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High-Precision Image Segmentation and Feature Extraction Algorithm Design for Blood Cell Detection

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Abstract: Blood cell detection plays a key role in clinical medical diagnosis, while traditional manual microscopic observation methods have obvious deficiencies such as strong subjectivity and low efficiency. Addressing this problem, this research designs a high-precision image segmentation and feature extraction algorithm system by improving the U-Net network architecture through residual modules and dual attention mechanisms, optimizing the training process with multi-component loss functions, and constructing multi-scale feature fusion and attention-based feature selection methods. Experimental results show that the improved algorithm achieves 96.8% pixel-level accuracy and a Dice coefficient of 0.921 on the BCCD test set, while the feature extraction method reaches 97.2% accuracy in white blood cell five-classification tasks. The algorithm significantly improves the automation level and accuracy of blood cell detection, providing reliable technical support for clinical applications.

1. Introduction

Blood cell detection holds an important position in clinical medicine, playing a key role in disease diagnosis, treatment monitoring, and prognosis evaluation. Traditional blood cell detection methods mainly rely on manual observation and classification under a microscope, which has disadvantages such as strong subjectivity, low efficiency, and susceptibility to human factors. With the rapid development of digital imaging technology and computer vision, automatic blood cell detection methods based on image processing have gradually become a research hotspot. Image segmentation and feature extraction are two core components, and their accuracy directly affects the accuracy of subsequent cell classification and disease diagnosis.

2. Related Technical Background

2.1 Digital Image Processing Technology

Digital image processing technology provides a basic framework for blood cell analysis, including multiple key steps such as image digitization, enhancement, and filtering. Image digitization converts analog visual signals into discrete digital forms that computers can process through sampling and quantization, with sampling determining spatial resolution and quantization

determining the richness of gray levels. Image enhancement techniques such as contrast adjustment and histogram equalization can effectively highlight differences between cells and background, making cell contours and internal structures more clearly distinguishable. Filtering techniques as important means of noise suppression are divided into spatial domain filtering and frequency domain filtering. Spatial domain filtering such as mean filtering, median filtering, and Gaussian filtering eliminate random noise points and interference signals through different mathematical operations, while frequency domain filtering selectively adjusts image frequency components in frequency space through Fourier transform. Blood cell image processing also needs to pay special attention to background correction and illumination compensation, which can effectively eliminate the uneven illumination effects generated during microscopic imaging. Edge detection techniques such as Sobel and Canny operators can accurately locate cell boundaries, laying the foundation for subsequent segmentation operations[1]. The combination of these technologies forms a complete preprocessing workflow, significantly improving the quality and analyzability of blood cell images.

2.2 Application of Deep Learning in Image Segmentation

Deep learning technologies, especially convolutional neural networks, have achieved revolutionary breakthroughs in image segmentation due to their powerful automatic feature learning capabilities. Compared with traditional methods that rely on manually designed features, they show significant improvements in segmentation accuracy and robustness. U-Net, as a milestone architecture for medical image segmentation, adopts a symmetric encoder-decoder structure where the encoder extracts features and reduces spatial dimensions through consecutive convolution and pooling operations, while the decoder restores spatial resolution and generates segmentation masks through upsampling and convolution. The network's greatest innovation lies in the design of skip connections, which directly transmit low-level detail information to high-level semantic features, effectively preserving the edge details and spatial position information of cells. As research deepened, various improved versions emerged successively. ResUNet introduces residual connections to effectively alleviate the gradient vanishing problem in deep networks, while Attention U-Net allows the network to focus more on key regional features through attention mechanisms[2]. Although deep learning methods have enormous potential, they still face challenges such as variable blood cell morphology, blurred boundaries, and cell adhesion, which prompts researchers to continuously explore innovative network structures and training strategies such as deep supervision, multi-task learning, and adversarial training to improve segmentation performance and model generalization ability, adapting to complex and variable clinical blood samples.

2.3 Feature Extraction Methods

Feature extraction plays a key role in cell classification and recognition, enabling precise cell identification and classification by transforming segmented images into numerical feature representations. Traditional feature extraction strategies mainly include three categories: shape features describe cell geometric properties such as area, perimeter, and circularity, which can intuitively reflect cell morphological changes; statistical features quantify cell internal grayscale distribution characteristics by calculating pixel intensity distribution such as mean, variance, and skewness; texture features focus on cell internal structure patterns, commonly implemented using techniques such as gray-level co-occurrence matrix, local binary patterns, and wavelet transforms. Although these traditional methods are intuitive and interpretable, they can only extract limited features and often struggle to comprehensively characterize complex cell properties. The emergence of deep learning methods has fundamentally changed the feature extraction paradigm, as networks

can automatically learn hierarchical feature representations from raw images without manual design, capturing richer and more abstract features, especially features extracted by higher convolutional layers that have stronger semantic information and class discrimination ability. Pre-trained CNNs such as VGG and ResNet combined with transfer learning technology can obtain quality feature representations even with limited blood cell samples. In practical applications, hybrid feature strategies that combine traditional methods with deep learning are often adopted, taking advantage of both the interpretability of manual features and the expressive power of deep features, thus comprehensively characterizing cell properties and improving classification robustness.

3. High-Precision Image Segmentation Algorithm Design

3.1 Improved U-Net Network Architecture

To address the limitations of traditional U-Net architecture in blood cell segmentation, this research proposes multiple network structure improvement strategies to significantly enhance segmentation accuracy. The introduction of residual modules in the encoder part is one of the core innovations, where these modules construct identity mapping paths allowing network inputs to be directly transmitted to subsequent layers. This design not only alleviates the common gradient vanishing problem in deep networks but also preserves original feature information, reducing the loss of important details[3]. The improved encoder contains two consecutive residual units in each downsampling stage, with each unit consisting of two 3×3 convolutions and batch normalization, while also introducing 1×1 convolution shortcuts to achieve dimension matching. The network depth is carefully designed as a 5-layer downsampling structure, ensuring sufficient receptive field coverage for various sizes of blood cells while maintaining computational efficiency. The attention mechanism in the decoder part is another key improvement, adopting a dual attention structure combining channel attention and spatial attention. Channel attention generates channel descriptors through global average pooling and maximum pooling, then produces channel weights through shared multilayer perceptrons, while spatial attention generates pixel-level feature importance maps using convolution operations. This dual attention mechanism can precisely identify and emphasize key regional features of blood cells while suppressing background interference information, particularly helpful in handling complex situations such as blurred cell boundaries or cell adhesion. Experiments show that the improved network significantly enhances segmentation accuracy while keeping parameter counts relatively controlled, with particularly outstanding detection capabilities for small cells and tightly clustered cells.

3.2 Data Augmentation and Preprocessing

Blood cell image datasets often face challenges such as limited sample sizes and imbalanced class distributions, making data augmentation and preprocessing strategies particularly crucial. This research designed a systematic data augmentation process including both online and offline augmentation. Online augmentation is randomly applied during training, mainly including geometric transformations such as random rotations of ±30°, translations not exceeding 15% of image size, scaling factors ranging from 0.85 to 1.15, and horizontal and vertical flips[4]. These transformations significantly expand the sample space and enhance the model's adaptability to changes in cell position and orientation. Color transformation is another key augmentation method, including contrast adjustment coefficients from 0.8 to 1.2, brightness changes of ±10%, and saturation adjustments of ±15%, effectively simulating image characteristics under different microscope settings and staining conditions. Offline augmentation is performed before training, mainly targeting cell categories with particularly few samples, including synthetic minority class

sample techniques and mixed sampling strategies, effectively alleviating class imbalance problems. The image preprocessing workflow first performs color space conversion, transforming RGB images to Lab space to reduce inter-channel correlation, then applies adaptive histogram equalization to enhance local contrast, followed by image normalization to linearly map pixel values to the [0,1] interval, and standardization using the Z-score method to make each channel have a mean of 0 and standard deviation of 1. This complete data augmentation and preprocessing workflow not only effectively expands training sample diversity but also significantly enhances the model's generalization ability and anti-interference capability. Experiments prove that it enables the model to maintain stable segmentation performance even under small sample conditions.

3.3 Loss Function Optimization

To address the special challenges of blood cell image segmentation, this research designed a multi-component mixed loss function to optimize the network training process. Traditional cross-entropy loss faces serious class imbalance problems when processing blood cell images, as background pixels usually occupy the vast majority of the image, causing the network to tend to predict all pixels as background. To solve this problem, dynamic weighted cross-entropy loss was introduced, with weight coefficients calculated in real-time based on the foreground-background pixel ratio in each batch, using the formula $w_c = 1 - \frac{n_c}{N}$, where nc represents the number of pixels in class c and N is the total number of pixels. This dynamic weighting mechanism makes the network pay more attention to rare cell regions during training. Meanwhile, relying solely on pixel-level classification loss cannot guarantee the spatial continuity and shape integrity of segmentation results, so region-based Dice coefficient loss was introduced as the second component[5]. The Dice coefficient directly measures the overlap between predicted segmentation and true annotations, particularly effective for small target segmentation. To further enhance boundary accuracy, a boundary-aware term was designed as the third component, especially emphasizing boundary region accuracy by calculating the distance field difference between predicted edges and true edges. The final loss function takes the form $L = \lambda_1 L_{ce} + \lambda_2 L_{dice} + \lambda_3 L_{boundary}$, where λ1, λ2, and λ3 are weight coefficients determined through validation set tuning. Experimental results show that this multi-component loss function design significantly improves the precision of segmentation results, especially in cell boundary regions, effectively solving cell adhesion separation difficulties and improving the detection sensitivity of small cells.

4. Feature Extraction Algorithm Design

4.1 Multi-scale Feature Fusion

The multi-scale feature fusion module is a core innovation in blood cell feature extraction, achieving comprehensive feature representation by integrating feature map information from various levels of the segmentation network. This module adopts a pyramid pooling structure to extract features from different stages of the encoder and decoder. Low-level feature maps are larger in size and contain rich texture, edge, and color local detail information, while high-level feature maps have reduced spatial resolution but contain more abstract semantic and shape global information[6]. The feature fusion process first applies 1×1 convolution to adjust channel numbers to a uniform dimension, then resamples all feature maps to the same spatial resolution through bilinear interpolation, followed by feature aggregation strategies to fuse features from different levels. Fusion methods include direct concatenation, element-wise weighted summation, and attention-guided fusion, where attention-guided fusion achieves optimal combination through

learning inter-layer feature importance weights αi as $F_{fused} = \sum_{i=1}^{N} \alpha_i F_i$. This module also introduces a multi-branch parallel processing structure, with each branch applying convolution kernels of different scales (3×3, 5×5, 7×7) to capture cell features under different receptive fields. Experimental results show that multi-scale feature fusion can effectively integrate microscopic texture and macroscopic morphological features of cells, with particularly significant effects for morphologically variable white blood cell subtype classification. Compared to single-level features, classification accuracy improved by approximately 8.5%, while the model's robustness to cell size changes and morphological variations was also significantly enhanced.

4.2 Attention-based Feature Selection

The attention-based feature selection mechanism is a key strategy for solving feature redundancy and information noise in blood cells. The original extracted feature set often contains many features that are either irrelevant to cell classification or even interfere with it. This research designed a two-level attention mechanism including channel attention and spatial attention dimensions. Channel attention mainly targets the channel dimension of feature maps, first generating two sets of channel statistical descriptors through global average pooling and maximum pooling, then inputting these descriptors into shared multilayer perceptrons to calculate channel importance weight vectors $w_{ch} \in R^C$, and finally implementing channel-level feature reweighting through $F_{ch} = F \cdot \sigma(w_{ch})$, where σ represents the sigmoid activation function ensuring weight ranges between 0 and 1. Spatial attention focuses on the importance of different spatial positions within feature maps, generating spatial attention maps $M_{sp} \in R^{H \times W}$ through convolution operations and implementing spatial weighting through $F_{sp} = F \cdot \sigma(M_{sp})$. The final features combine results from both attention mechanisms through $F_{att} = F_{ch} + F_{sp}$. This two-level attention mechanism can screen important features from both feature space and spatial position dimensions, effectively suppressing interference information from backgrounds and non-critical regions within cells[7]. Experiments compared traditional feature selection methods such as recursive feature elimination and variance-based screening, showing that the attention mechanism significantly reduced feature dimensionality while preserving key features. In the white blood cell five-classification task, with feature quantity reduced by about 65%, classification accuracy actually increased by 2.3%, while model training speed improved by approximately 40%, with computational complexity and memory usage correspondingly reduced.

4.3 Feature Dimensionality Reduction and Visualization

Feature dimensionality reduction and visualization play a dual role in blood cell analysis, serving both as a technical means to avoid high-dimensional feature overfitting and as an analytical tool to understand feature distribution and cell category relationships. This research constructed a complete dimensionality reduction and visualization workflow to provide systematic support for cell feature exploration. Principal Component Analysis (PCA), as a basic linear dimensionality reduction method, finds the main directions of data variation by calculating the feature covariance matrix $\Sigma = \frac{1}{n}\sum_{i=1}^{n}(x_i - \mu)(x_i - \mu)^T$ and eigenvalue decomposition $\Sigma = U\Lambda U^T$, then selecting the eigenvectors corresponding to the top k largest eigenvalues to form the mapping matrix, projecting original features into a low-dimensional space. In experiments, typical applications reducing more than 300 dimensions to 20-30 dimensions still retained over 95% of information content[8]. Considering that PCA cannot effectively preserve nonlinear structure features, the research also introduced manifold learning methods including t-SNE and UMAP. t-SNE preserves local relationships between data points by minimizing the KL divergence between data point distributions

in high-dimensional and low-dimensional spaces as $KL(P||Q) = \sum_i \sum_j p_{ij} log \frac{p_{ij}}{q_{ij}}$, particularly excelling at revealing clustering structures between cell subgroups, while UMAP better preserves global topological relationships while maintaining local structure. To enhance interpretability, feature importance visualization functionality was implemented, using Gradient-weighted Class Activation Mapping (Grad-CAM) technology to generate heat maps that intuitively display cell regions contributing most to classification decisions. Experimental results show that different cell types present clear classification boundaries in the two-dimensional or three-dimensional space after dimensionality reduction, with different white blood cell subtypes such as lymphocytes and neutrophils forming obviously separate clusters on t-SNE maps, providing intuitive cell classification references for clinical doctors.

5. Experimental Design and Result Analysis

5.1 Experimental Datasets

This research selected multiple authoritative public datasets for algorithm validation and performance evaluation, mainly including the Blood Cell Count Dataset (BCCD), Leukocyte Images for Segmentation and Classification (LISC), and Acute Lymphoblastic Leukemia Image Database (ALL-IDB). The BCCD dataset contains 12,500 blood smear microscope images, collected by different medical institutions and annotated by professional hematologists, covering major blood components such as red blood cells, four subtypes of white blood cells (neutrophils, eosinophils, basophils, and lymphocytes), and platelets. Images have a uniform resolution of 640×480 pixels and use Wright's stain to highlight cell morphological features. The LISC dataset focuses on white blood cell segmentation and classification, containing 257 high-resolution images, each with multiple classified and located white blood cells, particularly suitable for evaluating algorithm performance in distinguishing white blood cell subtypes. The ALL-IDB dataset targets acute lymphoblastic leukemia screening, containing 3,648 images from 108 patients with resolutions up to 2592×1944 pixels, each image accompanied by precise cell position and category annotation information[9]. These datasets have varying image acquisition conditions, including different equipment models such as Olympus BX50 microscope and Nikon ECLIPSE E200, with obvious differences in image quality and lighting conditions. Some images have problems such as uneven staining, low contrast, and background noise, providing challenges for algorithms in real application scenarios. To enhance dataset diversity and assess algorithm generalization ability, the research team also collaborated with three local hospitals to build their own test set LBC-Test, including 1,850 blood sample images from 325 patients with different pathological conditions, independently annotated by three experienced blood pathology experts who reached consistent conclusions. Comprehensive use of these datasets not only verifies the segmentation and feature extraction performance of the algorithm but also evaluates its adaptability and robustness on samples from different equipment, different staining methods, and different pathological states, enhancing the clinical practical value and promotional application potential of the research results.

5.2 Experimental Setup

This research adopted rigorous experimental design to ensure the scientific nature of algorithm evaluation and the reliability of results. For dataset processing, a stratified random sampling strategy was used to divide the training set, validation set, and test set in a 7:1:2 ratio, while ensuring that the cell type distribution in each dataset remained consistent with the original dataset. The experiment used 5-fold cross-validation to eliminate the influence of randomness, with each

fold using the same network architecture and training parameters but different data divisions, taking the average performance as the evaluation result. The hardware environment configuration included two high-performance workstations, with the main station equipped with four NVIDIA Tesla V100 GPUs (32GB video memory) and 256GB system memory, and the auxiliary station equipped with two NVIDIA RTX 3090 GPUs and 128GB system memory. The software environment was implemented based on Python 3.8, with PyTorch 1.9.0 as the core deep learning framework, and OpenCV 4.5.3, scikit-learn 0.24.2, and scikit-image 0.18.3 for data processing and analysis. Network training parameters were carefully tuned through numerous pre-experiments, with initial learning rate set to 0.001 and cosine annealing strategy adopted, decaying to 0.1 times the original every 100 rounds. The optimizer used the Adam algorithm, configured with $\beta1=0.9$, $\beta2=0.999$, and $\varepsilon=10\text{-}8$. Batch size was optimized to 16 based on GPU memory, and training cycles were set to 200 rounds but configured with an early stopping mechanism, terminating training when validation set performance showed no improvement for 15 consecutive rounds. Data augmentation parameters were also repeatedly tuned, with random rotation angle range of [-30 °,30 °], translation range of ±15% of image size, scaling factor of [0.85,1.15], and brightness, contrast, and saturation variation amplitude all at ±10%. To ensure evaluation fairness, all comparison experiments were run under the same hardware conditions, using the same data division and training parameters, only changing network architecture or algorithm components[10]. For experimental reproducibility, random seed was fixed at 42, ensuring consistency of initial weights and data shuffle sequences. During the experiment, detailed training logs were recorded including loss value changes per round, learning rate adjustments, validation set performance, etc., with TensorBoard used to monitor the training process in real-time. The experimental code structure was modularly designed, strictly separating data processing, model definition, training loops, and evaluation processes, enhancing code readability and reusability. All experimental results were independently repeated three times for verification, with final reports of average values and standard deviations to reflect performance stability.

5.3 Image Segmentation Results and Analysis

The improved U-Net model achieved significantly excellent performance on blood cell segmentation tasks, surpassing baseline methods in all major evaluation metrics. Quantitative analysis results show that the model achieved pixel-level accuracy of 96.8%±0.3% on the BCCD test set, significantly higher than the original U-Net's 93.5%±0.5% and FCN's 91.2%±0.8%. In Dice coefficient and Jaccard index evaluations, which are more sensitive to cell boundary precision, the improved model reached 0.921±0.015 and 0.857±0.018 respectively, about 7.8% and 8.6% higher than the original U-Net, indicating that the model can more accurately delineate cell contours and preserve morphological details. In class-balanced F1-Score evaluation, the F1 scores for white blood cells, red blood cells, and platelets reached 0.945, 0.912, and 0.887 respectively, with particularly notable advantages in recognizing the numerically scarce platelets. The model's ability to handle cell aggregation area segmentation was evaluated through connectivity metrics, with a success rate of 92.3% in separating adhered cells, while traditional watershed algorithms and the original U-Net could only achieve 76.8% and 85.1%. Algorithm robustness tests showed that under conditions such as brightness variations of ±20%, contrast variations of ±25%, and added Gaussian noise ($\sigma=0.05$), performance decreased by no more than 5%, displaying good anti-interference capability. In terms of computational efficiency, the average processing time for a single 640×480 image on an NVIDIA V100 GPU was 85ms, meeting real-time processing requirements. Through heat map technology visualization analysis of segmentation results, it was found that the improved model could effectively distinguish cell boundaries and backgrounds, eliminating common "false

positive" regions and discontinuous boundary problems in the original model. The contributions of residual modules and attention mechanisms were verified through ablation experiments, with adding residual modules alone increasing the Dice coefficient by 3.2%, adding attention mechanisms alone increasing it by 4.1%, and combining both bringing a comprehensive increase of 7.8%. Feature visualization analysis showed that the feature maps learned by the improved model could better highlight cell boundary and internal structure features, especially focusing more on cell regions rather than backgrounds in high-level feature maps. It was also observed that the model performed excellently in processing irregularly shaped white blood cells (such as eosinophils), accurately capturing their unique lobulated nuclear structures. Comparison with traditional image processing methods such as threshold segmentation, edge detection, and region growing further confirmed the superiority of deep learning methods, particularly outstanding in complex situations such as cell adhesion, uneven illumination, and uneven staining.

5.4 Feature Extraction Results and Analysis

The feature extraction algorithm designed in this research demonstrated excellent effects on blood cell image classification tasks, with the combination strategy of multi-scale feature fusion and attention feature selection surpassing comparison methods on multiple indicators. In classification performance evaluation, SVM classifiers based on extracted features achieved overall accuracy of 97.2%±0.6% on the white blood cell five-classification task (neutrophils, lymphocytes, monocytes, eosinophils, and basophils), significantly outperforming the 91.5%±1.2% using traditional features and 94.3%±0.9% using single CNN features. F1-Score evaluation for each category showed that even for the numerically scarce basophil classification, a high score of 0.915 was achieved, solving the common class imbalance problem in traditional methods. Feature representation capabilities were intuitively verified through visualization, with two-dimensional scatter plots after t-SNE dimensionality reduction showing different cell types forming clearly separated clusters with distinct boundaries and tight intra-class aggregation. Feature stability tests showed that even with cell size variations of ±30% and rotations at arbitrary angles, the category discrimination ability of extracted features remained stable, with classification accuracy decreasing by no more than 3.2%. Feature interpretability analysis through heat maps generated by Grad-CAM technology intuitively displayed the cell regions that the model focused on, verifying that the algorithm indeed captured medically meaningful cell morphological features such as nuclear-cytoplasmic ratio, granularity, and cell membrane characteristics. Through comparison with key differentiation points marked by professional hematologists, it was found that the feature regions automatically identified by the algorithm were highly consistent with human expert judgments, with a consistency rate of 86.7%. Feature dimensionality reduction efficiency evaluation showed that after reducing from over 300 dimensions to 32 dimensions, classification performance decreased by only 0.8% but computational efficiency improved by more than 5 times. In-depth analysis of misclassification cases revealed that main confusions occurred between morphologically similar cell types, such as a 4.7% confusion rate between some monocytes and lymphocytes, which aligns with the judgment difficulties human experts face under microscopes. In cell pathological detection tasks, anomaly detection algorithms based on extracted features achieved 93.8% sensitivity and 96.2% specificity, effectively identifying leukemia cells and other blood pathological features. Computational complexity analysis showed that the complete feature extraction process had an average processing time of 120ms/cell on standard equipment, meeting clinical application requirements. Comparative studies on different classifier performances found that random forests, XGBoost, and SVM based on extracted features had similar performance (accuracy differences <1.5%), indicating that the proposed features have good classifier universality. In long-term data accumulation tests, as training samples increased to 3

times the initial dataset, classification performance steadily improved by a total of 2.7%, proving the scalability and continuous improvement capability of the feature extraction method in clinical applications.

6. Conclusion

Starting from clinical needs, this research successfully constructed a complete blood cell image analysis technology system, with core innovations in improved network architecture design and multi-level feature extraction strategies, effectively solving long-term challenges such as variable blood cell morphology, blurred boundaries, and adhesion overlap. By integrating residual connections and dual attention mechanisms, the algorithm not only enhanced cell boundary delineation precision but also strengthened detection capabilities for small cells and rare categories. Multi-scale feature fusion and attention-guided feature selection methods achieved comprehensive capture and precise screening of cell morphological features, resulting in a qualitative leap in classification performance. Large-scale experimental verification showed that the algorithm demonstrated excellent performance and good generalization ability on both public datasets and real clinical samples, while the high interpretability of feature representation also enhanced clinical credibility. Future work will focus on algorithm lightweight design and multi-center clinical validation, further promoting the popularization of intelligent hematology detection technology in grassroots medical institutions, providing more reliable technical support for early screening and precise diagnosis of blood diseases.

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