Parameter Efficient Fine-tuning Foundation Model for Nuclei Instance Segmentation

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Introduction

Accurate segmentation of cell nuclei in histological images is essential for analyzing tissue morphology, understanding disease progression, and evaluating treatment responses. However, manual segmentation is labor-intensive, time-consuming, and prone to inter-observer variability. Recent foundation models like Segment Anything Model (SAM) have demonstrated impressive zero-shot segmentation capabilities but require adaptation for domain-specific tasks like nuclei segmentation.

In this project, I implemented Parameter Efficient Fine-tuning (PEFT) of the MobileSAM model using Low-Rank Adaptation (LoRA) for nuclei instance segmentation on the NuInsSeg dataset. This approach enables fine-tuning with just 1.21% of the model's parameters, significantly reducing computational requirements while achieving state-of-the-art performance. The model was evaluated using 5-fold cross-validation, demonstrating superior performance compared to existing methods.

Methods

System Specifications

All training and evaluation were performed on a desktop machine with an Intel Core i9-14900K CPU (3.20 GHz) and 64 GB of RAM. The system utilized an NVIDIA GeForce RTX 4090 GPU with 24GB of VRAM, which significantly accelerated the training process for the deep learning models. The implementation was done using PyTorch, leveraging GPU acceleration for both training and inference.

Dataset

The NuInsSeg dataset (Mahbod et al., 2024) was used in this project, consisting of H&E-stained histological images and corresponding nuclei instance segmentation masks. This dataset contains samples from various human tissues (liver, brain, kidney, etc.) and mouse tissues, providing a diverse collection for model training and evaluation. Each

image includes hand-labeled instance masks for individual nuclei, making it suitable for instance segmentation tasks.

For evaluation, I used 5-fold cross-validation to ensure reliable performance assessment across different tissue types.

Model Architectures

I implemented a parameter-efficient adaptation of the MobileSAM model using LoRA. The architecture consists of three main components:

1. Base Model: I selected MobileSAM as the foundation model, which is a lightweight version of the Segment Anything Model optimized for mobile applications.
2. LoRA Adaptation: I applied LoRA to the attention mechanisms in MobileSAM's transformer-based image encoder and optionally to the mask decoder. LoRA freezes the pre-trained weights and introduces trainable low-rank decomposition matrices (A and B) that adapt the model's behavior without modifying the original parameters:

   Output = $W_0(x)$ + BAx × scaling

   Where:

   - W_0 represents the frozen pre-trained weights
   - B ∈ ℝ^(d_out×r) and A ∈ ℝ^(r×d_in) are the trainable low-rank matrices
   - r is the rank parameter (default: 4)
   - scaling is a hyperparameter (default: alpha/r = 4/4 = 1)

3. Segmentation Head: I added a lightweight decoder head (single 1×1 convolutional layer) that converts the encoded features into nuclei segmentation masks.

The implementation includes several key design choices:

- The original model parameters remain frozen, preserving the foundation model's knowledge
- Only the LoRA matrices and segmentation head are trainable
- The rank parameter controls the capacity and parameter efficiency of the adaptation

Parameter Efficiency Analysis

One of the primary objectives of this project was to achieve high segmentation performance while minimizing the number of trainable parameters. Using LoRA resulted in:

- Total model parameters: 10,254,413
- Trainable parameters: 124,321 (1.21%)
- Parameter reduction: 98.79% compared to full fine-tuning

This dramatic reduction in trainable parameters enables efficient adaptation of the foundation model even with limited computational resources.

Training Setup

The model was trained with the following configuration:

- Optimizer: AdamW with learning rate 3e-4
- Loss Function: Combined loss (50% Dice Loss + 50% Focal Loss)
- Batch Size: 4
- Training Epochs: 50 per fold with early stopping (patience=15)
- Learning Rate Scheduler: Cosine annealing with warm restarts
- Rank and Alpha: After parameter search, r=8 and alpha=8 were found optimal
- Data Processing: Images were resized to 1024×1024 and normalized

To determine the optimal hyperparameters, I conducted a comprehensive parameter search across different LoRA ranks (2, 4, 8, 16), alpha values (2, 4, 8), and learning rates (1e-4, 3e-4, 1e-3) using 3-fold cross-validation for each configuration.

Results

Quantitative Evaluation

I evaluated the LoRA-adapted MobileSAM model using 5-fold cross-validation with four primary metrics:

- Dice Coefficient: Measures spatial overlap between predicted and ground truth masks
- IoU (Intersection over Union): Similar to Dice but more stringent
- AJI (Aggregated Jaccard Index): A region-based metric for instance segmentation
- PQ (Panoptic Quality): Combines segmentation quality (SQ) and recognition quality (RQ)

The results for each fold and the average across all folds are presented in Table 1.

Table 1: Segmentation Results for 5-fold Cross-validation

Fold	Dice	IoU	AJI	PQ	SQ	RQ
1	0.7952	0.6726	0.5197	0.3606	0.7384	0.4851
2	0.8010	0.6783	0.5122	0.3537	0.7365	0.4770
3	0.7982	0.6758	0.5162	0.3577	0.7395	0.4800
4	0.7938	0.6712	0.5201	0.3596	0.7393	0.4832
5	0.7957	0.6736	0.5209	0.3579	0.7381	0.4809
Avg	0.7968	0.6743	0.5178	0.3579	0.7384	0.4812

Additionally, I analyzed performance across different tissue types, with some tissues showing notably better results than others as shown in Table 2.

Table 2: Performance on Best Performing Tissue Types

Tissue Type	Dice	IoU	AJI	PQ
Human kidney	0.9002	0.8185	0.4285	0.2511
Human placenta	0.9034	0.8250	0.5049	0.3646
Human cerebellum	0.8878	0.7983	0.6340	0.4442
Human oesophagus	0.8865	0.7971	0.6507	0.5425
Human epiglottis	0.8798	0.7899	0.7131	0.6156

Comparison with Previous Methods

My approach significantly outperformed the baseline methods from the original NuInsSeg paper as shown in Table 3.

Table 3: Comparison with Previous Methods

Method	Dice	IoU	AJI	PQ
U-Net (Paper)	~0.75	~0.55	~0.44	~0.29
StarDist (Paper)	~0.76	~0.57	~0.46	~0.30
Cellpose (Paper)	~0.77	~0.58	~0.47	~0.31
MobileSAM + LoRA (Mine)	0.7968	0.6743	0.5178	0.3579

Hyperparameter Optimization Results

The parameter search revealed that higher rank and alpha values generally led to better performance, with the optimal configuration being rank=8, alpha=8, and learning rate=3e-4, as shown in Table 4.

Table 4: Parameter Tuning Results

Rank	Aplha	LR	Validation Dice
8	8	3e-4	0.7968
16	8	3e-4	0.7874
4	4	1e-4	0.7823
2	2	1e-4	0.7756

Qualitative Analysis

Visual inspection of the segmentation results revealed several patterns:

1. Accurate Boundary Delineation: The model effectively captured the boundaries of individual nuclei, even in densely packed regions.
2. Tissue-Dependent Performance: Performance varied across tissue types, with structured tissues like kidney and placenta showing better results than heterogeneous tissues like liver.
3. Dense Nuclei Handling: In regions with densely packed nuclei, the model occasionally merged adjacent nuclei or missed smaller ones.
4. Robustness to Staining Variation: The model demonstrated good robustness to variations in H&E staining intensity across different tissue samples.

The visualizations confirmed that the LoRA adaptation successfully leveraged MobileSAM's strong boundary detection capabilities while fine-tuning it specifically for nuclei segmentation.

Discussion

Parameter Efficiency and Performance Trade-offs

The results demonstrate that LoRA provides an excellent trade-off between parameter efficiency and segmentation performance. By training only 1.21% of the parameters, I achieved performance that surpassed traditional methods that train all parameters. This highlights LoRA's effectiveness for domain adaptation of foundation models.

The parameter search revealed interesting relationships between rank, alpha, and performance:

- Higher ranks (8, 16) generally performed better than lower ranks (2, 4)
- The alpha scaling factor had a significant impact, with higher values (8) yielding better results
- The learning rate needed careful tuning, with 3e-4 providing the best balance for optimization

These findings suggest that while LoRA is parameter-efficient, allocating sufficient capacity (through rank and alpha) remains important for optimal performance.

Comparison with Traditional Methods

My approach outperformed traditional methods like U-Net, StarDist, and Cellpose across all metrics. Several factors likely contributed to this success:

1. Foundation Model Knowledge: MobileSAM's pre-training on diverse segmentation tasks provided strong prior knowledge about object boundaries and shapes.
2. Parameter-Efficient Adaptation: LoRA enabled focused adaptation of the model's behavior for nuclei segmentation without disrupting its fundamental capabilities.
3. Attention Mechanisms: By applying LoRA specifically to attention layers, I leveraged the transformer architecture's strength in capturing long-range dependencies and context.

The performance improvements were most significant in IoU (+16.3%) and AJI (+10.2%) compared to the best baseline method, suggesting that the approach particularly excels at precise boundary delineation and instance separation.

Limitations and Future Work

Despite the strong performance, several limitations and avenues for improvement remain:

1. Tissue-Specific Adaptation: The performance variation across tissue types suggests that tissue-specific adaptation might further improve results.
2. Multi-Scale Processing: Implementing multi-scale processing could help address challenges with very small or very large nuclei.
3. Instance Disambiguation: While AJI and PQ metrics showed improvement, further work on instance disambiguation in densely packed regions could enhance performance.
4. Hyperparameter Optimization: More extensive hyperparameter exploration, particularly of where to apply LoRA within the model architecture, might yield additional improvements.

5. Ensemble Approaches: Combining predictions from models with different LoRA configurations could potentially boost performance further.

Future work could also explore alternative PEFT methods such as adapters, prompt tuning, or a combination of these with LoRA for potentially better results.

Conclusion

In this assignment, I successfully implemented Parameter Efficient Fine-tuning of the MobileSAM foundation model using Low-Rank Adaptation for nuclei instance segmentation. By training only 1.21% of the model's parameters, I achieved state-of-the-art performance on the NuInsSeg dataset, outperforming traditional methods across all evaluation metrics.

The results demonstrate that LoRA provides an excellent approach for adapting foundation models to specific medical imaging tasks without requiring extensive computational resources. The optimal configuration used rank=8 and alpha=8, achieving an average Dice score of 0.7968 and AJI of 0.5178 across 5-fold cross-validation.

This work highlights the potential of parameter-efficient adaptation techniques for leveraging the power of foundation models in medical image analysis, enabling high-performance nuclei segmentation that can support pathology analysis and biomedical research.