OG-SAM: Enhancing Multi-Organ Segmentation with Organogenesis-Based Adaptive Modeling

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Introduction

OG-SAM addresses critical challenges in multi-organ segmentation by integrating biological priors of organogenesis into the Segment Anything Model (SAM). Traditional methods (e.g., thresholding, CNNs, Transformers) struggle with nuanced organ relationships and morphological variability due to shared embryonic origins and size disparities. For instance, the liver and pancreas (both endoderm-derived) exhibit textural differences that complicate segmentation. OG-SAM overcomes these via:

1.OrganAdapt:Dynamically parameter sharing/specialization across organs based on developmental hierarchies.

2.GoF Module: Adaptively fuses multi-scale features using organ-specific parameters to address size variability.

As a query-based plug-in, OG-SAM uses organ classes as prompts to gate adaptations, enhancing boundary accuracy.

Methodology

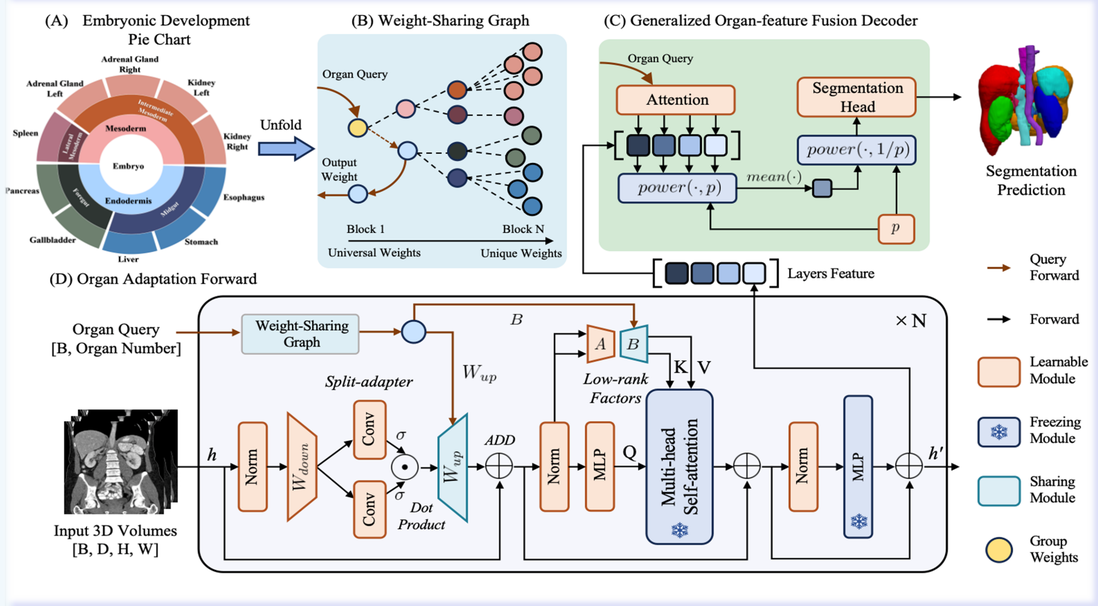
Parameter-Efficient Adaptation

Leverages SAM's ViT-B backbone with LoRA (form. 2) and Adapters (form. 3), reducing computational costs while maintaining expressivity (form. 4).

$$\Delta\theta = AB^T,\ A \in R^{d\times r},\ B \in R^{d\times r}, \quad (2)$$

$$h' = h + H(h) = h + W_{up}(\sigma(W_{down}h)), \quad (3)$$

$$h_{i+1} = f^{i}\Theta(h_i + H(h_i)), \text{where}\ \Theta = \theta_0 + AB^T, \quad (4)$$



OG-SAM integrates two core components:

OrganAdapt(§2.3):

The hierarchical development of organs (Fig.1A), where an embryo gradually developing into distinct organs.

Weight-Sharing Graph:

Mirrors embryonic development (Fig.1B), where early layers share weights across germ layers (e.g., endoderm), later layers specialize organ-specifically.

Our Organ Adaptation (Fig. 1D) consists of three key components, each split by additive operations: the Split-Adapter, Low-Rank Factors, and a MLP。

（Split-Adapter: Processes input features via convolutional branches and dot-product operations (form. 5), updating features while preserving anatomical coherence.）

（Low-Rank Factors: Projects features into Key/Value representations for attention mechanisms (form. 6), optimizing parameter efficiency.）

$$h_a = W_{up}(\sigma(\text{Conv1}(\tilde{h})) \odot \sigma(\text{Conv}_2(\tilde{h})) + h, \text{ where } \tilde{h} = W_{down}N(h), \quad (5)$$

$$Q = W_q(N(h_a)),\ [K, V] = BA(N(h_a)), \quad (6)$$

2.Generalized Organ-feature Fusion (§2.4):

Extracts pyramidal features from SAM blocks, computes attention scores via MLPs (form. 7).

Fuses features using learnable parameter p(form. 8), enabling organ-specific aggregation (e.g., prioritizing fine scales for small organs like adrenal glands).

$$S = W_2(\sigma(W_1Q_o)), \quad (7)$$

$$f' = (G)^{1/p}, \text{ where } G = (\textstyle\sum_i (S_i f_i)^p)/(\sum_i S_i), \quad (8)$$

Experiments and Results

Setup and Implementation

Dataset: BTCV Challenge (13 abdominal organs, 30 CT volumes).

Metrics: Dice Score (↑), HD95 (↓) indicating a higher accuracy.

Implementation:The model was used to made 200epochs of training.

Key Results

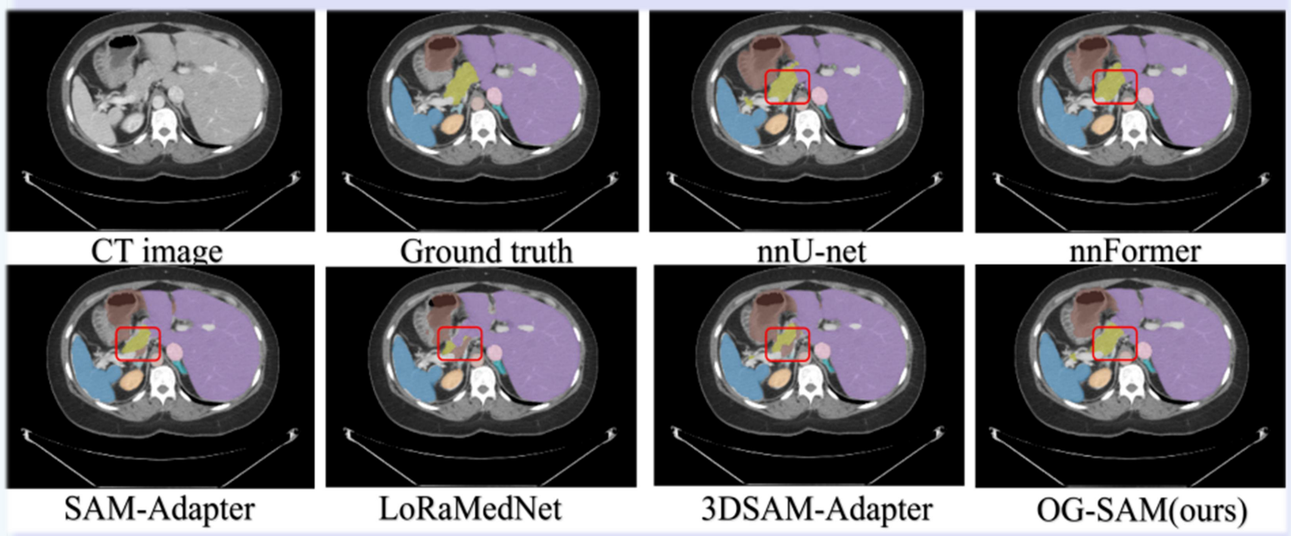
Baselines: CNN/Transformer-based (nnU-Net, SwinUNETR) and SAM fine-tuned models (3DSAM-adapter).

1.Superior Performance:

Achieves 85.5% average Dice (↑1.0% vs. SOTA) and 2.91mmHD95 (↓1.0mm vs. SwinUNETR).

Excels in challenging organs: Gallbladder (80.1% Dice ↑15.7%), Adrenal Glands (70.3% Dice ↑5.4%).

Robust boundary delineation (Fig. 2):



2.Ablation Studies:

Further explore the effectiveness of each component.

Removing GoF ↓ Dice by 0.5%, ↑ HD95 by 0.07mm.

Excluding weight-sharing ↓ Dice by 0.9%, ↑ HD95 by 53.57mm (critical for anatomical coherence).

Without Split-Adapter ↓ Dice by 5.2%, ↑ HD95 by 73.16mm (confirms feature-disentangling efficacy).

Conclusion

OG-SAM pioneers biologically inspired adaptation for multi-organ segmentation:

OrganAdapt aligns parameter sharing with organogenesis, ensuring anatomical consistency.

GoF dynamically fuses multi-scale features via organ-specific modulation.

As a plug-in, it enables efficient specialization without full retraining. Limitations include dependency on organ-query design and unexplored 3D extensions. Future work will incorporate non-parenchymal structures (e.g., blood vessels) and expand to thoracic/pelvic organ segmentation, advancing scalable precision medicine.