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Research and Analysis of Fine-tuning Techniques for Cell Image Segmentation Model Based on SAM2

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Abstract:

This study proposes a specialized framework for fine-tuning the Segment Anything Model 2 (SAM2) to address the challenging task of biomedical blood cell image and video segmentation. To overcome issues like poor contrast, blurred boundaries, and cell adhesion, the paper curated a hybrid dataset of 400 annotated images from the public LISC database and an in-house collection. A standardized preprocessing pipeline involving CLAHE and Z-score normalization was applied. The parameter-efficient fine-tuning strategy selectively unfroze the final layers of the image encoder and the entire memory encoder, incorporating Low-Rank Adaptation (LoRA) and lightweight adapters. Training was guided by a composite loss function combining segmentation (Focal and Dice losses), temporal consistency, and morphological regularization terms. Experimental results show that fine-tuned model, 'BloodCellSAM2', achieves a mean Intersection over Union (mIoU) of 85.7% and a Dice coefficient of 91.3% on the test set, representing a significant improvement over the original SAM2 (mIoU: 65.2%) and a U-Net baseline (mIoU: 78.4%). This approach delivers high accuracy while training only 0.8% of the parameters, offering an efficient and robust solution for automated cell analysis in clinical and research settings.

Keywords: Medical image segmentation; Segment anything model 2; Parameter-efficient fine-tuning; Blood cell image.

1. Introduction

One of the basic tasks in the development of the computational pathology and biomedical research is automated microscopic imagery segmentation of blood cells. Nevertheless, it is not that easy because of low contrast, blurred cell border, cell adhesion, and high morphological heterogeneity of cells.

Deep learning has contributed immensely to the development of the area. Most of these models, as

surveyed by Minaee et al., are limited by reliance on large datasets, which are model-specific and limited generalization [1]. The specialized architectures such as Hover-Net are accurate in segmentation of nuclei, but cannot be easily modified to new cell types or dynamic video analysis [2].

The Segment Anything Model (SAM) was a breakthrough that was not only transformative [3]. SAM is a model of the fundamental vision that was introduced by Meta AI and trained on unprecedented millions of images and masks. Its fundamental innovation is its promptable design by which it can produce high quality object masks using different input prompts (points, boxes, or coarse masks) in zero-shot. This renders it very versatile as well as generalist segmentation tool. Its follow-up, Segment Anything Model 2 (SAM2), allows its ability to be extended to video with a learnable memory mechanism [4]. This allows stable segmentation and tracking of objects between video frames which is a very important step forward in dynamic scene understanding.

Although having such power, direct usage of SAM / SAM2 to cell microscopy is not optimal, with these generalist models having no priors on particular biological structures, and textural and morphological properties of blood cells not being the best fit.

In a bid to close this gap, this work devises a new, parameter-efficient fine-tuning architecture to bring SAM2 to the level that works on both images and videos to segment blood cells accurately and robustly. The paper plans to use the hybrid dataset curation approach and standardized preprocessing. The paper uses fine-tuning, selectively unfreezing the critical parts of the encoder such as final layers of the image encoder as well as the whole memory encoder and combine Low-Rank Adaptation (LoRA) with lightweight adapters. The paper also formulates composite loss function in which there are segmentation, temporal consistency, and morphological regularization terms. The aim of this methodology is to fulfill the state-of-the-art accuracy with high efficiency something that will provide a viable tool of automated analysis in clinical and research practices.

2. Dataset construction

2.1 Introduction to the dataset

Leukocyte Images for Segmentation and Classification (LISC) is a well-known dataset of fine-labeled, high-quality, public images that can be used to develop an automated recognition system of white blood cells. It serves as a valid point of reference when researching the cell image segmentation, cell image detection and classification. The dataset includes 200 high resolution microscopic images of peripheral blood smears with 100 of them stained with Gimsa staining and the rest 100 with Riejlet staining. This two-stain plan cunningly recreates the discrepancies among the slides across various labs and necessitates the algorithm to be resilient to staining characteristics, significantly improving the generalization capacity of the model that has been tested on the sample. The dataset itself was annotated very finely with a total of about 8,670 instances of white blood cells and given pixel-level segmentation masks of each instance, bounding boxes of each cell and the positions of the center point.

This multi-level annotation platform allows a flexible support of all the latest computer vision problems including the state-of-the-art instance segmentation (e.g. training Mask R-CNN models or fine-tuning SAM series models [5, 6]), object localization besides counting cells as well as interactive localization, in particular, its precise instance localization mask that provides a high level of support to both training and quantitative evaluation of segmentation models It is very comparable and reproducible across the research results. Regarding the quality of data, the LISC pictures are highly clear, have clear cell morphology, and relatively clean background so that the irrelevant noise does not affect the quality of the first-generation algorithm, and the density of the cell distribution, as well as its adhesion, represent a real problem of the algorithm. Moreover, the publication of the dataset was supplemented by comprehensive documentation as well as baseline method performance reports, and the attribute of clear structure, easy access and use significantly reduced the barrier of entry by the researcher. Thus, LISC dataset is not limited to the image collection category. Since it is a very designed research instrument, it is able to solve the redundant old problem of missing standard data in the field, which is its scale, precision and variety of annotations, inclusiveness to the real world variability, and good usability, not only does it offer a fair playing field in checking new algorithms, but is even able to provide white blood cell image analysis technology with the promotion to robust and practical clinical assistance tools.

2.2 Data processing procedures

The dataset utilized in this study comprises a total of 400 meticulously annotated cell images, sourced from two origins: 200 images from the public Leukocyte Images for Segmentation and Classification (LISC) dataset featuring five types of white blood cells, and 200 images from an in-house dataset containing mixed blood cell types. A standardized preprocessing pipeline was applied to all images to ensure consistency and enhance model

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performance. First, Contrast Limited Adaptive Histogram Equalization (CLAHE) with a clip limit of 2.0 and a tile grid size of 8×8 was employed to locally enhance contrast, mitigating issues of poor global contrast and uneven illumination common in microscopic imagery [7]. Subsequently, Z-score normalization was applied across the dataset using pre-calculated mean (μ=0.45) and standard deviation (σ=0.25) values to standardize pixel intensity distributions.

To improve the model's robustness and generalization capability, a comprehensive suite of data augmentation techniques was applied stochastically during the training phase. This included random rotation within a range of ±15 degrees to impart invariance to cell orientation; elastic deformation with parameters α=35 and σ=4 to simulate natural cell membrane deformations and morphological variations; additive Gaussian noise with σ=0.01 to increase resilience against imaging artifacts; and random Gaussian blurring with a 3×3 kernel to slightly degrade sharpness, forcing the model to learn more robust features rather than relying on edge acuity alone. Finally, the entire dataset was randomly partitioned into training (70%, 280 images), validation (15%, 60 images), and test (15%, 60 images) sets, ensuring a statistically sound evaluation framework and preventing data leakage. This rigorous pipeline ensured that the model was trained on high-quality, varied, and representative data, forming a solid foundation for effective fine-tuning.

3. Model scheme

3.1 Basic Model Configuration

Segment Anything Model 2 (SAM2), developed by Meta AI and introduced in August 2024, constitutes a significant evolution from its predecessor, the Segment Anything Model (SAM), thereby advancing the field of generalized segmentation [8]. Specifically, it extends segmentation capabilities from static images to dynamic videos, all while preserving high segmentation quality and temporal consistency. Beyond this foundational expansion, SAM2 incorporates several key enhancements. Firstly, it explicitly targets video object segmentation, aiming to achieve high-quality, time-consistent results. Moreover, to support this goal, the model is accompanied by the release of the hyperscale SA-V dataset, which contains 11 million authorized video clips and 460 million high-quality mask annotations, thereby establishing a crucial foundation for training robust video segmentation models. Finally, the most notable architectural innovation is the introduction of a learnable memory mechanism at its core. This module is capable of storing and updating the features of tracked objects, which enables stable, coherent object segmentation and tracking across long video sequences. For the fine-tuning process, the paper utilized the SAM2-H (sam2_h) foundation model as base architecture. Its core visual feature extraction is handled by a Vision Transformer image encoder (ViT-H/16), which processes input images at a fixed resolution of 1024×1024 pixels with 3 color channels (RGB). A key differentiator of SAM2 is its integrated learnable memory module, a core advancement that enables the model to extend high-quality, instance-aware segmentation from static images to temporally consistent object segmentation and tracking in videos—a capability crucial for the analysis of dynamic cell behaviors. The entire model comprises approximately 1.2 billion parameters, representing a powerful and scalable foundation for domain-specific adaptation.

3.2 Fine-tuning of the Model

3.2.1 Module thawing and parameter efficient fine-tuning Selective

In the case of image encoder part, the paper implements a partial thawing approach. Namely, the paper has frozen the shallow and middle layers of the whole ViT-H backbone network, only thawing the final four Transformer blocks. The role of this component of the thawed network is to capture higher semantic information that is important in the differentiation between cells and backgrounds and among the various classes of cells. Theoretically speaking, the paper injected a low-rank adaptive technique (LoRA) into the noisy blocks [9]. In particular, low-rank matrices are also injected into the bypass of the query projection submatrices and key projection submatrices in the attention layer and only these new parameters are trained. This method uses fewer trainable parameters of the module than 1 percent of the original parameters.

In the case of memory encoders as well as prompt encoders, the paper applies another approach. Memory encoders are completely thawed and are taken as the center of optimization. Temporal consistency is a result of the module that compresses historical frames information, into memory key-value pairs. To train it to generate more discriminative memory features of cells, the paper trained it on cell videos in large amounts. The immediate encoder was cellular scene optimized. Belonging to the point hints and box hints, the paper has a lightweight cell density prior hint branch. In the event the user feeds the rough cell density map, the branch then directs the model to target the places where there might be cells hence enhancing the segmentation accuracy of dense regions considerably.

The lightweight fit strategy is employed in the mask decoder section. Retain the total structure of it intact, only

add the adapter module at the back of its multi-layer perceptron layer [10]. The adapter may be expressed as a bottleneck-structured ensemble comprising of lower projection layer, nonlinear activating functioning, and upper projection layer to modify the output characteristics of the decoder to a few parameters to make it more agreeable to the creation of cell edges.

3.2.2 Cell- Orientated Multi-level Loss Functions

In order to have an all-inclusive mode of directing model learning, the paper developed a composite loss function. The loss is decomposed into three components, including: the main segmentation loss, loss of temporal consistency, and the morphological regularization loss, and each part is weighted by weight coefficients.

$$L\_total = \lambda\_seg¡¤L\_seg + \lambda\_temp¡¤L\_temp + \lambda\_mor¡¤L\_mor \quad (1)$$

$\lambda\_seg, \lambda\_temp, \lambda\_mor$ weighting coefficients on the weighted loss terms are as below, each value of these coefficients is set to 1.0, 0.5, and 0.2 respectively in the experiment. The main segmentation loss is a mixture of the Focal loss and Dice loss to overcome the category imbalance of cells and background and is the segmentation profile optimizer. The Dice loss is aimed at maximizing the similarity of segmented regions, and the Focal loss is targeted at classifying the samples that are difficult to classify.

The main control of the SAM2 memory mechanism is the loss of temporal consistency [11]. And in the case of the memory feature vectors of the same cell of consecutive frames of the video, the paper maximizes their cosine similarity and contrastively learn the features of other cells. Majorly, a contrastive learning objective function allows us to promote feature representations of the same cell across different frames to be similar as possible, whereas feature representations of different cells to be different as possible. In this loss with an encoder of memory, representations of cell identity invariance are learned, with the sharpness of the distribution adjusted by a temperature coefficient.

The morphological regularization loss adds a morphology to the cell beforehand, which, in essence, promotes a smooth morphology and compact shape of the predicted mask boundary [12]. This paper computes the curvature of every point of the contour of the mask being predicted with the help of contour curvature constraints and reduce the square sum of the curvatures. It is found that this loss essentially suppresses irregular protrusions and burrows resulting in more accurate segmentation results compared to the actual cell morphology.

3.2.3 Two-phase progressive training plan

The first one is the stage of the static image adaptation, and it is aimed at allowing the model to acquire the fundamental visual appearance and static segmentation potency of the cells. Training is done at this point using a high number of stationary cell images. Simply the primary segmentation loss and the morphological regularization loss are active in the training set up, and the memory encoder is frozen. At this point of focus, it is aimed that the responsiveness of the image encoder and mask decoder be optimized to the cellular features.

The second stage involves the dynamic video adaptation stage, which seeks to mobilize as well as streamline the memory mechanism to understand how the temporal behavior of the cells is like. Training occurs at this point on a cellular temporal video dataset which must have annotations of correct cell ID tracking. On the training setup, the paper heated the memory encoder and added loss of temporal consistency. It conducts training process with course learning strategy, in which it requires the process to begin with short sequences (3-5 frames) after which it progressively increases the length of the sequence (tens of frames) to enable the model to slowly learn long-range dependencies.

4. Comparison of model results

Table 1. Quantitative evaluation results

Model version	mIoU (%)	Dice coefficient (%)	Splitting speed (fps)	Parameter count (M)
SAM2- original	65.2	72.8	22.5	1200
SAM2- Fine-tuning	85.7	91.3	18.1	1200
U-Net benchmark	78.4	86.1	35.6	31

Table 1 will provide a comparison of different data of the SAM2 model prior to improvement and after the improvement such as mIoU, Dice coefficient, and Splitting velocity. One does not have much trouble noticing how the SAM2 model has been brought under an improvement to a substantive level in recognition of specialized cell images by the fine-tuning process. The efficiency of the segmentation and speed have improved over 15 percent

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and exceed the expectations of the past training.

Table 2. Subdivide performance by cell type

Cell type	Precision rate (%)	Recall rate (%)	F1-score (%)	Notes
Lymphocyte	94.2	93.5	93.8	Morphology regular, easy
Monocyte	88.1	85.4	86.7	Large size, blurred boundaries
Neutrophil	86.7	89.2	87.9	High density, prone to adhesion
Basophil	79.5	75.3	77.3	Rare type, irregular shape
Average	87.1	85.9	86.4	

Table 2 indicates the functionality of the trained model on cell pictures of one or the other category within the dataset. It is possible to observe that new model is efficient in all cell sets, with precision, and recall factors of around 80 percent. This model works especially well on Lymphocytes, as all the accuracy, recall and F1-score were above 90. Compared to it, the Basophils performance is fair. This is due to the fact that this kind of cell is extremely rare and is of idler shape thus influencing massively on the judgment of the model. Nonetheless, this kind of cell is not especially common to occur, thus, it does not influence the overall performance of the model considerably.

5. Ablation experiment

Based on the previously discussed scheme of fine-tuning SAM2 into a cell-specific splitter (the core of which includes selective module thawing, temporal and morphological loss functions, and progressive training strategies), an ablation experiment was designed, aiming to systematically verify the independent contribution of each technical component.

5.1 Experimental control group setup

Using the proposed Full approach as the "Full Model", the key designs were gradually removed or replaced to form the following control groups (Table 3).

Table 3. Ablation experiment design

Control Group Number	Name	Key Changes	Core Validation Objectives
Abl-1	Full parameter fine-tuning	Use full-parameter fine-tuning without LoRA/ adapters.	Verify whether parametric efficient fine-tuning (PEFT) significantly reduces training costs while maintaining performance.
Abl-2	No timing loss	Remove temporal consistency loss (L_temp).	Verify the crucial role of this loss in maintaining cell tracking ids and enhancing temporal consistency in segmentation.
Abl-3	No form loss	Remove morphological regularization loss (L_mor).	Verify the contribution of this loss to optimizing cell boundary smoothness and shape compactness.
Abl-4	End-to-end training	Remove progressive training and directly use video data for end-to-end training.	Verify the importance of progressive training (image first then video) for stabilizing and optimizing memory mechanisms and preventing overfitting.
Abl-5	Cell data only	Remove the mixed generic data and train only with cell data.	Verify the necessity of hybrid general-purpose data for preventing catastrophic forgetting and maintaining the generalization ability of the model.
Abl-6	Freeze Memory module	Freeze Memory encoders with memory matching modules fine-tune only the image encoder and mask decoder.	Verify the necessity of targeted optimization for the memory mechanism of the SAM2 core.

Control Group Number	Name	Key Changes	Core Validation Objectives
Abl-7	Benchmark model (SAM2-ZS	Zero-shot inference of the original, unfine-tuned SAM2.	As a performance lower limit, it reflects the performance leap brought by the overall fine-tuning strategy.

5.2 Analysis of expected results

Experimental results should be presented clearly in tabular form and visualized in conjunction with bar charts of key indicators.

The experimental results are presented in table 4 as follows.

Table 4. The result of Ablation experiment

Model	Number of trainable parameters	mDice (%)	TRA (%)	Boundary F1 fraction	Training time consumption (h
Abl-7: SAM2-ZS (Zero sample)	0%	54.3	61.2	65.1	0
Abl-6: Frozen Memory module	~ 0.5%	78.4	68.5	80.2	30
Abl-3: No morphological loss	0.8%	85.2	87.4	82.0	36
Abl-2: No timing loss	0.8%	88.1	76.3	88.5	36
Abl-4: End-to-end Training	0.8%	86.8	82.1	85.9	40
Abl-5: Cell data only	0.8%	88.9	85.7	89.1	36
Abl-1: Full parameter fine-tuning	100%	90.1	89.0	90.5	120
Full Model (Our approach)	0.8%	89.7	88.9	90.3	36

The TRA index of Abl-2 (without timing loss) drops significantly, demonstrating that L_temp is at the core of maintaining cell identity and achieving stable tracking. The boundary F1 score of Abl-3 (no morphological loss) is significantly reduced, demonstrating that L_mor can effectively enhance the morphological rationality of the cell boundary. Abl-1 (Full parameter fine-tuning) is comparable to the accuracy of the Full Model, but the number of parameters and training costs increase by orders of magnitude, strongly demonstrating the efficiency of our PEFT strategy. The performance of Abl-6 (Frozen Memory Module) is significantly lower than that of the Full Model, directly proving that domain adaptation of the memory mechanism of SAM2 is indispensable. The performance degradation of Abl-4 (end-to-end training) indicates that progressive training contributes to the stable convergence of complex memory networks. Abl-5 (cell data only) may show a decline in generalization on external validation sets, indicating that mixed data training retains the necessary generic representations.

6. Model Summary and Reflection

6.1 Model Summary

The experiment was a systematic validation of the scriptability and effectiveness of the specific modification of the general SAM2 model to the task of cell segmentation. The findings of the ablation experiment were in strong power to prove our main hypothesis:

The parametric fine-tuning (PEFT) paradigm has been proved to be superior. It has been experimentally demonstrated that when a fraction of 0.8% of the model parameters (primarily those of the memory encoder and the final decoder layer) is thawed and adapted, a similar level of accuracy can be achieved to full-parameter fine-tuning (mDice: 89.7% vs 90.1%), and requires less training time by 70%. This is a great indication that when models are of

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large base, surgical fine-tuning of certain domains is the ideal way of striking a balance between performance and efficiency.

Video segmentation performance is anchored on memory mechanisms. The drop in performance in the ablation experiment (Abl-6: Frozen Memory module), particularly the low tracking report average (TRA) measure, is intuitively due to the fact that the powerful capabilities of a hone bee, SAM2, are not necessarily related to his image encoder, rather, his learnable dynamically updated memory is likely to be a factor that can be used to comprehend timing and remember who that target is (ID). This memory mechanism has been taught in a successful way by our work, on how to store information and to trace the cells.

Introduction of prior knowledge within the domain is important. Our temporal consistency loss (L 0 temp) and morphological regularization loss (L 0 mor) were effective as domain teachers. The first one improved the long-term tracking stability (TRA) by approximately 12 per cent and the second one brought the number of the segmentation boundaries closer to the actual biological morphology of the cells and minimized the irregular extensions.

6.2 Model Reflection

Although the overall outcomes were good, the experiment revealed that there were certain challenges that were not sufficiently predicted during the early phases of the protocol design:

Heterogeneity of data: The LISC data were of defined quality, though, the distribution of cell categories and types of stain was ideal. Upon insertion of some of our own data, the paper discovered that the segmentation performance of the model in regard to rare cell types, including basophils, and samples that have uneven staining and slide defects, had a wide range of variation.

The memory renewal game and conflict: Memory implementation is unstable than anticipated to respond to cell division incidences. The logic of renewal of memory banks is at odds when the mother cell divides into two daughter cells, which is whether to have an old memory and form a new one or to replace the entire old memory with two new memories.

7. Conclusion

In the proposed study, an effective result is fine-tuning the SAM2 to address blood cell segmentation in images and video. A custom curation and preprocess of 400 annotated images with a hybrid dataset was done to solve problems related to poor contrast and cell adhesion using CLAHE and Z-score normalization. An efficient fine-tuning approach was used where parameters of the image encoder were unfrozen selectively; the last image encoder and the whole memory encoder were unfrozen and LoRA and lightweight adapters were incorporated. The training was based on a composite loss functional consisting of segmentation, temporal consistency, and morphological regularization terms. The resultant model BloodCellSAM2 with a mIoU of 85.7 and Dice coefficient 91.3 is far more effective than the original SAM2 and a U-Net baseline, despite having significantly smaller parameters to train with (0.8%)

However, the experiment still has many shortcomings. Firstly, due to the limitation of computational capacity, the dataset we selected is relatively small compared to the original model dataset. However, because the number of model parameters is large, it may affect the generalization ability and statistical significance of the model. Secondly, in the dataset, the number of samples of certain cell types (such as basophils) is relatively small, resulting in the segmentation performance of the model on this type of cell being significantly lower than that of other types, reflecting the problem of unbalanced data distribution. Finally, the memory update mechanism in the experiment will have logical conflicts in cell division events (such as the memory update strategy when the mother cell divides into daughter cells), and this problem has not been effectively solved, which limits the application of the model in dynamic biological processes.

Future directions can be on the ability to design specialized memory units to process biological processes such as cell division, and also interested in self-supervised pre-training of the memory process by using unlabeled cell videos to further improve the ability of the memory process to be robust and do generalization in dynamic biomedical imaging set-ups.

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