

# How to build the best medical image segmentation algorithm using foundation models: a comprehensive empirical study with Segment Anything Model

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Code: <https://github.com/mazurowski-lab/finetune-SAM>

## Abstract

*Automated segmentation is a fundamental medical image analysis task, which enjoys significant advances due to the advent of deep learning. While foundation models have been useful in natural language processing and some vision tasks for some time, the foundation model developed with image segmentation in mind - Segment Anything Model (SAM) - has been developed only recently and has shown similar promise. However, there are still no systematic analyses or “best-practice” guidelines for optimal fine-tuning of SAM for medical image segmentation. This work summarizes existing fine-tuning strategies with various backbone architectures, model components, and fine-tuning algorithms across 18 combinations and evaluates them on 17 datasets covering all common radiology modalities. Our study reveals that (1) fine-tuning SAM leads to slightly better performance than previous segmentation methods, (2) fine-tuning strategies that use parameter-efficient learning in both the encoder and decoder are superior to other strategies, (3) network architecture has a small impact on final performance, and (4) further training SAM with self-supervised learning can improve final model performance. We also demonstrate the ineffectiveness of some methods popular in the literature and further expand our experiments into few-shot and prompt-based settings. Lastly, we released our code and MRI-specific fine-tuned weights, which consistently obtained superior performance over the original SAM, at <https://github.com/mazurowski-lab/finetune-SAM>.*

## 1. Introduction

Medical image segmentation refers to identifying the region of interest, typically anatomical structures or tumors,

in an image. This process is essential in the field of medical image analysis, contributing significantly to the effectiveness of computer-aided diagnosis [1]. The introduction of deep learning techniques has led to a variety of automated segmentation methods [57, 85], further enhancing the precision and efficiency of analyzing medical images. Despite the progress made, it is still difficult to determine the most effective method for developing an optimal segmentation model, especially with the recent introduction of vision foundation models dedicated to segmentation. Therefore, in our study, we aim to explore and define the optimal strategies for developing automated segmentation algorithms specifically designed for medical images and with a focus on foundation models.

In the era of deep learning, a common practice for automated medical image segmentation is to directly train UNet [70] or its variants [75, 83] for a dataset and task. Recently, there has been a growing interest in the field of customizing vision foundation models towards specific segmentation tasks [29, 96]. Foundation models are (typically transformer-based [82]) neural networks pre-trained with extremely large datasets, such that they can generalize to a wide range of tasks and datasets. The seminal Segment Anything Model (SAM) [45] was proposed as the first large model designed with segmentation tasks in mind. SAM employs a prompt-based training method, aiming to generate target object’s segmentation masks in response to user-provided prompts, e.g. points or bounding boxes. It has demonstrated comparable or even superior zero-shot performance to fully supervised models in processing natural images. However, SAM performance is less impressive when applied directly to medical images [21, 39, 61], and the requirement of prompts makes its direct usage with medical imaging segmentation tasks challenging.

Removing the prompt requirement in SAM is relatively

straightforward as we can use “dummy” prompt embeddings as inputs during fine-tuning, a strategy verified by concurrent work [96]. However, the approaches proposed for adapting SAM to medical imaging tasks vary widely. Some works focused on adapting SAM’s decoder only [92], while others chose to modify the entire network [96]. Some works introduced an additional pre-training stage [59] using multiple medical images while others usually do not. Though some prior survey work [49, 98] have attempted to list different strategies and categorize them into various groups, questions remain regarding (1) which fine-tuned strategy is the most effective, (2) whether these models can achieve better performance than traditional UNets and (3) whether using additional data is helpful.

In this work, we aim to answer these questions by considering three common dataset availability scenarios in the medical imaging field: (1) only a single labeled dataset; (2) multiple labeled datasets for different tasks; and (3) multiple labeled and unlabeled datasets. The first scenario reflects the most common deep learning scenario of adapting SAM to the dataset of interest, and the latter two scenarios bring the opportunity to first incorporate broad medical domain knowledge into SAM using supervised/self-supervised training before adapting it to a specific dataset. Figure 1 summarizes the strategies and experiment setups we include. To avoid terminology confusion, we name these strategies as **task-specific supervised training**, **task-expansive prompt-based learning**, and **task-agnostic self-supervised learning** respectively.

When considering the design choice during task-specific supervised training, our work aligns with several concurrent works [49, 98, 99]. However, our work differs from theirs in that we conduct comprehensive experiments over 17 medical imaging datasets across various modalities for a fair comparison, rather than simply compiling disparate results, and provide an organized and new catalog that could summarize existing approaches. The choice of each category is shown in Figure 2 and will be discussed in Section 2.2. Our category definition reflects the common design choices when building a segmentation algorithm from SAM, and we can categorize most existing works based on the proposed criteria, shown in Table 1.

When incorporating extra medical knowledge into SAM, we explore two main setups of pre-training approaches: task-expansive prompt-based learning and task-agnostic self-supervised learning, depending on the availability of labels. Note that our objective is not to propose a novel pre-training strategy, as such strategies are often constrained by the availability of computation resources and datasets. Instead, our focus is on identifying if additional pre-training with more available medical data is helpful and if it is, to determine what is the best combination of pre-training and task-specific fine-tuning. Therefore, we adopt the strategies

used during SAM’s development and one of the most commonly applied pre-training strategies in this field. Namely, we use the same interactive training pipeline where prompts are simulated from the masks for task-expansive prompt-based learning; and masked autoencoding (MAE) [31] as the objective for task-agnostic self-supervised learning. We evaluate these approaches on the same 17 datasets.

Our study is extended to two crucial scenarios when deploying a segmentation algorithm for annotation purposes: few-shot learning and interactive segmentation. The first scenario reflects the case of annotating a new dataset with only a limited number of annotations, while the latter examines the effectiveness of using tools to assist the annotation process. In both scenarios, we limit the evaluation datasets to MRI. When conducting few-shot learning, we limit the number of training samples to 5 and re-examine the effectiveness of setups 1-3 described in Figure 1. In the interactive segmentation scenario, we focus on task-specific supervised training with either box or point as input prompts.

In conclusion, we systematically study different approaches to fine-tune SAM in the medical imaging field. Our paper investigates an important question: what is the best practice to develop an automated segmentation algorithm based on foundation models? We find the answers depend on the availability of the datasets and consider three scenarios: (1) only a single labeled dataset; (2) multiple labeled datasets (with different objects of interest); and (3) multiple labeled and unlabeled datasets. We propose task-specific supervised training, task-expansive prompt-based learning followed by task-specific supervised training, and task-agnostic self-supervised learning followed by task-specific supervised training as the solution to each scenario respectively. By conducting systematic experiments on each strategy, we observe several useful guidelines and summarize them in Section 5.

## 2. Method

In this section, we first recapitulate SAM’s structure. Next, we describe the selected methods under different data availability scenarios.

### 2.1. SAM and removal of prompts

To begin with, we first briefly present an overview of the Segment Anything Model (SAM) [45] before introducing the fine-tuning strategies. SAM consists of three components: (1) image encoder, (2) prompt encoder, and (3) mask decoder. The image encoder, built on a robust Vision Transformer (ViT) framework, effectively converts a 2D image into a latent feature representation. Notably, in SAM’s original architecture, the image encoder offers flexibility in model size, with options including ViT-H(uge), ViT-L(arge), and ViT-B(ase) [22]. The prompt encoder is flexible, accommodating different prompt types such as

## Common Experimental setup based on varying levels of dataset availability

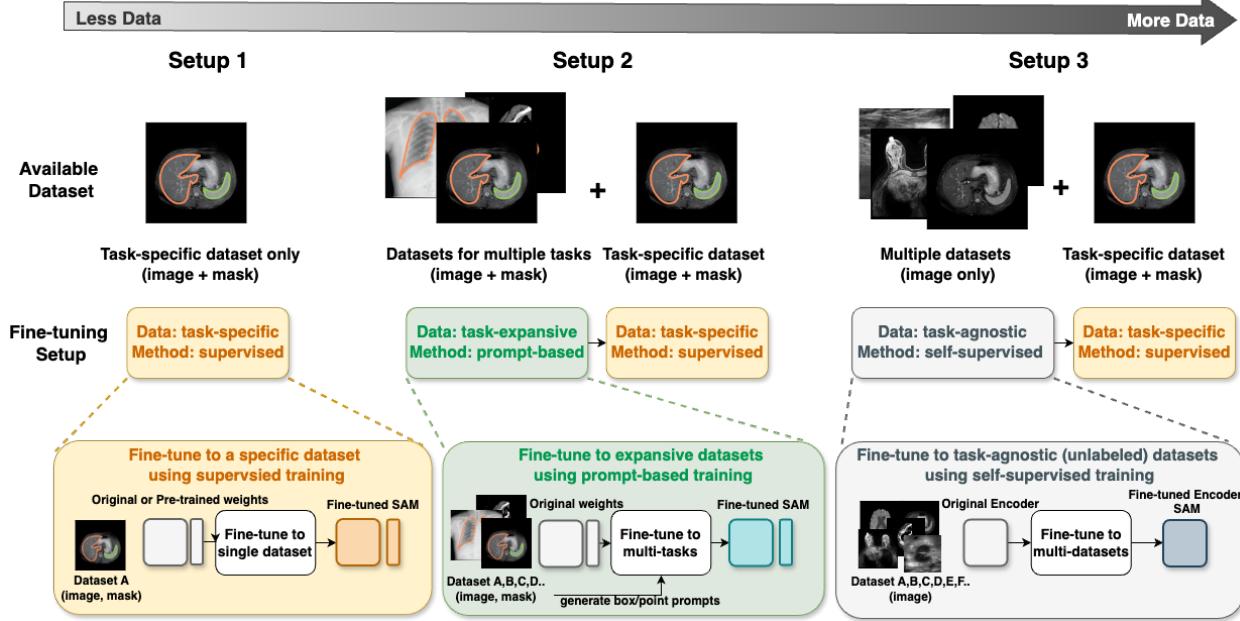


Figure 1. Overview of general fine-tuning strategies based on different levels of dataset availability.

point, box, or mask prompts. Depending on the input type, it generates either sparse embeddings for point/box prompts or dense embeddings for mask prompts. Lastly, the mask decoder is a transformer decoder using two-way cross-attention that integrates image and prompt embeddings to produce a multi-channel mask output, each channel representing varying confidence levels.

### 2.1.1 Interactive segmentation to automated segmentation

When converting SAM to auto-mode (without prompts), we can simply use the default embeddings generated by using “None” as inputs to the prompt encoder, *i.e.*

```
sparse_embeddings, dense_embeddings =
sam.prompt_encoder(points=None,
boxes=None, masks=None),
```

where the “sparse\_embeddings” and “dense\_embeddings” serve as inputs to SAM’s mask decoder. Empirical evidence shows the effectiveness of this simple approach [96]. More advanced methods, including adding a detection network to automatically generate box prompts or a self-prompt module into SAM’s structure [27, 72, 87], are feasible but will introduce extra complexity into SAM’s structure, hampering our analysis on the effectiveness of fine-tuning strategies. Moreover, we believe our work offers a potentially effective strategy, *i.e.* feeding the generated prompts to the

fine-tuned SAM instead of the original one, for this research direction.

### 2.2 Variables in task-specific supervised training

We consider three aspects in task-specific supervised training that can affect the performance, as shown in Figure 2. The choice of each category is discussed next.

#### 2.2.1 Image Encoder Architecture

In this work, we select ViT-B and ViT-H from SAM’s provided checkpoints because they represent the most efficient and effective versions of SAM’s encoder respectively. Additionally, we explore a more compact option: ViT-T(iny). This backbone is introduced in MobileSAM [94], where the authors distill the knowledge from SAM’s pre-trained ViT-H to ViT-T, a customized vision transformer with 1% of the network parameters and offers an inference speed 50 times faster compared to the original SAM. The lightweight nature can widen the application of SAM, ease the computational requirements, and, more importantly, raise interesting research questions, such as whether distillation can maintain or even lead to the superior performance of SAM during fine-tuning.

#### 2.2.2 Model Component

When selecting which set(s) of SAM’s parameters to update, the most straightforward way is to select one or multi-

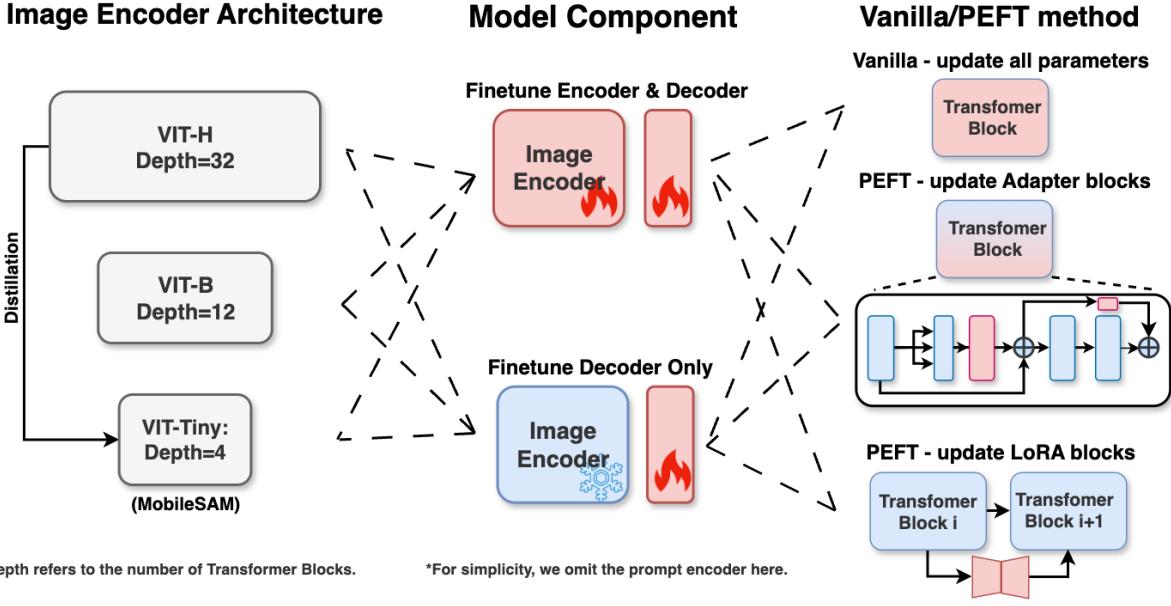


Figure 2. Visualization of task-specific fine-tuning architectures selected in our study: including 3 encoder architecture  $\times$  2 model components  $\times$  3 vanilla/PEFT methods = 18 choices.

ple components from SAM. As discussed in Section 2.1.1, we use the default prompt embeddings and thus can keep the prompt encoder as is.

Some methods state the effectiveness of maintaining the encoder’s weights and only adapting the lightweight mask decoder of SAM’s architecture, as shown in Table 1. These approaches are grounded in the understanding that SAM’s encoder, trained on a comprehensive collection of natural images, is adequately powerful and knowledgeable in the general imaging domain with zero-shot ability to perform feature extraction, and updating the lightweight decoder can enhance performance in specific applications. Also, it is suggested that fine-tuning the encoder of SAM would demand considerably higher computational resources. However, due to the significant appeal difference between natural images and medical images, it remains unclear if SAM’s encoder could effectively capture the distinctive features of medical images without any modifications to the image encoder. Therefore, we consider these two choices: *mask decoder only* and *mask decoder plus image encoder*.

### 2.2.3 Vanilla or Parameter-efficient Fine-tuning Method

When conducting model fine-tuning or transfer learning, the easiest and most intuitive way is to update all model parameters involved when feeding medical domains of data, which is vanilla fine-tuning [6].

Recently, parameter-efficient fine-tuning (PEFT) tech-

niques have gained an increasing amount of attention. Compared with vanilla fine-tuning, PEFT keeps most of the network parameters fixed and only updates a small percentage, *i.e.* less than 5%, of them. Such a strategy significantly reduces the computational cost and is beneficial in preventing catastrophic forgetting as well as over-fitting [23]. The simplest PEFT techniques involve selecting and fine-tuning a subset of the parameters from the original pre-trained model. These selective methods concentrate on identifying the optimal parameters for fine-tuning, aiming to strike an ideal balance between parameter efficiency and overall model performance. For instance, BitFit [93] proposed fine-tuning only the bias term in a transformer-based network, and Tinytl [12] shares a similar idea but focuses on CNN-based networks. Touvron et al. [79] have demonstrated the effectiveness of selectively fine-tuning only the attention layers in Vision Transformers (ViTs), whereas alternative approaches suggest that exclusively optimizing the normalization layers [7].

Rather than updating certain selected layers, recent research [54] indicates that incorporating extra modules into the large models appears to be more beneficial because it re-configures models towards a downstream task than solely updating network parameters. Among these additional module methods, Adapters, which were originally introduced for learning multi-domain representations [68,69], have emerged as a particularly prevalent choice. In addition to the conventional Adapter block [35], Low-Rank Adaptation (LoRA), known for its efficient low-rank matri-

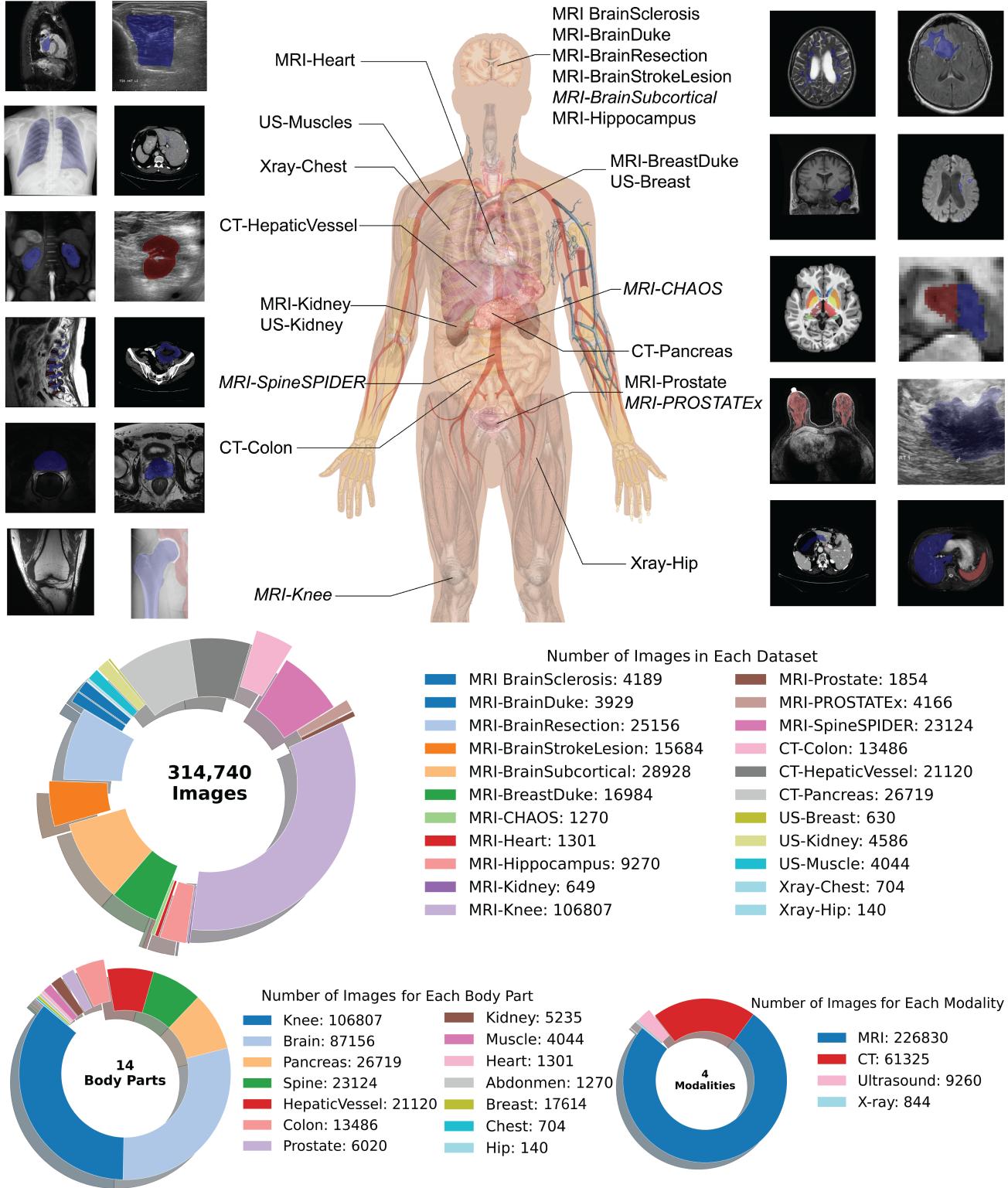


Figure 3. A visual summary of the collected datasets, including the visual example from each dataset and the number of images under different criteria.

Category	Methods	Dataset	Backbone
Decoder + Vanilla	SAM for medical images? [39]	COSMOS 1050K	ViT-H / ViT-B
	Generalist Vision Foundation [73]	Multiple	ViT-H
	How to efficiently [38]	ACDC [8]	ViT-H
	All-in-SA [19]	Monuseg [47]	ViT-H
	AdaptiveSAM [64]	Multiple	ViT-B
	SkinSAM [37]	HAM10000 [80]	ViT-B
	DeSAM [27]	Multi-Prostate	ViT-H
	SurgicalSAM [92]	EndoVis [3]	ViT-H
	SAM3D [11]	Multiple	ViT-B
	SAM Fewshot [88]	Multiple	N/A
Decoder + LoRA	BLO-SAM [97]	Multiple	ViT-B
Encoder + Vanilla	AutoSAM [72]	Multiple	ViT-H
	SAMUS [56]	Multiple	N/A
En/Decoder + Vanilla	Polyp-SAM [55]	Multi-Colonoscopy	ViT-L / ViT-B
	CellViT [34]	Multi-nuclei	ViT-H
En/Decoder + LoRA	Customized SAM [96]	Multi-Organ	ViT-H / ViT-B
	MA-SAM [14]	BTVC [24]	ViT-H
	Cheap Lunch [25]	BraTS 18 [62]	ViT-B
En/Decoder + Adapter	Medical SAM Adapter [86]	BTVC [24]	ViT-H
	SAM Fails to Segment? [17]	kvasir-SEG [42]	ViT-H
	Learnable Ophthalmology SAM [67]	Multiple	N/A
	Auto-Prompting SAM [53]	Multiple	LightWeight ViT
	SAM-Med2D [18]	SAM-Med2D [18]	ViT-B
	3DSAM-adapter [28]	Multi-CT	ViT-B
	SAM-Path [95]	Multiple	LightWeight ViT
	Self-Sampling Meta [51]	ABD-30 [48]	ViT-B
	Cross-modality [74]	MRI	ViT-B

Table 1. Summary of existing fine-tuning methods, grouped by the component-method combinations. En/Decoder means both the encoder and decoder are optimized.

ces added into self-attention layers that require even fewer parameters, has also gained popularity [36]. Additionally, AdaptFormer [15], which integrates a scalable Adapter into the multi-layer perceptron (MLP) layer of the attention block specifically for vision transformers, has shown that adding just 2% extra parameters can surpass the performance of fully fine-tuned networks across various natural imaging benchmarks. In our study, we aim to investigate the effectiveness of applying PEFT for fine-tuning SAM within the medical imaging domain. Considering Adapter and LoRA are the most popular PEFT methods adopted in LLMs and vision foundation transformers [91], we choose to include them as well as the simplest Vanilla for our experiments. In summary, we select the following methods:

1. Vanilla - a “baseline” approach that updates all parameters.
2. Adapter / LoRA - these approaches involve adding extra layers with original parameters fixed.

#### 2.2.4 Summary

To sum up, we choose the following combinations to fine-tune SAM’s performance for specific datasets or tasks, as illustrated in Figure 2: (1) Variations in the image encoder’s architecture, including ViT-H, ViT-B, and ViT-T from MobileSAM [94]. (2) Different approaches to the fine-tuning scope of the network, encompassing both the encoder and decoder updates, as well as the decoder only. (3) Diverse parameter updating settings, comprising Vanilla, PEFT with Adapter blocks, and PEFT with LoRA blocks. By integrating these three variables, we present a total of  $3 \times 2 \times 3 = 18$  distinct architectures for fine-tuning SAM on task-specific supervised training setup.

### 2.3. Task-general Prompt-based Learning

When multiple **labeled** datasets are available, an approach to adapting SAM to the medical imaging field involves additional pre-training, *i.e.* starting with SAM’s pre-trained weights and continuing the learning process with a compilation of the medical datasets, followed by task-

Alias in our paper	Description and citation	# of images	# of masks
Datasets used for dataset-specific fine-tuning and pre-training:			
MRI-BrainSclerosis (MRI-Scler.)	Brain Sclerosis with Lesion Segmentation [63]	4189	1813
MRI-BrainDuke (MRI-Brain)	Brain with FLAIR Abnormality Segmentation Masks [10]	3929	1372
MRI-BrainResection (MRI-Resect.)	EPISURG Segmentation on the Resection CaViTy [66]	25156	5377
MRI-BrainStrokeLesion (MRI-Stroke.)	ISLES 2022: Stroke Lesion Segmentation [33]	15684	4827
MRI-BreastDuke (MRI-Breast)	Breast Cancer Screening [52, 71]	16984	16984
MRI-Heart	Medical Segmentation Decathlon Cardiac [4]	1301	1301
MRI-Hippocampus (MRI-Hippo.)	Medical Segmentation Decathlon Hippocampus Head and Body [4]	9270	6622
MRI-Kidney	T2-weighted Kidney MRI [20]	649	647
MRI-Prostate (MRI-Prost.)	Original Multi-Parametric MRI Images of Prostate [50]	1854	1854
CT-Colon	Medical Segmentation Decathlon Colon [4]	13486	1285
CT-HepaticVessel (CT-vessel)	Medical Segmentation Decathlon Hepatic Vessel [4]	21120	13042
CT-Pancreas (CT-Panc.)	Medical Segmentation Decathlon Pancreas [4]	26719	8792
US-Breast	Breast Ultrasound Images Dataset [2]	630	630
US-Kidney	Kidney Segmentation in Ultrasound Images [77]	4586	4585
US-Muscle	Transverse Musculoskeletal Ultrasound images [60]	4044	4043
Xray-Chest	Montgomery County and Shenzhen Chest X-ray Datasets [41]	704	704
Xray-Hip	X-ray Images of the Hip Joints [30]	140	140
Datasets used for pre-training only:			
MRI-BrainSubcortical	14 Brain Sub-cortical Structures [76]	28928	5891
MRI-CHAOS	Segmentation of Liver, Kidneys and Spleen from MRI data [44]	1270	992
MRI-Knee	MRNet Knee MRI Examinations [9]	106807	Not used
MRI-ProstateX	ProstateX Dataset of Prostate MR Studies [5]	4166	3195
MRI-SpineSPIDER	SPIDER - Lumbar Spine Segmentation in MR Images [81]	23124	12763

Table 2. Description of the collected datasets. The first 17 datasets are used throughout the paper for training and evaluation and the remaining 5 are used exclusively for supervised or self-supervised pre-training.

specific supervised training, as is similar in [18, 59]. The procedure is illustrated in Figure 1 setup 2. The motivation for adopting a two-step training approach, rather than utilizing automated fine-tuning on multiple datasets, lies in the fact that various datasets, despite featuring medical images of the same anatomical area and being captured using the same imaging technique, may concentrate on entirely distinct objectives. For example, two brain MRI datasets might each focus on segmenting different entities, such as the hippocampus in one and tumors in the other. Applying automated segmentation to these datasets could introduce ambiguity, and make the training challenging.

Therefore, we use a prompt-based segmentation setup during task-expansive prompt-based learning, which involves providing prompts to identify the targeted area of interest interactively. This approach addresses the issue of the above-mentioned ambiguity. Furthermore, this choice conceptually aligns with the second phase of SAM’s second-stage training process [45], allowing it to be considered as an extra step of supervised training specifically tailored for medical images within the SAM framework.

To simulate a prompt, we first randomly selected a type of object if the ground truth mask contains multiple objects. Then, for each contiguous region of the selected object, we generate a box or a point prompt with equal probability. The generation of box prompts follows SAM’s strategy: a tight box containing the target box is created first, followed by some random noises added to both locations. The random noises are generated with the standard deviation equal to

10% of the box coordinates and to a maximum of 20 pixels. For point generation, we follow [61] to first compute the distance of each pixel to its closest edge within the object region and sample a pixel with a distance above the median distance. This operation allows us to sample a point prompt around the center of the object. Such a design choice is different from that of the SAM, which samples the first point prompt uniformly and subsequent points from the error region between the previous mask prediction and the ground truth mask. Since our ultimate goal is to learn an automated segmentation algorithm, we do not need the iterative process to refine the predictions based on prompts.

Considering the differences across various medical imaging modalities, alongside the observation that images within the same modality often share similar visual features [46], we emphasize the value of modality-specific dataset knowledge in pre-training, a practice also common in the literature [78]. Specifically, we focus on the supervised pre-training on MRI, which consists of most of the collected datasets.

## 2.4. Task-agnostic Self-supervised Learning

When using multiple **unlabeled** medical image datasets, we can utilize the same idea as in the last section to conduct additional pre-training before applying task-specific supervised training. As the label information is unavailable in this scenario, we adapt the self-supervised learning (SSL) techniques, referred to as task-agnostic self-supervised learning. SSL refers to training a network with-

out any human-collected labels. This is an effective strategy since the number of available datasets can increase dramatically. Popular SSL methods generally fall into two categories: contrastive learning [16, 32, 65] or masked image modeling [31, 90]. In the medical image field, further methods are tailored to fit the characteristics of medical images [78], including dimension discrepancy [89], structure similarity [43], etc.

Among these methods, we select the Masked Autoencoder (MAE) [31] as our self-supervised pre-training strategy for three reasons: (1) the computation of CL is infeasible given the input size of SAM, *i.e.*  $1024 \times 1024$ ; (2) SAM also utilized an MAE pre-trained vision transformer as the initial model; (3) there is increasing evidence showing the effectiveness of using MAE during medical image segmentation [84, 100, 101]. MAE first divides input images into non-overlapping patches and removes most of them, and its goal is to reconstruct these original inputs given the remaining ones. For the same reason as in task-expansive prompt-based learning, we also conduct training with MRIs only and evaluate all datasets.

### 3. Dataset

We select 22 datasets from publicly available sources online, including TCIA (The Cancer Imaging Archive), Kaggle, Zendo, Grand Challenge, and Mendeley Data. Figure 3 presents a visual summary of the datasets used in this paper. In total, we collect 14 magnetic resonance images (MRI) datasets, 3 computed tomography (CT) datasets, 3 ultrasound (US) datasets, and 2 X-ray datasets. Our datasets cover images from 14 main human anatomical locations. Examples of all 22 datasets are also included in the same figure, in addition to the image count of each dataset, each anatomical location, and each modality. The details of each dataset are listed in Table 2, including the citation, description, number of images, and number of masks. All datasets employ expert annotated segmentation masks except for the MRI-Knee dataset, which is used exclusively for self-supervised pre-training and thus their numbers of masks are indicated as “not used”.

Since SAM is a 2D-based segmentation network, 3D volumes are first extracted to 2d slices. We convert Nifti, mha, and Dicom volumes by normalizing all pixel values to 0–255 and further upsampling each slice to  $1024 \times 1024$  using nearest-neighbor interpolation to meet SAM’s required input size. The pixel values are repeated three times across the three channels for all grayscale images. We split each dataset into training, validation, and test sets by dividing patients into 7 : 1 : 2 splits accordingly.

In our study, we utilize this curated medical imaging datasets across various levels of data availability as follows:

1. *Specific Dataset Fine-tuning:* This involves datasets

applied for fine-tuning on a single labeled dataset, including all datasets listed in the first section of Table 2.

2. *Prompt-based Supervised Training with Multiple Labeled Datasets:* This category includes all MRI datasets that come with available masks, utilized for supervised pre-training.
3. *Self-Supervised Learning with Both Labeled and Unlabeled Datasets:* This level pertains to the use of all MRI datasets mentioned in our table for self-supervised learning, incorporating both labeled and unlabeled datasets.

## 4. Experiment

In this section, we conduct various experiments to assess the effectiveness of fine-tuning strategies across multiple datasets and configurations. First and foremost, we analyze the behaviors of these strategies when conducting task-specific supervised training. Next, we examine the effectiveness of applying task-expansive prompt-based learning or task-agnostic self-supervised learning before task-specific supervised training. These experiments are further extended to the few-shot learning and interactive segmentation setting. Throughout the paper, we use the dice similarity score (DSC%) as the evaluation metric.

### 4.1. Which fine-tuning combination is the best if applying task-specific supervised training only?

#### 4.1.1 Implementation details

When conducting task-specific supervised training, in addition to finding the most effective fine-tuning strategy, we also want to compare the performance against conventional UNet-based algorithms. Therefore, we have chosen three well-known and frequently used automated segmentation models for comparison: UNet [70], nnUNet [40], and SwinUNet [13]:

1. *UNet* serves as the baseline of the convolutional neural network-based segmentation algorithm.
2. *nnUNet* configures a UNet-based algorithm according to the specific attributes of the input datasets and approximates the performance of UNet with the optimal design choice.
3. *SwinUNet* replaces the encoder of UNet with a swin-transformer [58].

For PEFT with Adapter blocks, we implemented it based on [87], which added adapter blocks to SAM’s attention blocks. In the image encoder, adapter blocks were added into transformer blocks right after the multi-attention head

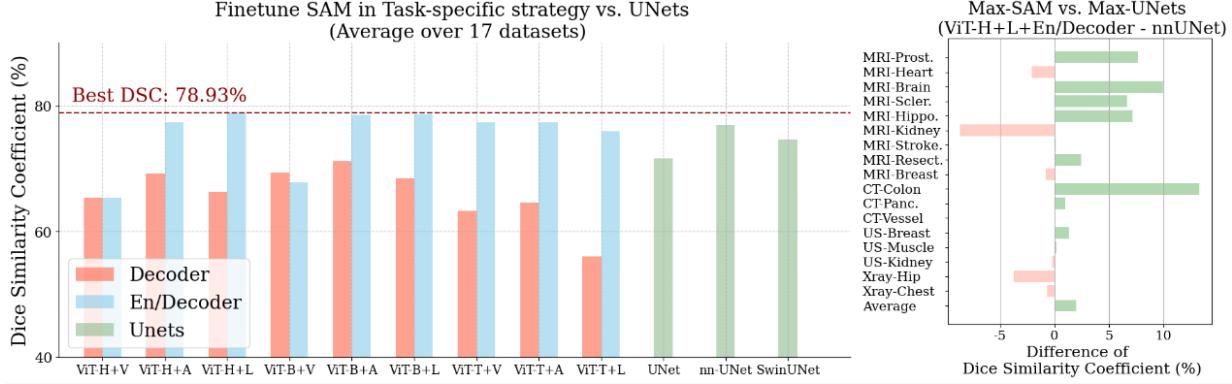


Figure 4. Left: Visualization of the performance of various task-specific supervised training strategies and UNet and its variances. Right: Difference between the best fine-tuned SAM model (ViT-H + En/Decoder + LoRA) and the best UNet-based model (nnUNet) across individual datasets.

Model			# of param.	# of trainable param.	GPU allocated (MB)	Single iteration time (s)
ViT-H	Decoder	Vanilla	640.95M	3.92M (0.61%)	22206	1.82
		Adapter	641.08M	0.13M (0.021%)	17210	1.88
		LoRA	640.97M	0.65M (0.10%)	17214	1.81
	En/Decoder	Vanilla	640.95M	640.95M (100.0%)	99,208	5.2
		Adapter	650.93M	9.98M (1.53%)	69,144	3.8
		LoRA	641.63M	1.31M (0.20%)	68,540	3.82
ViT-B	Decoder	Vanilla	93.60M	3.92M (4.19%)	11158	0.44
		Adapter	93.73M	0.13M (0.14%)	11532	0.45
		LoRA	93.62M	0.65M (0.69%)	11530	0.44
	En/Decoder	Vanilla	93.60M	93.60M (100.0%)	37306	1.16
		Adapter	97.28M	3.68M (3.79%)	33454	1
		LoRA	93.77M	0.80M (0.86%)	30578	0.95
ViT-T	Decoder	Vanilla	9.99M	3.92M (39.22%)	1404	0.08
		Adapter	10.12M	0.13M (1.13%)	1398	0.09
		LoRA	10.01M	0.65M (6.49%)	1400	0.08
	En/Decoder	Vanilla	9.99M	9.99M (100.0%)	10102	0.25
		Adapter	10.31M	0.32M (3.12%)	4018	0.16
		LoRA	10.04M	0.79M (7.82%)	4036	0.15

Table 3. Specifics of parameters and computer resources occupied for 18 combinations of fine-tuning choices. GPU allocated are measured when setting batch size as 4, and time for forward/backward is measured on a single A6000.

or within the MLP residual block with a scalable parameter [15]. In the default setting, we added Adapter blocks at the first two and last two transformer blocks (layers) in the image encoder. In the mask decoder, Adapters were added after the multi-head attention head. For PEFT with LoRA blocks, we implemented it based on SAMed [96], which inserted LoRA layers into the “query” and “value” projection layers of each transformer block in the image encoder and mask decoder.

In the pre-processing step of our datasets, we removed all data lacking target objects, specifically those images where the corresponding masks only consist of the background, for both training and testing purposes. We also followed the same normalization mean and standard deviation as the original SAM. We utilized dice loss and cross-

entropy loss with equal weights. For all experiments across various datasets, we adapted a basic learning rate of 1e-4 with a warmup of 200 iterations and applied AdamW with 0.1 weight decay for the remaining iterations. The batch size was set to 4. Histogram equalization and color jitter were the augmentations used during training. The maximum epochs were set to 200 epochs, incorporating an early stopping mechanism that halted training if there was no improvement in the highest validation DSC for 20 consecutive epochs. For settings that require heavy computing resources, such as ViT-H with the vanilla setting, we adopted Distributed Data Parallel (DDP) combined with model parallel to split batches or the model into 2-3 GPUs. The specifics regarding the total number of parameters in the model, the number of parameters subject to updates for each

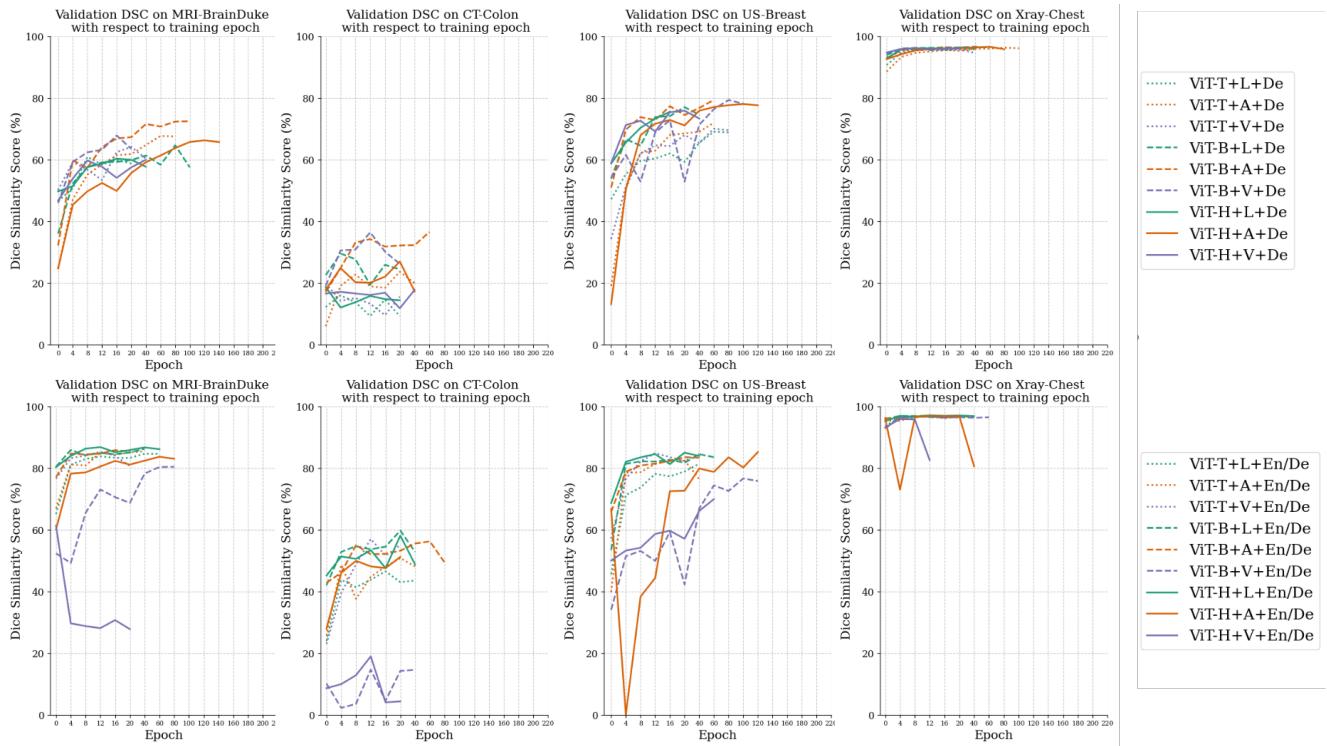


Figure 5. Validation loss with respect to training epoch for different combinations of fine-tuning strategies. We select one representative dataset from each modality for visualization, and the behavior is consistent across different datasets.

combination, and the computing resources needed are detailed in Table 3.

#### 4.1.2 Results

Figure 4 shows the performance of various task-specific fine-tuning approaches across each dataset and the performance of various UNet-based algorithms. The detailed results of each architecture-component-method fine-tuning strategy over 17 datasets can be found in the Appendix. Note that we provide the numerical results for all figure-based results in the Appendix. By comparing the red and blue bars, we first observe an almost definite (except in the ViT-B + Vanilla setting) improvement in the average performance when changing from only updating the decoder parameters to that of both the encoder and decoder. This discovery indicates that SAM’s original image encoder, initially trained on a vast collection of natural images, is not well-suited for efficiently extracting features from medical images, aligned with previous studies [61]. Therefore, freezing it and directly adapting the mask decoder for downstream tasks in the medical domain results in sub-optimal performance.

When comparing the performances among Vanilla, Adapter, and LoRA, we observe little difference between the two PEFT methods (Adapter and LoRA), and the rank be-

tween Vanilla and PEFT methods depends on the choices of backbones. When using the standard-size backbone (ViT-H or ViT-B), we observe an absolute advantage of using PEFT techniques. For example, when comparing the middle three blue bars in Figure 4, we observe using PEFT with Adapter or LoRA achieves 77.35% and 78.93% DSC respectively, while vanilla fine-tuning yields only 65.39% DSC. We also conduct an additional study to insert the Adapter block after each layer and observe little difference. However, the difference between vanilla fine-tuning and PEFT is significantly reduced when using ViT-T, the small backbone introduced by MobileSAM [94]. We hypothesize the large gap between Vanilla and PEFT methods with a standard-size backbone is caused by the model collapse and knowledge-forgotten issues when fine-tuning all parameters of a large model [23, 26]. To support our hypothesis, we track the change of validation DSC on all datasets, and the examples of each modality are shown in Figure 5. It reveals that ViT-H + En/Decoder + Vanilla would cause a model collapse at an early stage. For instance, when applied to the MRI-BrainDuke dataset, this configuration results in a significant reduction in performance, with a decrease of approximately 35% in DSC.

Next, our results reveal that the choice of encoder network architecture has minimal impact on performance when other choices remain the same. For instance, under the

same settings of updating both encoder and decoder with Adapter (EN/Decoder + Adapter), we observe similar DSC scores across different encoders: ViT-H, ViT-B, and ViT-T. This similarity in performance occurs despite ViT-H having a significantly larger encoder with 6.8 times network parameters compared with ViT-B and 64 times parameters compared with ViT-T, as listed in Table 3. We deduce that while ViT-H excels in foundational settings for multiple segmentation tasks, it may be too parameter-rich for singular medical imaging segmentation tasks, given the typically smaller dataset sizes in the medical imaging field. Such property can also make the training difficult. As shown in Figure 5 top right, it takes 140 epochs to train the ViT-H + En/Decoder + Adapter setting, which is approximately 30 times longer when conducting the same setting with ViT-B, yet the latter gives slightly better performance (80.53% DSC vs. 81.21% DSC when using ViT-H and ViT-B as the backbone respectively). Given the uniform results across our 17 datasets, we deduce that using PEFT (Adapter or LoRA) to fine-tune SAM within a smaller framework offers more benefits. This strategy strikes an optimal balance between efficiency and performance, especially for medical image segmentation tasks where datasets typically range from a couple hundred to tens of thousands of images.

Lastly, when comparing the results of automated segmentation by directly training on UNets, we observe that fine-tuning SAM with the En/Decoder generally yields better average performance. To further study the optimal performance across individual datasets, we select the best SAM-based method (ViT-H+LoRA+En/Decoder) vs. the best UNet-based method (nnUNet) in Figure 4, right block. It appears that SAM excels in tasks where the objects of interest are complicated, such as MRI-Brain Sclerosis or CT-Colon. Conversely, nnUNet demonstrates higher precision in tasks with simpler targets, including Xray-Hip or MRI-Kidney.

## 4.2. Is task-expansive prompt-based learning helpful for further automated segmentation?

As discussed in Section 2.3, we utilize an interactive segmentation setting for task-expansive prompt-based learning. In this section, we provide the implementation details and analysis of its performance.

### 4.2.1 Implementation details

When implementing task-expansive prompt-based learning, we utilized a collection of datasets and their corresponding masks. Our experimental setup focused on training with all MRI datasets listed in Table 2 except “MRI-Knee”. In this collection criteria, we include 13 MRI datasets including 45k training image and non-empty mask pairs, and 7.9k evaluation images and mask pairs. We selected ViT-B as

the encoder architecture since (1) it achieved similar performance to ViT-H in the data-specific fine-tuning setting; (2) MobileSAM was a distilled version of SAM which was not provided by initial SAM and thus less representative.

Under this multi-dataset supervised training setting, we configured a batch size of 3, utilizing DDP across 3 A6000 GPUs for training. The training was stopped when the validation performance was not improved for 5 epochs. To train the network, we fixed the prompt encoder and updated the image encoder and mask decoder in a vanilla setting (same as SAM’s supervised training stage). We generated a box or point prompt for each image as described in Section 2.3. Additionally, in this setting, we incorporated MedSAM [59] as a parallel approach since its training algorithm was similar to the proposed task-expansive prompt-based learning but with a different database.

In this experimental setup, our methodology follows a two-phase procedure, depicted in Figure 1 Setup 2: (1) Phase 1: task-expansive prompt-based learning. (2) Phase 2: task-specific supervised training for each dataset, beginning from pre-trained weights. We name the weights after phase 1 as **SupSAM**. The implementation details in the task-specific setting were identical to those of the previous section (Section 4.1). In phase 2, we had 2 model component choices (En/Decoder or Decoder only) and 3 Vanilla/PEFT choices in the automated setting. We evaluated the final automated segmentation performance after phase 2.

### 4.2.2 Results

The results are shown in Figure 6 and Figure 7, in which we list the performance of the original method when starting from SAM’s initial weights in gray. We further illustrate the difference, highlighted in green (when positive) or red (if negative), when changing the initial weights from the original SAM to those acquired from task-expansive prompt-based learning or MedSAM, respectively. When task-specific supervised training is applied solely to the decoder (the upper 3 blocks in both figures), we observe a consistent performance decrease in both scenarios. Since in this case, phase 2 fine-tuning is applied exclusively to the decoder, it appears that weights learning through supervised training fail to adequately prepare the image encoder with the medical imaging domain knowledge necessary for automated feature extraction. Thus, attempting to conserve computational resources while starting with a publicly available, prompt-based medical model, such as MedSAM, becomes unnecessary if the goal is to update only the small decoder for customized datasets.

When fine-tuning both the encoder and decoder during phase 2 task-specific supervised training (Figure 6 and 7, bottom 3 blocks), we observe either a negative or no ef-

## The impact on using different supervised learning weights: SAM vs. SupSAM

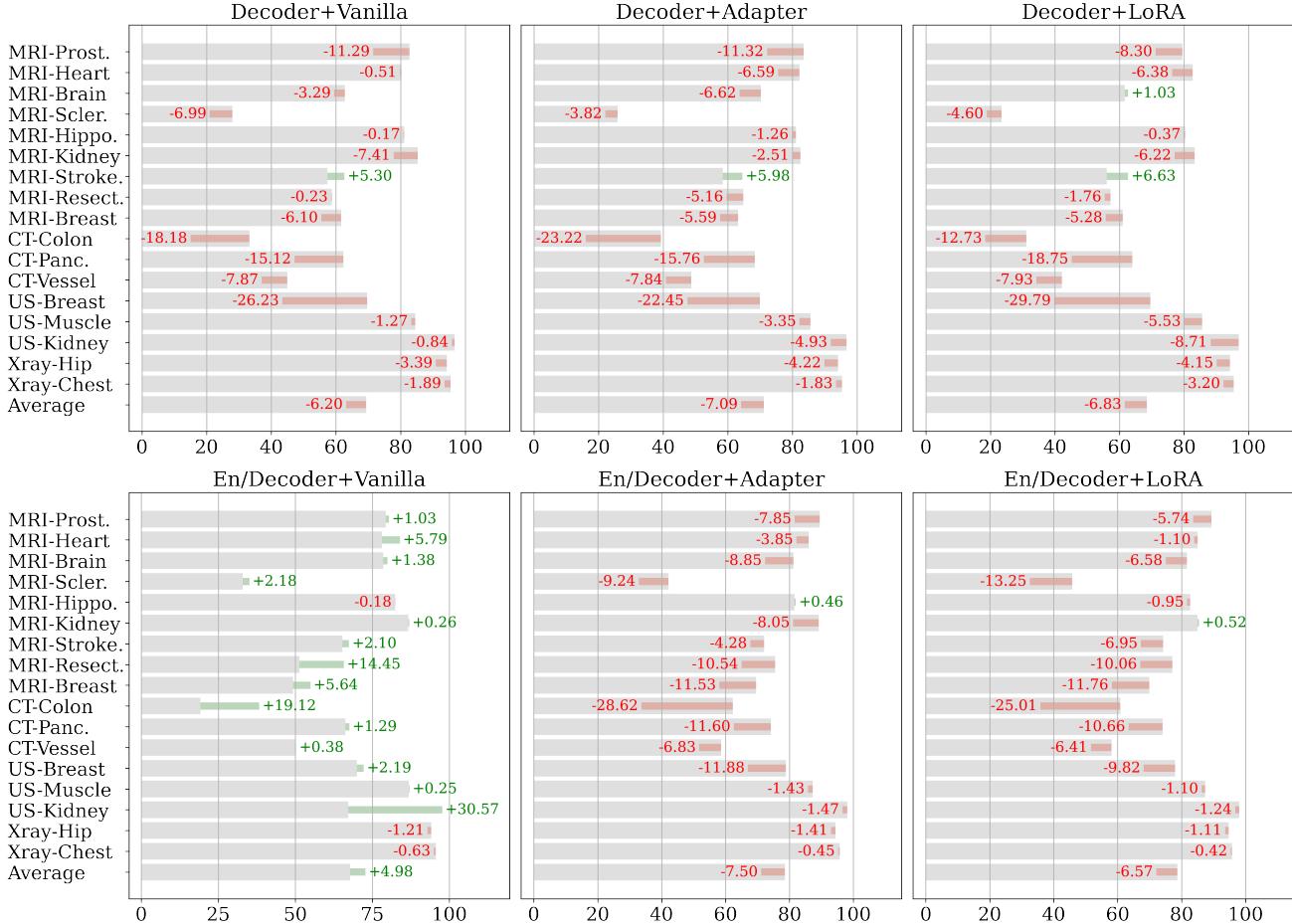


Figure 6. The performance of applying various task-specific supervised training strategies to SAM (in gray), and the performance difference of switching from SAM’s initial weights to ones learned through SupSAM, weights learned through task-expansive prompt-based learning (in red or green).

fect when utilizing a different pre-trained weights when using PEFT methods and a positive effect when using Vanilla fine-tuning. However, the latter setting leads to worse overall performance and thus offers little practical value. Despite the decrement being alleviated when using MedSAM, the overall trend shows the ineffectiveness of prompt-based learning when the ultimate goal is automated segmentation (MedSAM has around 34 times larger training set yet results in no performance change at best). We infer that the observed performance enhancement in En/Decoder-Vanilla is attributed to supervised pre-training potentially nudging the weights closer to the medical domain, thereby reducing the likelihood of model collapse. Nonetheless, given that this configuration still results in the lowest segmentation performance compared to the PEFT setting, this improvement does not offer practical benefit.

Our research indicates that supervised pre-training across various labeled medical images, despite working well in the original setting (MedSAM [59] is verified in its paper and ours is verified in Section 4.2), fails to enhance automated segmentation performance. We believe the ineffectiveness of additional supervised pre-training is due to the difference in the tasks: (1) The weights learned from interactive (prompt-based) mode vs. automated mode might be different and could not commute with each other effectively. Additionally, extended pre-training might disrupt the original weights’ transferability. (2) Furthermore, training the network on multiple segmentation tasks simultaneously could lead to conflicts within the training process thus making the training more challenging.

## The impact on using different supervised learning weights: SAM vs. MedSAM

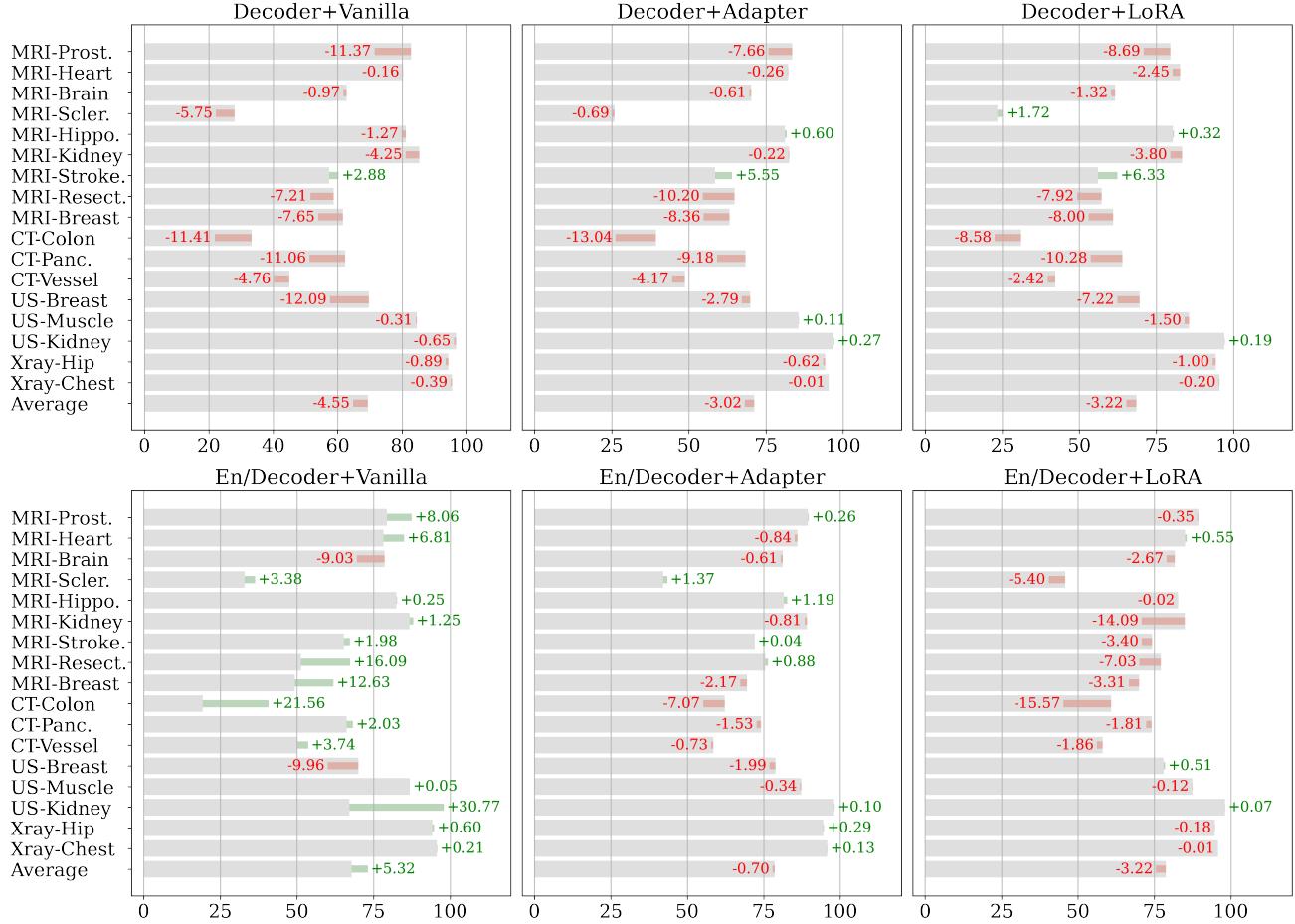


Figure 7. The performance of applying various task-specific supervised training strategies to SAM (in gray), and the performance difference of switching from SAM’s initial weights to ones learned through MedSAM [59] (in red or green).

### 4.3. Is task-agnostic self-supervised learning helpful for further automated segmentation?

As discussed in Section 2.4, we select masked autoencoder (MAE) as the method for task-agnostic self-supervised learning. In this section, we provide the implementation details and analyze its performance.

#### 4.3.1 Implementation details

In this stage, all MRI datasets in Table 2 were used during training. The mask information was ignored and only the images from the training set were utilized. Blank slices were further removed since they were not informative for the reconstruction task. This resulted in 159, 104 images for training.

Following the previous section, we only select ViT-B as the encoder architecture. To employ MAE’s objective,

we introduced an additional decoder to reconstruct the inputs, which was discarded after training. The additional decoder’s structure, mask ratio, and learning rate schedule all follow that of the original paper. Since the shape of SAM’s input was restricted to  $1024 \times 1024$ , we set the batch size to 2. To accommodate for the small batch size, we set the accumulative iteration, *i.e.* the number of iterations to only compute gradients without updating the network parameters, to 16. The training was conducted on 8 A6000 for 50 epochs.

In this experimental setup, our methodology follows a similar two-phase procedure: (1) Phase 1: task-agnostic self-supervised learning. (2) Phase 2: task-specific supervised training for each dataset, beginning from pre-trained weights. We name the weights after phase 1 as **SSLSSAM**, which is shared publicly at <https://github.com/mazurowski-lab/finetune-SAM>.

The impact on using supervised learning weights vs. self-supervised learning weights:

### SAM vs. SSLSAM

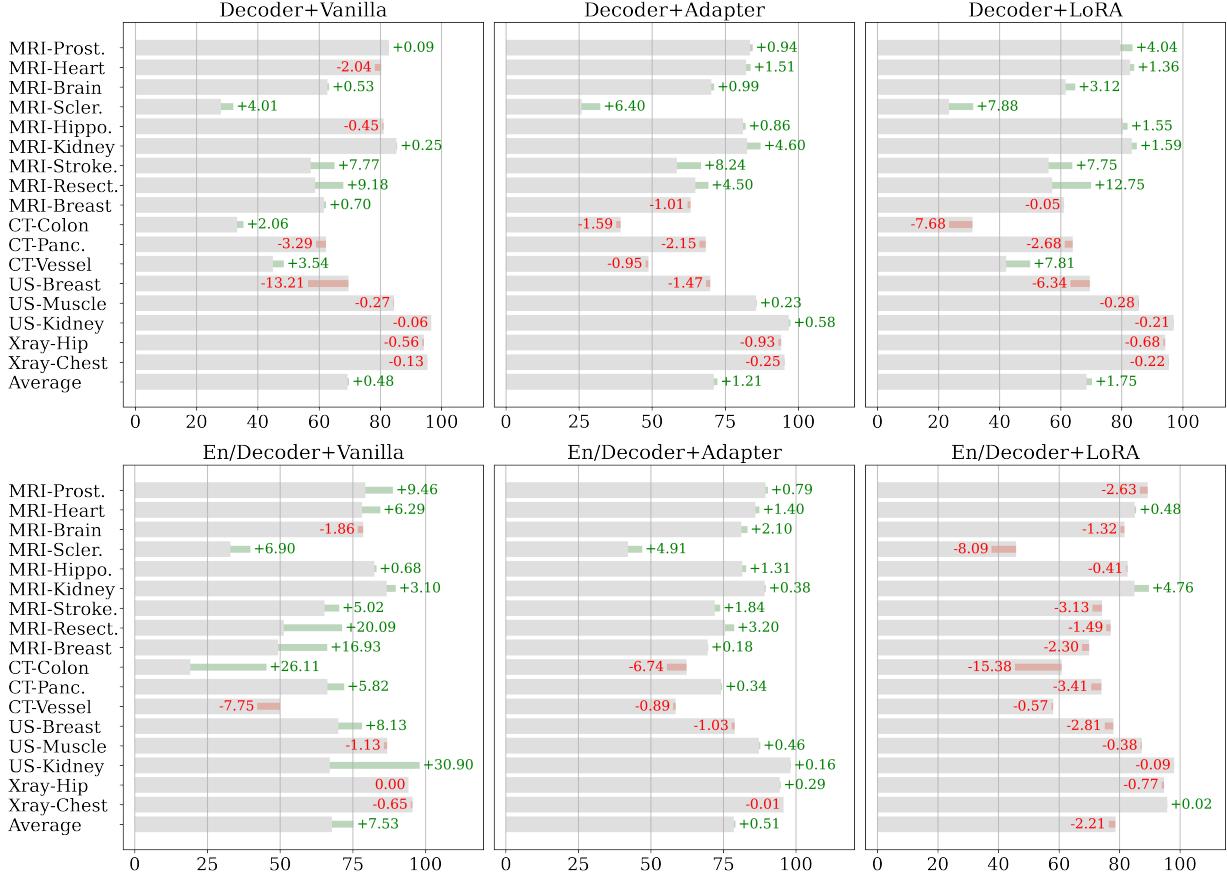


Figure 8. The performance of applying various task-specific supervised training strategies to SAM (in gray), and the performance difference of switching from SAM’s initial weights to ones learned through SSLSAM, weights learned through task-agnostic self-supervised learning (in red or green).

#### 4.3.2 Results

Figure 8 presents the results of using SSLSAM as the weights before task-specific supervised training. We observe an improvement in the average performance of all MRIs across all architecture combinations besides En/Decoder + LoRA. Noticeably, when selecting En/Decoder + Adapter as the fine-tuning strategy, we observe consistent improvements over all MRI datasets, and the model achieves an average performance of 78.09%, which surpasses the leading ViT-H based method by 1.08% and the best UNet-based method (nnUNet) by 3.58%. Contradictory to task-expansive prompt-based learning, the features learned during SSL are task agnostic, and since we only pre-train the encoder, there is no dependence on the task condition, which we have shown to hurt the performance. In the non-MRI data sets base, we observe a minor decrease in performance. This may be due to the specificity of the MRI.

#### 4.4 Which fine-tuning setup works the best in the few-shot learning setting?

##### 4.4.1 Implementation details

One of the popular scenarios for adopting fine-tuning strategies is when the target dataset has a limited number of annotated images, known as few-shot fine-tuning. Few-shot fine-tuning gets even more attention in the field of medical imaging segmentation, given the difficulty in securing a substantial quantity of expert annotations. We explore the effectiveness of different fine-tuning procedures in the following setting.

Our study primarily investigates 5-shot learning, selecting five images and their corresponding annotations randomly from the training set and validation set, respectively. In the case of datasets derived from 3D volumes, these samples were chosen from distinct volumes to ensure diversity. In addition to the constraint of using only 5 train-

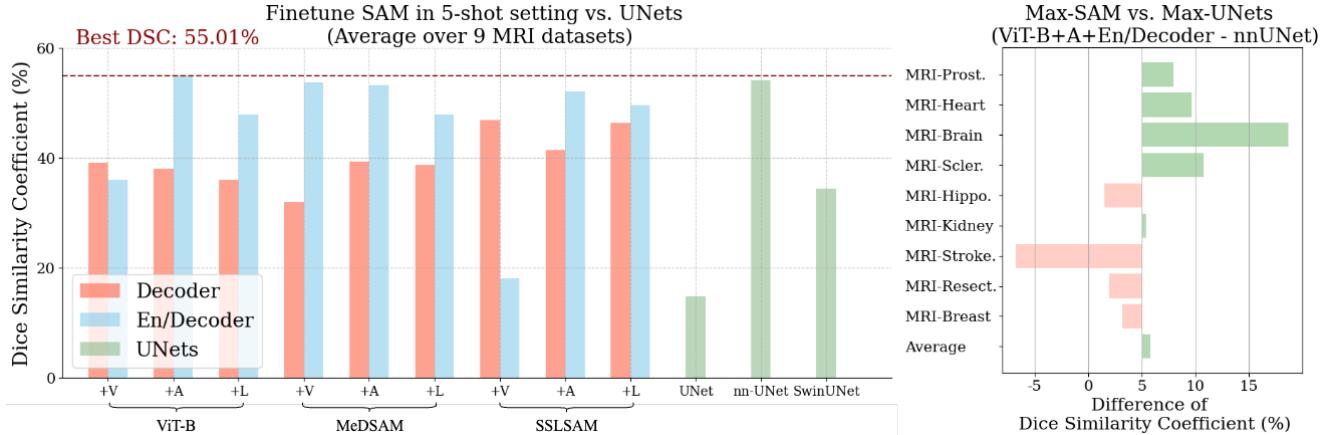


Figure 9. Left: Visualization of the performance of fine-tuned models compared with UNets in 5-shot setting (Section 4.4). Right: Difference between the best fine-tuned SAM model (ViT-B-A-En/Decoder) and the best UNet-based model (nnUNet) across individual datasets.

ing/validation images, we also modified the training hyperparameters better suited for the few-shot setting. Specifically, we set a maximum of 1000 epochs for training, a batch size of 2, and did not include any early stopping criteria.

In this setting, we also investigated the previous three setups within a few-shot framework, including (1) task-specific fine-tuning exclusively, and (2) two pre-trained setups: task-expansive prompt-based learning and task-agnostic self-supervised learning, each followed by additional task-specific fine-tuning. Notably, we cannot use the weights learned from task-expansive prompt-based learning as its training pipeline requires all labeled images. Thus, we consider the MedSAM weights as an alternative. In this section, we investigate three key questions: (1) whether additional pre-training offers superior initial weights for the few-shot setting, (2) which fine-tuning strategy proves most effective in a few-shot context, and (3) whether fine-tuning foundation models still work better than UNets in the few-shot setting?

#### 4.4.2 Results

Figure 9 shows the results for 5-shot setting, comparing the fine-tuning of SAM’s models with direct training on UNets. The results demonstrate that using ViT-B + En/Decoder + Adapter on the initial SAM yields optimal performance across all configurations. Comparing the results with UNets’, especially with the best-performing nnUNet, fine-tuned SAM still manages to achieve a slight improvement. This observation aligns with the findings presented in Section 4.1.

Consistently, the observation that MedSAM is ineffective persists in this few-shot scenario. While SSLSAM has

shown effectiveness in the full-dataset setting, its efficacy diminished and even became detrimental in the few-shot scenario. This observation aligns with the understanding that the task-agnostic training disrupts the model’s connection with the segmentation tasks. While beneficial as initial weights for full-dataset training, this approach may not adequately rebuild these connections with only five images, resulting in lower performance. In summary, we observe the ineffectiveness of additional pre-training (either using task-expansive prompt-based learning or task-agnostic self-supervised learning) with limited training data. This can be contradictory to the common belief that imposing medical knowledge to the network in advance will be beneficial in the few-shot learning scenario.

#### 4.5. What if I can provide prompts to SAM?

Despite the primary goal of this paper is to find the best practice to build an automated segmentation algorithm from the foundation models, we conduct a non-trivial extension that studies the effectiveness of various task-specific supervised training strategies in the interactive segmentation setting.

##### 4.5.1 Implementation details

We considered two types of prompts: point or box. To generate a prompt, we utilized the same strategy as in task-expansive prompt-based learning. The generated prompts were fed to the prompt encoder to obtain the prompt embeddings during both training and inference. The prompt encoder was fixed. We also limited the evaluation data to MRI only since this task was not our main focus.

We included the performance of applying prompts to the original SAM and its oracle performance; the latter reflects

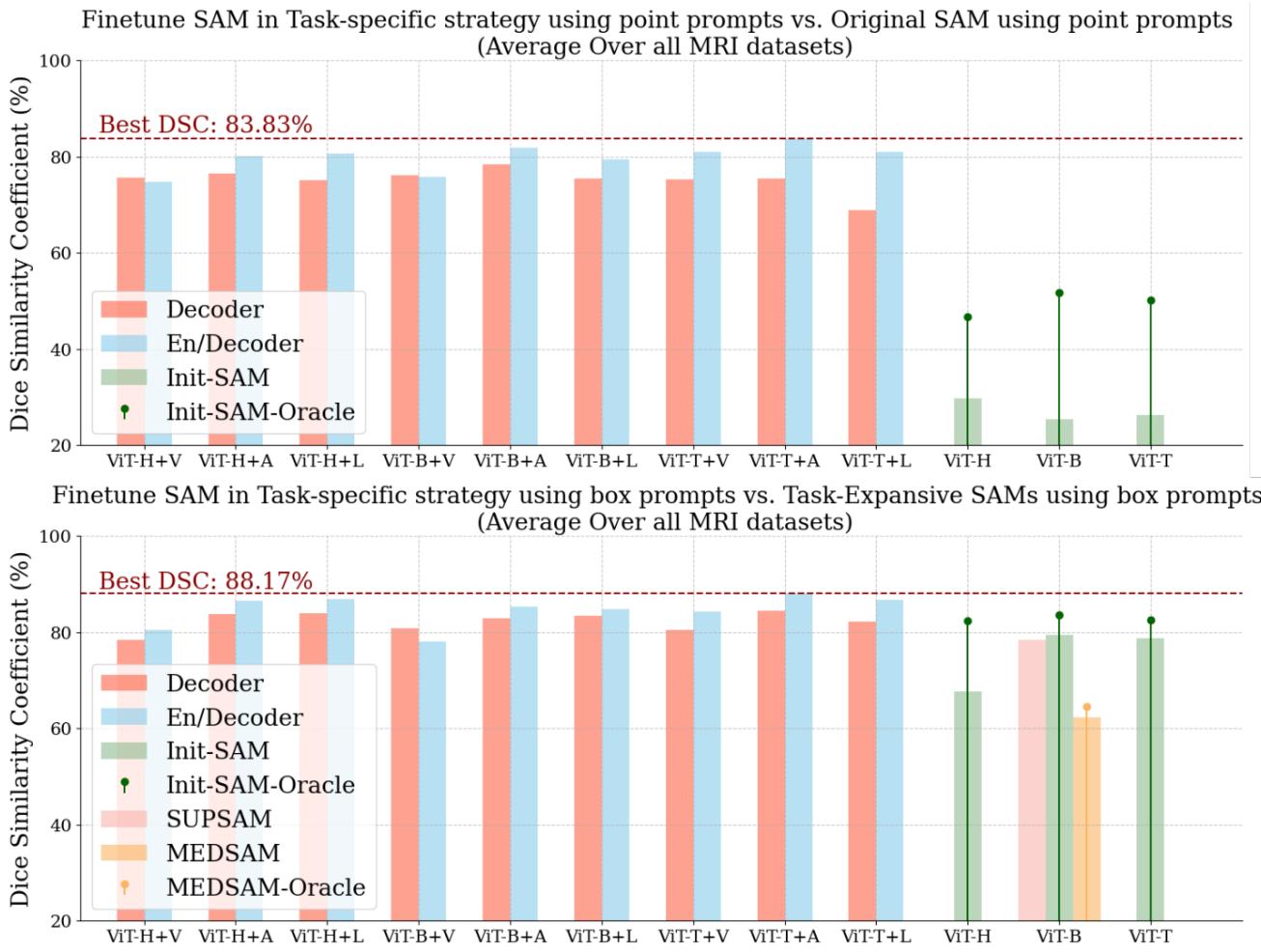


Figure 10. Performance of the task-specific fine-tuning strategies and initial SAM when using point/box prompts.

the hypothetical performance when conducting an extra step to determine the best prediction from the network. Additionally, we include weights acquired from task-expansive prompt-based learning and MedSAM in the box-prompt setting. When applying task-specific supervised training to SAM, we followed Section 4.1 to include all strategies.

#### 4.5.2 Results

Figure 10 shows the performance of all task-specific supervised training strategies in the interactive mode, as well as that of the original SAM as a reference. First, we observe the performance of SAM with point prompts is not satisfying. Replacing the point prompts with box ones significantly improves the performance. In this setting, we also examine the weights acquired from task-expansive prompt-based learning and observe similar performance (less than 0.92% DSC difference compared to that of the initial SAM). This observation confirms that the inefficiency of task-

expansive prompt-based learning is inherently from having different tasks in mind.

To be noted, the best automated task-specific supervised training strategy yields an average performance of 77.01% on all MRI datasets, which is better than the original SAM with point prompts and on par with that with box prompts.

Conducting task-specific supervised training is also shown to be effective in the interactive segmentation scenario, especially when points are used as the prompts. Moreover, we find the best task-specific supervised training strategy is ViT-T + En/Decoder + Adapter in both scenarios, achieving 83.83%/88.17% DSC when using a point/box as the prompt.

## 5. Conclusion

In summary, we systematically study different strategies to fine-tune the Segment Anything Model (SAM) in the medical imaging field. Our extensive experiments re-

veal several interesting observations and provide a guideline for developing an automated segmentation algorithm from SAM. Our findings are based on dataset availability, and are summarized as follows:

When only a single dataset is available for fine-tuning, we find that:

1. Fine-tuning SAM, if with proper strategies, leads to better segmentation performance than training from scratch with nnUNet [40].
2. Increasing the size of network architecture leads to a marginal increase in segmentation performance while exponentially longer training time.
3. Using parameter-efficient fine-tuning (PEFT) techniques has a clear advantage over fine-tuning all parameters on medium-to-large-size architectures (ViT-H or ViT-B) but not on the small architecture (ViT-T).
4. Optimizing both the encoder and decoder (En/De) has clear advantages over only the decoder, with the latter being a popular choice in the literature.
5. In summary, we recommend using **ViT-B + En/Decoder + PEFT** as the fine-tuning framework because of its leading performance and moderate computation cost.

When having multiple datasets, we can incorporate general medical knowledge into SAM through additional pre-training, and find that:

1. Using additional labeled data for other tasks with prompt-based learning is an inefficient strategy to further improve SAM's performance.
2. Using additional unlabeled data with self-supervised learning can improve SAM's performance when the test data is from the same modality as the pre-trained data and has no effect otherwise.

When we adjust the fine-tuning task into few-shot learning, we find that:

1. Fine-tuning SAM significantly outperforms UNet, and still maintains a slight improvement compared with nn-UNet in the 5-shot setting.
2. Additional task-expansive prompt-based learning or task-agnostic self-supervised learning do not contribute to improvements in the final few-shot learning task.

Lastly, in the interactive segmentation scenario, we observe that:

1. Fine-tuned SAM brings substantial performance improvements compared to SAM and MedSAM in the interactive segmentation setting.
2. Our recommendation framework is **ViT-T + En/Decoder + PEFT** given its superior performance and low computation cost.

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## 6. Graphic Abstract

We provide a graphic abstract in Figure 11 for better understanding.

## 7. Appendix

In the appendix, we provide the numerical results of all experiments.

Tables 4, 5, 6 present the results of applying task-specific supervised training to ViT-H, ViT-B, and ViT-T respectively, and table 7 shows the performance of UNets. Figure 4 summarizes the results of these 4 tables.

Tables 8, 9, 10 show the performance of replacing SAM’s weights with SupSAM (acquired from task-expansive prompt-based learning), MedSAM (from [59]), and SSLSAM (acquired from task-agnostic self-supervised learning) respectively. Since all weights utilize the same encoder architecture (ViT-B), we show the difference by conducting Table 5 minus the corresponding table in Figure 6, 7, and 8 respectively.

Tables 12 and 11 show the performance of applying task-specific supervised training in the few-shot learning setting, which is summarized in Figure 9.

Tables 13 shows the performance of initial SAM in the point-based segmentation setting, with tables 14, 15, and 16 shows applying task-specific supervised training in the same setting. Tables 17, 18, 19, and 20 are conducted in the same setting but with box as the prompt. All results are summarized in Figure 10.

Dataset	ViT-H							
	Decoder			En/Decoder				
	V	A	L	V	A	A*	L	
MRI-Prost.	82.58	82.42	78.60	73.56	88.97	88.80	89.64	
MRI-Heart	80.86	80.61	80.53	73.69	77.90	86.22	85.07	
MRI-Brain	45.32	60.19	50.87	53.89	80.53	82.65	84.09	
MRI-Scler.	21.16	22.01	22.51	27.81	42.74	48.44	47.24	
MRI-Hippo.	81.25	80.30	79.01	81.22	81.61	82.56	83.33	
MRI-Kidney	82.34	84.08	82.82	87.65	88.81	90.29	83.02	
MRI-Stroke.	47.52	53.06	47.22	56.51	71.64	67.82	72.39	
MRI-Resect.	43.96	60.09	54.23	57.26	75.03	67.77	76.62	
MRI-Breast	59.48	61.10	59.05	61.78	69.00	69.11	71.71	
CT-Colon	22.67	35.08	26.77	24.12	55.44	54.30	60.91	
CT-Panc.	61.78	67.43	64.06	64.45	73.92	73.01	75.74	
CT-vessel.	40.94	44.75	42.15	40.96	58.16	54.67	58.53	
US-Muscle	84.50	85.52	85.05	86.66	86.16	86.92	87.49	
US-Kidney	96.97	97.08	96.53	67.12	98.13	98.34	98.18	
Xray-Hip	93.78	94.35	93.00	92.02	93.96	94.33	94.73	
Xray-Chest	95.29	95.35	95.22	94.85	95.81	95.45	95.74	
Average	65.36	69.24	66.34	65.39	77.35	77.58	78.93	

Table 4. The performance of SAM under different fine-tuning strategies in the automated mode across different datasets. V = vanilla, A = Adapter, L = LoRA. A\* is a variant of A in which we applied Adapter after each network layer.

Dataset	ViT-B							
	Decoder			En/Decoder				
	V	A	L	V	A	L		
MRI-Prost.	82.77	83.44	79.51	79.36	89.50	89.37		
MRI-Heart	80.29	82.16	82.72	78.16	79.28	85.04		
MRI-Brain	62.73	70.23	61.65	78.57	81.21	81.65		
MRI-Scler.	27.95	25.92	23.44	32.90	42.12	45.83		
MRI-Hippo.	81.08	81.09	80.35	82.45	81.52	82.69		
MRI-Kidney	85.29	82.50	83.32	86.70	89.19	84.93		
MRI-Stroke.	57.33	58.47	56.05	65.32	72.05	74.24		
MRI-Resect.	58.74	64.76	57.23	51.28	75.53	71.23		
MRI-Breast	61.60	63.16	61.02	49.30	69.54	69.95		
CT-Colon	33.25	39.29	31.12	19.18	62.30	60.87		
CT-Panc.	62.28	68.34	63.97	66.25	74.16	74.07		
CT-vessel.	44.95	48.71	42.16	49.89	58.56	58.08		
US-Breast	69.64	69.93	69.56	70.02	78.87	77.97		
US-Muscle	84.53	85.53	85.61	86.80	87.24	87.37		
US-Kidney	96.70	96.76	96.99	67.12	98.08	98.05		
Xray-Hip	94.29	94.11	94.27	94.14	94.44	94.73		
Xray-Chest	95.45	95.29	95.45	95.58	95.73	95.78		
Average	69.35	71.16	68.50	67.82	78.59	78.69		

Table 5. The performance of SAM under different fine-tuning strategies in the automated mode across different datasets. V = vanilla, A = Adapter, L = LoRA.

Dataset	ViT-B							
	Decoder			En/Decoder				
	V	A	L	V	A	L		
MRI-Prost.	81.36	80.01	77.17	88.90	89.37	86.70		
MRI-Heart	80.75	80.39	76.24	85.15	84.93	84.35		
MRI-Brain	52.68	58.43	28.12	78.32	79.42	77.14		
MRI-Scler.	21.20	18.22	15.29	42.60	41.05	41.92		
MRI-Hippo.	78.97	78.39	76.00	82.90	82.96	82.56		
MRI-Kidney	82.49	79.93	67.54	89.85	88.39	88.38		
MRI-Stroke.	42.13	46.35	34.08	71.02	72.14	70.37		
MRI-Resect.	40.35	40.56	37.10	74.34	75.74	72.93		
MRI-Breast	53.06	52.89	45.23	66.92	68.28	66.18		
CT-Colon	14.97	23.09	23.16	55.99	53.76	49.63		
CT-Panc.	59.01	64.54	55.43	72.08	73.21	70.36		
CT-vessel.	37.25	36.55	32.25	56.62	57.25	55.09		
US-Breast	61.42	67.38	49.64	77.55	74.50	71.15		
US-Muscle	84.68	85.50	59.94	86.72	86.71	87.18		
US-Kidney	96.11	96.37	92.60	97.45	98.06	97.88		
Xray-Hip	94.07	93.83	91.04	92.33	94.33	94.61		
Xray-Chest	95.08	95.26	91.50	95.87	95.75	95.72		
Average	63.27	64.57	56.02	77.33	77.40	76.01		

Table 6. The performance of SAM under different fine-tuning strategies in the automated mode across different datasets. V = Vanilla, A = Adapter, L = LoRA.

## How to build the best medical image segmentation algorithm using foundation models: a comprehensive empirical study with Segment Anything Model

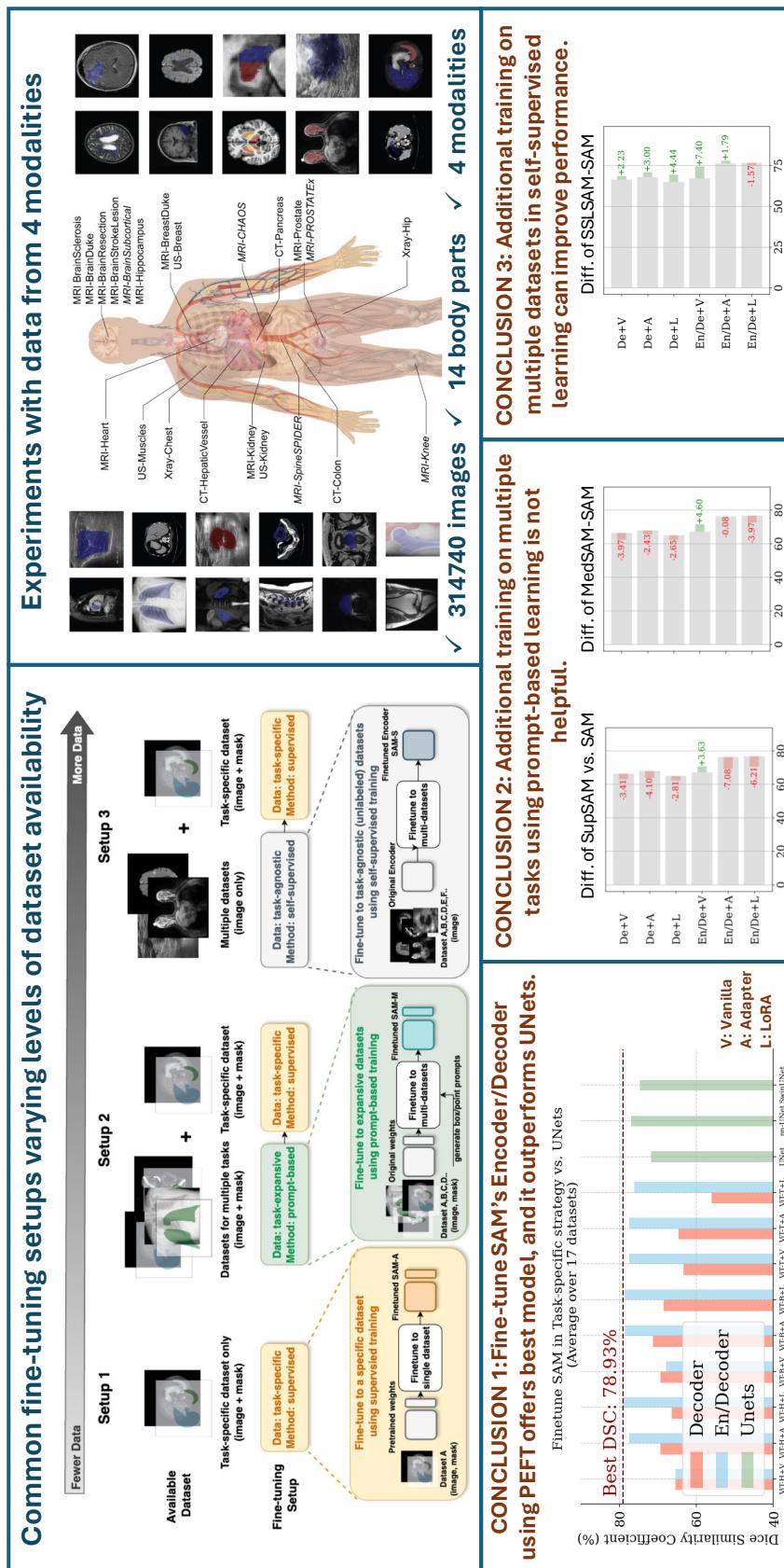


Figure 11. The graphical abstract for the paper.

Dataset	UNet	nnUNet	SwinUNet
MRI-Prost.	82.59	81.98	82.03
MRI-Heart	82.85	87.14	84.10
MRI-Brain	79.00	74.13	75.83
MRI-Scler.	2.95	40.56	36.73
MRI-Hippo.	80.59	76.18	83.25
MRI-Kidney	87.03	91.69	83.83
MRI-Stroke.	69.67	72.27	70.45
MRI-Resect.	68.15	74.15	65.91
MRI-Breast	58.68	72.49	70.33
CT-Colon	43.64	47.58	46.39
CT-Panc.	70.06	74.78	68.54
CT-vessel.	57.06	58.44	56.06
US-Breast	64.83	76.03	72.02
US-Muscle	83.99	87.30	86.62
US-Kidney	96.74	98.37	97.75
Xray-Hip	94.36	98.46	94.29
Xray-Chest	95.51	96.40	95.62
Average	71.63	76.94	74.69

Table 7. The performance of UNet, nnUNet, and SwinUNet across different datasets.

Dataset	ViT-B					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	71.48	72.12	71.21	80.39	81.65	83.63
MRI-Heart	79.78	75.57	76.34	83.95	82.16	83.94
MRI-Brain	59.44	63.61	62.68	79.95	72.36	75.07
MRI-Scler.	20.96	22.10	18.84	35.08	32.88	32.58
MRI-Hippo.	80.91	79.83	79.98	82.27	81.98	81.74
MRI-Kidney	77.88	79.99	77.10	86.96	81.14	85.45
MRI-Stroke.	62.63	64.45	62.68	67.42	67.77	67.29
MRI-Resect.	58.51	59.60	55.47	65.73	64.99	67.07
MRI-Breast	55.50	57.57	55.74	54.94	58.01	58.19
CT-Colone	15.07	16.07	18.39	38.30	33.68	35.86
CT-Panc.	47.16	52.58	45.22	67.54	62.56	63.41
CT-Vessel	37.08	40.87	34.23	50.27	51.73	51.67
US-Breast	43.41	47.48	39.77	72.21	66.99	68.15
US-Muscle	83.26	82.18	80.08	87.05	85.81	86.27
US-Kidney	95.86	91.83	88.28	97.69	96.61	96.81
Xray-Hip	90.90	89.89	90.12	92.93	93.03	93.62
Xray-Chest	93.56	93.46	92.25	94.95	95.28	95.36
Average	63.14	64.07	61.67	72.80	71.10	72.12

Table 8. The performance of applying various task-specific supervised training to SSLSAM, weights acquired from task-expansive prompt-based learning.

Dataset	MedSAM					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	71.40	75.78	70.82	87.42	89.76	89.02
MRI-Heart	80.13	81.90	80.27	84.97	85.17	85.59
MRI-Brain	61.76	69.62	60.33	69.54	80.60	78.98
MRI-Scler.	22.20	25.23	25.16	36.28	43.49	40.43
MRI-Hippo.	79.81	81.69	80.67	82.70	82.71	82.67
MRI-Kidney	81.04	82.28	79.52	87.95	88.38	70.84
MRI-Stroke.	60.21	64.02	62.38	67.30	72.09	70.84
MRI-Resect.	51.53	54.56	49.31	67.37	76.41	70.10
MRI-Breast	53.95	54.80	53.02	61.93	67.37	66.64
CT-Colone	21.84	26.25	22.54	40.74	55.23	45.30
CT-Panc.	51.22	59.16	53.69	68.28	72.63	72.26
CT-Vessel	40.19	44.54	39.74	53.63	57.83	56.22
US-Breast	57.55	67.14	62.34	60.06	76.88	78.48
US-Muscle	84.22	85.64	84.11	86.85	86.90	87.25
US-Kidney	96.05	97.03	97.18	97.89	98.18	98.12
Xray-Hip	93.40	93.49	93.27	94.74	94.73	94.55
Xray-Chest	95.06	95.28	95.25	95.79	95.86	95.77
Average	64.80	68.14	65.27	73.14	77.90	75.47

Table 9. The performance of applying various task-specific supervised training to MedSAM, weights acquired from [59].

Dataset	SSLSAM					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	82.86	84.38	83.55	88.82	90.29	86.74
MRI-Heart	78.25	83.67	84.08	84.45	87.41	85.52
MRI-Brain	63.26	71.22	64.77	76.71	83.31	80.33
MRI-Scler.	31.96	32.32	31.32	39.80	47.03	37.74
MRI-Hippo.	80.63	81.95	81.90	83.13	82.83	82.28
MRI-Kidney	85.54	87.10	84.91	89.80	89.57	89.69
MRI-Stroke.	65.10	66.71	63.80	70.34	73.89	71.11
MRI-Resect.	67.92	69.26	69.98	71.37	78.73	75.64
MRI-Breast	62.30	62.15	60.97	66.23	69.72	67.65
CT-Colone	35.31	37.70	23.44	45.29	55.56	45.49
CT-Panc.	58.99	66.19	61.29	72.07	74.50	70.66
CT-Vessel	48.49	47.76	49.97	42.14	57.67	57.51
US-Breast	56.43	68.46	63.22	78.15	77.84	75.16
US-Muscle	84.26	85.76	85.33	85.67	87.70	86.99
US-Kidney	96.64	97.34	96.78	98.02	98.24	97.96
Xray-Hip	93.73	93.18	93.59	94.14	94.73	93.96
Xray-Chest	95.32	95.04	95.23	94.93	95.72	95.80
Average	69.82	72.36	70.24	75.36	79.10	76.48

Table 10. The performance of applying various task-specific supervised training to SSLSAM, weights acquired from task-agnostic self-supervised learning.

Dataset	ViT-B				MedSAM				SSLSAM			
	Decoder		En/Decoder		Decoder		En/Decoder		Decoder		En/Decoder	
	V	A	V	A	V	A	V	A	V	A	V	A
MRI-Prost.	68.15	66.77	73.11	45.47	57.93	58.73	70.20	71.73	67.46	62.69	73.88	69.67
MRI-Heart	62.55	56.94	72.34	19.14	59.65	64.70	66.28	67.93	68.90	69.00	61.30	35.30
MRI-Brain	38.29	31.54	60.31	49.32	43.01	17.10	64.50	64.16	50.19	31.62	55.09	0.09
MRI-Scler.	1.49	2.34	16.17	2.26	3.58	4.17	14.89	13.08	2.39	2.59	12.70	0.98
MRI-Hippo.	51.86	60.12	67.79	70.45	51.93	14.40	60.49	65.05	51.42	42.91	64.73	0.00
MRI-Kidney	74.45	74.46	76.21	67.70	66.98	68.40	74.20	77.95	66.70	73.90	77.10	0.00
MRI-Stroke.	15.46	8.59	25.54	25.20	15.79	11.60	34.02	31.28	26.60	14.03	25.50	31.60
MRI-Resect.	35.33	27.01	51.30	11.30	17.75	13.90	52.14	53.13	46.40	36.81	50.30	4.44
MRI-Breast	43.83	45.00	52.25	33.61	37.60	35.30	42.27	40.08	42.50	40.17	48.80	21.00
Average	43.49	41.42	55.00	36.05	39.36	32.03	53.22	53.82	46.95	41.52	52.16	18.12

Table 11. The performance of applying task-specific supervised training to the ViT-B architecture with different initial weights.

Dataset	UNet	nnUNet	SwinUNet
MRI-Prost.	6.34	70.13	2.67
MRI-Heart	1.26	67.69	59.94
MRI-Brain	6.49	46.60	53.69
MRI-Scler.	0.77	10.40	1.64
MRI-Hippo.	34.05	71.29	46.58
MRI-Kidney	47.95	75.81	47.51
MRI-Stroke.	2.01	37.30	38.99
MRI-Resect.	2.66	54.34	22.16
MRI-Breast	32.40	54.06	37.39
Average	14.88	54.18	34.51

Table 12. The performance of UNet, nnUNet, and SwinUNet across different datasets.

Dataset	ViT-H		ViT-B		ViT-T	
	H	O	H	O	H	O
MRI-Prost.	52.63	67.65	35.52	68.94	41.06	65.71
MRI-Heart	49.20	58.75	48.39	65.24	43.50	63.42
MRI-Brain	34.20	54.57	29.23	58.55	30.33	58.38
MRI-Scler.	1.80	3.91	1.58	5.28	1.72	4.50
MRI-Hippo.	34.78	55.15	17.34	59.33	22.20	59.94
MRI-Kidney	41.41	73.31	44.17	76.22	46.07	70.85
MRI-Stroke.	21.38	39.85	21.75	49.98	20.17	44.43
MRI-Resect.	27.86	45.84	17.38	60.82	26.07	55.89
MRI-Breast	5.00	21.61	12.83	21.81	5.00	28.57
Average	29.81	46.74	25.35	51.80	26.24	50.19

Table 13. The performance of SAM with different choices of encoder architectures with point prompts. H = Highest confidence, O = Oracle mode.

Dataset	ViT-H					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	87.74	86.89	86.82	79.84	89.55	88.10
MRI-Heart	84.77	85.07	86.46	83.77	85.60	86.40
MRI-Brain	74.44	72.87	72.66	74.15	80.76	75.09
MRI-Scler.	62.95	62.64	62.64	51.42	60.77	64.26
MRI-Hippo.	83.13	82.03	82.95	83.99	81.88	83.26
MRI-Kidney	88.49	87.37	89.06	89.31	86.87	92.01
MRI-Stroke.	61.18	66.09	60.47	73.87	78.22	81.52
MRI-Resect.	73.38	75.20	68.06	66.57	79.96	77.09
MRI-Breast	64.84	69.56	67.61	70.12	77.14	78.13
Average	75.66	76.41	75.19	74.78	80.08	80.65

Table 14. The performance of applying task-specific supervised training during point-based segmentation with ViT-H as the encoder architecture.

Dataset	ViT-B					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	87.23	87.22	87.10	88.54	89.57	87.48
MRI-Heart	84.90	85.20	84.98	86.04	87.54	85.41
MRI-Brain	76.05	76.48	77.71	73.82	83.70	77.61
MRI-Scler.	58.41	59.18	62.78	59.42	66.95	60.98
MRI-Hippo.	82.06	82.98	83.66	84.23	84.04	83.43
MRI-Kidney	89.34	89.04	86.93	88.81	90.80	89.77
MRI-Stroke.	69.08	69.67	52.63	72.62	79.19	78.12
MRI-Resect.	73.11	77.15	73.02	71.36	81.56	75.39
MRI-Breast	64.57	67.79	69.79	56.86	73.38	76.28
Average	76.08	77.19	75.40	75.74	81.86	79.39

Table 15. The performance of applying task-specific supervised training during point-based segmentation with ViT-B as the encoder architecture.

Dataset	ViT-T					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	87.76	84.06	78.06	90.46	90.81	84.38
MRI-Heart	85.19	85.50	79.28	87.72	88.03	86.60
MRI-Brain	74.38	72.63	59.00	84.12	85.78	83.98
MRI-Scler.	61.29	63.85	50.53	64.78	72.56	71.04
MRI-Hippo.	82.97	80.71	79.20	84.95	87.36	77.90
MRI-Kidney	88.30	87.60	81.25	91.12	91.48	89.69
MRI-Stroke.	63.80	65.78	64.84	76.22	81.61	81.21
MRI-Resect.	74.08	74.48	68.94	80.66	81.62	79.82
MRI-Breast	59.92	64.80	59.12	69.55	75.23	73.61
Average	75.30	75.49	68.91	81.06	83.83	80.91

Table 16. The performance of applying task-specific supervised training during point-based segmentation with ViT-T as the encoder architecture.

Dataset	ViT-H		ViT-B		ViT-T		MedSAM		SupSAM
	H	O	H	O	H	O	H	O	-
MRI-Prost.	87.09	91.60	89.75	92.20	88.50	90.99	87.02	92.51	91.82
MRI-Heart	67.29	85.62	83.03	85.96	83.49	86.82	73.99	75.73	83.74
MRI-Brain	73.44	84.51	81.74	85.48	81.70	84.50	77.13	78.32	80.57
MRI-Scler.	39.13	78.58	75.15	79.91	76.43	79.72	38.52	41.28	56.26
MRI-Hippo.	71.19	81.37	78.48	82.31	78.52	81.75	70.76	72.69	84.75
MRI-Kidney	87.51	89.58	87.84	90.02	87.40	89.31	70.36	72.44	87.46
MRI-Stroke.	55.97	81.09	78.14	82.21	77.50	82.15	55.88	57.95	78.06
MRI-Resect.	71.97	85.68	83.58	87.09	81.58	84.85	66.92	68.20	78.90
MRI-Breast	54.69	63.38	56.87	66.96	54.09	63.06	19.52	21.12	64.70
Average	67.59	82.38	79.40	83.57	78.80	82.57	62.23	64.47	78.47

Table 17. The performance of SAM with different choices of encoder architectures with box prompts. H = Highest confidence, O = Oracle mode. MedSAM and SupSAM is applicable since both utilize box during training.

Dataset	ViT-H					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	91.61	94.18	94.52	91.08	94.82	95.16
MRI-Heart	64.24	90.66	88.91	86.21	89.17	91.88
MRI-Brain	77.84	82.93	83.21	73.03	87.09	88.14
MRI-Scler.	62.29	73.70	74.06	62.53	74.84	72.18
MRI-Hippo.	84.95	86.02	88.32	88.14	88.61	89.45
MRI-Kidney	89.44	89.59	90.06	89.51	90.06	90.15
MRI-Stroke.	81.05	81.14	81.95	81.66	87.70	86.42
MRI-Resect.	81.66	81.29	81.47	83.23	86.93	87.70
MRI-Breast	72.91	74.71	72.89	69.55	79.70	80.68
Average	78.44	83.80	83.93	80.55	86.55	86.86

Table 18. The performance of applying task-specific supervised training during box-based segmentation with ViT-H as the encoder architecture.

Dataset	ViT-B					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	94.13	94.43	94.76	92.76	94.78	94.58
MRI-Heart	90.27	90.52	90.35	90.18	90.48	90.05
MRI-Brain	82.68	82.85	84.71	76.32	87.98	85.27
MRI-Scler.	68.58	71.80	69.12	61.74	69.43	72.00
MRI-Hippo.	86.38	87.02	89.04	85.89	88.24	88.68
MRI-Kidney	91.37	90.33	89.44	91.63	91.53	90.89
MRI-Stroke.	72.45	81.19	75.46	67.33	85.84	82.76
MRI-Resect.	77.15	77.35	83.83	76.86	84.91	85.49
MRI-Breast	64.57	69.88	73.70	59.66	74.00	73.14
Average	80.84	82.82	83.38	78.04	85.24	84.76

Table 19. The performance of applying task-specific supervised training during box-based segmentation with ViT-B as the encoder architecture.

Dataset	ViT-T					
	Decoder			En/Decoder		
	V	A	L	V	A	L
MRI-Prost.	93.37	94.45	94.07	93.51	94.98	94.13
MRI-Heart	88.75	91.26	90.10	90.50	91.02	91.05
MRI-Brain	78.92	82.23	79.38	84.15	88.69	88.01
MRI-Scler.	75.41	76.24	74.59	74.29	79.49	78.49
MRI-Hippo.	86.64	88.01	87.59	87.60	90.38	86.85
MRI-Kidney	90.27	89.37	87.13	92.15	92.33	91.22
MRI-Stroke.	70.94	81.77	81.40	81.44	89.33	88.13
MRI-Resect.	76.44	85.68	82.91	81.00	86.77	87.62
MRI-Breast	62.81	70.90	63.12	74.09	80.54	74.74
Average	80.39	84.43	82.25	84.30	88.17	86.69

Table 20. The performance of applying task-specific supervised training during box-based segmentation with ViT-T as the encoder architecture.