



OPEN Meta transfer learning for brain tumor segmentation using nnUNet in meningioma and metastasis cases

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In recent years, numerous algorithms have emerged for the segmentation of brain tumors, driven by advancements in deep learning techniques, where the objective is to identify and delineate various tumor sub-regions. While deep learning models like nnUNet have shown promising results in glioma segmentation, their effectiveness in segmenting other brain tumor subtypes, such as meningiomas and metastases, remains uncertain, especially when the available dataset lacks representative examples. To address this challenge, we propose a meta-transfer learning approach, which involves fine-tuning the nnUNet model on datasets containing meningiomas and metastases while leveraging the knowledge acquired from glioma segmentation. This approach aims to enhance the adaptability of nnUNet, allowing it to generalize better to diverse brain tumor types and potentially improving the accuracy of diagnosis and treatment planning for patients with meningiomas and metastases. Our proposed method significantly improves segmentation performance, achieving Dice coefficients of 0.8621 ± 0.2413 for Whole Tumor (WT) in meningiomas and 0.8141 ± 0.0562 for WT in metastases. These results set a new benchmark in brain tumor segmentation and pave the way for more robust and generalizable medical image analysis tools.

Keywords Brain tumor segmentation, nnUNet, BraTs2023, Meningioma, Metastasis, Meta-transfer learning

Brain tumor segmentation from magnetic resonance imaging (MRI) data is vital in medical image analysis, serving as a cornerstone for diagnosis, treatment planning, and patient monitoring¹. Among the various types of brain tumors, gliomas, meningiomas, and metastases are the three most prevalent, each possessing unique characteristics and imaging features that challenge existing segmentation techniques. While the literature on brain tumor segmentation is extensive, the majority of research has predominantly focused on gliomas, given their aggressive nature and high prevalence in adult populations². This focus has led to the development of sophisticated deep learning approaches, such as convolutional neural networks (CNNs) and U-Net-based architectures³, which have achieved remarkable results in glioma segmentation.

However, despite the success of these methods, other tumor types, particularly meningioma and metastasis, remain underexplored. The existing approaches typically leverage variations of the U-Net architecture, known for its encoder-decoder structure with skip connections that effectively capture multi-scale features and preserve fine details in segmentation tasks. Researchers have further enhanced the U-Net framework by integrating advanced techniques like residual connections⁴, attention mechanisms⁵, and region-based training tailored for brain tumor segmentation tasks. Additionally, there has been an emerging interest in transformer-based models, such as Swin UNETR⁶ and TranBTS⁷, which replace or augment traditional CNN-based approaches with transformer architectures that excel at modeling long-range dependencies within medical images.

While these advanced architectures have shown promise, they also present significant challenges. Transformer-based models, for example, often require large amounts of training data and are computationally intensive, which is a notable drawback in medical imaging, where labeled data is scarce and expensive to obtain⁸. Consequently, there is a growing interest in exploring meta-learning strategies that enable models to generalize effectively with limited labeled data. So we can identify three practical limitations that remain for *non-glioma*

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subtypes. (i) Data scarcity and imbalance: labelled MRI for meningioma and metastasis is comparatively limited, making conventional fine-tuning brittle and prone to overfitting. (ii) Domain shift: models trained on glioma often degrade when transferred across scanners/sites or histologies, reducing reliability in real deployments. (iii) Adaptation strategy: prevailing approaches rely on standard fine-tuning or compute-intensive transformer variants; the former does not explicitly optimise for rapid adaptation with few labels, while the latter typically requires substantial data and resources. Consequently, a *data-efficient, generalisable* adaptation mechanism—with calibrated baselines and ablations—for meningioma and metastasis segmentation remains lacking, motivating the approach proposed next.

To address these challenges and the gap in research on non-glioma brain tumors, we propose a meta-transfer learning approach that leverages the strengths of the nnU-Net framework⁹, a state-of-the-art segmentation network, and the Model-Agnostic Meta-Learning (MAML) algorithm¹⁰. The nnU-Net framework is renowned for its modality-agnostic design and automated preprocessing capabilities, allowing it to generalize well across different datasets and tasks without extensive hyperparameter tuning. By incorporating the MAML algorithm, our approach aims to fine-tune the nnU-Net model for effective segmentation of meningioma and metastasis tumors while still maintaining high performance on glioma segmentation tasks (Fig. 1).

Our contributions in this paper are threefold:

1. We extend the nnU-Net model's capabilities through a meta-transfer learning approach, enabling it to segment meningioma and metastasis brain tumors alongside gliomas accurately.
2. We demonstrate the efficacy of our approach on publicly available datasets, achieving state-of-the-art segmentation performance for these underexplored tumor types.
3. We underscore the potential of meta-learning to enhance the modality-agnostic representation learning capabilities of the nnU-Net architecture, broadening its applicability to a broader array of brain tumor types.

Through this work, we aim to advance the field of brain tumor segmentation by developing a more robust and generalizable framework that can handle a diverse range of tumor types, addressing the pressing need for practical clinical tools in medical image analysis.

Related work

Meta-transfer learning

Meta-transfer learning (MTL) has gained traction in the medical imaging community for its ability to generalize well in low-data regimes. The core idea behind MTL is to combine meta-learning, which adapts models to new tasks with minimal training samples, with transfer learning that leverages knowledge from previously learned tasks. Unlike standard transfer learning, which fine-tunes a pretrained nnU-Net on a single target cohort, our meta-transfer learning (MTL) trains the *initialisation* itself to adapt rapidly to new tumour types with few labels. Concretely, a bilevel objective uses an inner loop (task-specific update on meningioma/metastasis episodes) and an outer loop (meta-update on held-out data) to encourage generalisable features. Model-Agnostic Meta-Learning (MAML)¹¹ remains a widely used meta-learning framework that enables fast adaptation of models with a few gradient updates. Several variants such as Reptile, Meta-SGD, and LEO have also been applied in medical contexts with varying success.

Recent studies such as Yan et al.¹² introduced a meta-learning pipeline for few-shot meningioma segmentation using a 3D U-Net with CNN-transformer blocks and Reptile optimization, showcasing promising results with limited data. In our work, we incorporate MAML into the nnUNet framework and further enhance it by integrating the Focal Tversky Loss (FTL) to mitigate class imbalance. This hybridization enables robust segmentation performance even with small training sets.

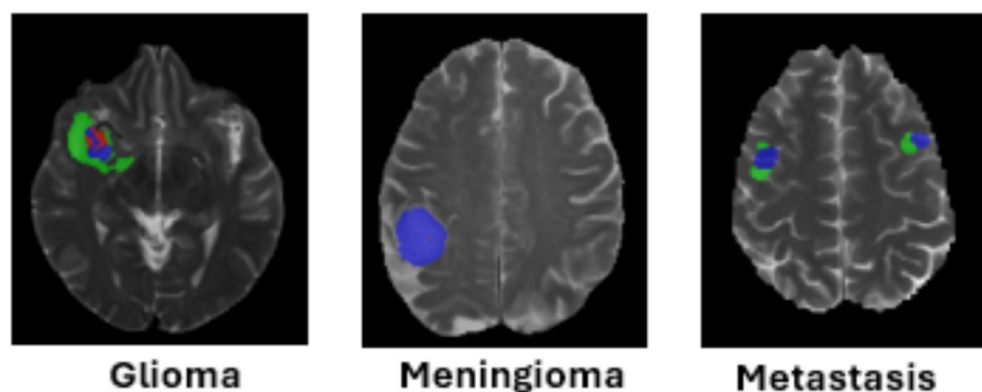


Fig. 1. MRI images and segmented masks of three different tumor types: glioma, meningioma, and metastasis. Each tumor type presents unique structural characteristics, highlighting their appearance and behavior variability.

Our proposed Meta-nnUNet demonstrates the effectiveness of MTL in segmenting previously underexplored brain tumor types such as meningioma and metastasis, maintaining high accuracy while reducing training epochs and dataset size—addressing a common constraint in clinical datasets.

Brain tumor segmentation

The field of brain tumor segmentation has been largely shaped by the BraTS (Brain Tumor Segmentation) challenges^{13,14}, which have established benchmarks for multi-modal MRI-based tumor delineation. Deep learning models like U-Net¹⁵, nnUNet¹⁴, and Swin UNETR¹⁶ have set state-of-the-art standards for glioma segmentation, particularly for the Whole Tumor (WT), Enhancing Tumor (ET), and Tumor Core (TC) regions.

However, segmentation efforts have predominantly centered on gliomas. The BraTS2023 challenge expanded its scope to include meningioma and metastasis cases^{17,18}, thereby introducing a new set of challenges due to differences in tumor morphology and class imbalance in labels. Our study utilized a carefully selected subset of the BraTS2023 dataset, focusing on meningioma (320 cases) and metastasis (88 cases). The Meta-nnUNet model achieved competitive Dice scores of 0.8621 for meningioma and 0.8141 for metastasis on the WT region, setting a new performance benchmark in these tumor types.

These results highlight the capability of MTL to effectively generalize learned representations across diverse tumor types and imaging conditions. Compared to traditional transfer learning, MTL significantly reduces the dependency on large annotated datasets while preserving segmentation performance, thereby offering a scalable solution for brain tumor analysis in real-world, data-limited environments.

Methods and materials

Data and preprocessing

For our study, we utilized the Brain Tumor Segmentation (BraTS) datasets from the 2020 and 2023 challenges^{13,17–20}. The BraTS 2020 dataset, which primarily includes glioma tumors, was used for pretraining our model. Gliomas are the most common and aggressive type of primary brain tumors, and the BraTS 2020 dataset contains multi-modal MRI scans, including T1, T1-contrast enhanced (T1ce), T2, and FLAIR sequences, from 369 patients. Each scan is annotated with three primary tumor regions: Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). The MRI images are standardized with dimensions of $240 \times 240 \times 155$ voxels, and intensity normalization is performed using z-score normalization. This dataset served as the primary source for pretraining our model on glioma segmentation.

For the fine-tuning and testing phases, we employed a subset of the BraTS 2023 dataset, focusing on meningioma and metastasis tumors. The BraTS 2023 dataset is an expanded version of previous BraTS challenges, comprising approximately 1,000 meningioma cases and 165 metastasis cases with multi-parametric MRI scans (T1, T1ce, T2, and FLAIR). The dataset features updated and corrected annotations from BraTS 2020, consolidating four previous labels into three (WT, TC, and ET) for consistency across all tumor types. These adjustments ensure standardized labeling across the dataset, facilitating more accurate training and evaluation of segmentation models.

From this dataset, we selected 320 meningioma cases and 88 metastasis cases for our experiments. The selection followed a strict criterion aimed at mitigating class imbalance and ensuring high-quality annotations. Specifically, we included only cases containing complete label sets for WT, TC, and ET, excluding cases with missing or partial annotations to prevent class imbalance during model training and evaluation. This approach ensured consistency across tumor regions and aligned with our objective to assess the model's performance under data-scarce conditions.

The selected meningioma and metastasis cases underwent preprocessing steps similar to the glioma data, including resampling to a uniform voxel size of $1 \times 1 \times 1 \text{ mm}^3$, co-registration to a common anatomical space, and intensity normalization using z-score scaling to ensure consistency across modalities.

To evaluate the model's performance effectively, we partitioned the selected meningioma and metastasis cases into training, validation, and testing sets, allocating 60% for training, 20% for validation, and 20% for testing. In contrast to previous studies that employed five-fold cross-validation, we adopted a single partitioning strategy. This decision was made to maintain consistency throughout the experiments and streamline the evaluation process. The single split ensured that the model was trained and validated on distinct subsets of the dataset, providing a clear and robust assessment of its performance across different tumor types without the variability introduced by multiple cross-validation folds. This approach also allowed for efficient experimentation while preserving the integrity of the evaluation.

Given the challenge of acquiring large labeled datasets in medical imaging, particularly for less common tumor types like meningioma and metastasis, we deliberately employed a smaller subset of the available data. Approximately 32% of the available meningioma data and 53% of the available metastasis data from the BraTS 2023 dataset were used for training, validation, and testing. This selection approach highlights the ability of our meta-transfer learning model to generalize effectively and perform well under data-scarce conditions, which is a significant advancement in medical image analysis. Our approach demonstrates that the model can transfer knowledge learned from glioma segmentation (BraTS 2020) to new tumor types (meningioma and metastasis) using limited labeled data, ensuring its applicability in real-world clinical settings.

Software and computational environment

All experiments were implemented using Python (version 3.10.12, <https://www.python.org/>) and PyTorch (version 2.1.0, <https://pytorch.org/>). We used the nnU-Net framework (version 1.7.0, <https://github.com/MIC-DKFZ/nnUNet>) for baseline training and initial segmentation modeling. For meta-transfer learning and fine-tuning, custom PyTorch modules were developed and deployed on AWS EC2 instances (g4dn.12xlarge) equipped with NVIDIA Tesla T4 GPUs, 192 GiB RAM, and 48 vCPUs. Model training and evaluation were

performed using Ubuntu 20.04 as the operating system. All software dependencies and preprocessing routines followed nnU-Net's standard configurations, with adjustments made for custom tumor types and label harmonization in the BraTS 2023 dataset²¹.

Methodology

Overview

The nnUNet framework is a state-of-the-art deep learning-based method designed for medical image¹⁴. It automatically configures its architecture, preprocessing, and postprocessing strategies based on the dataset characteristics, making it a versatile tool for various segmentation tasks. In our study, we initially trained the nnUNet model on the glioma dataset using the traditional nnUNet trainer, achieving robust segmentation performance.

Meta-learning and transfer learning

To enhance the model's ability to generalize across different brain tumor types, such as meningioma and metastasis, we developed a customized nnUNet trainer incorporating meta-learning and transfer learning concepts.

Meta-learning, often called "learning to learn," aims to develop models that can adapt quickly to new tasks with minimal data. This is particularly important in medical imaging, where acquiring large, labeled datasets can be challenging. Meta-learning facilitates this by enabling the model to adapt its learned features to the unique characteristics of new datasets. Specifically, meta-learning optimizes the model's initial parameters θ such that, after a few gradient descent updates on a new task T_i , the adapted parameters θ'_i perform well on that task. Mathematically, this can be expressed as:

$$\theta'_i = \theta - \alpha \nabla_{\theta} \mathcal{L}_{T_i}(f_{\theta})$$

where $\mathcal{L}_{T_i}$ is the loss function for task T_i , and α is the learning rate in the inner loop. The goal of meta-learning is to find the optimal θ that minimizes the overall loss across all tasks after adaptation:

$$\min_{\theta} \sum_{T_i \sim p(T)} \mathcal{L}_{T_i}(f_{\theta'_i})$$

Transfer learning complements this by leveraging the knowledge gained from training on one dataset (in our case, the glioma dataset) to improve performance on another related dataset (such as meningioma or metastasis). The transfer learning process can be mathematically described by initializing the model parameters θ_0 with the pretrained parameters from the source task (glioma dataset) and fine-tuning them on the target task:

$$\theta_{\text{target}} = \theta_{\text{source}} - \eta \nabla_{\theta} \mathcal{L}_{\text{target}}(f_{\theta_{\text{source}}})$$

where $\mathcal{L}_{\text{target}}$ is the loss function for the target dataset (meningioma or metastasis), and η is the learning rate during fine-tuning. This process allows the model to retain useful features from the source dataset while adapting to the specific characteristics of the target dataset.

Network architecture

This study employed the nnUNet architecture, a highly adaptive deep-learning framework specifically designed for medical image segmentation tasks. The nnUNet architecture is based on a fully convolutional network (FCN) with an encoder-decoder structure, further enhanced by adopting Model-Agnostic Meta-Learning (MAML)¹⁰. For training, we utilized the Focal Tversky Loss (FTL)²², which is particularly effective in handling class imbalance instead of the Cross-Entropy Loss.

Additionally, we developed a novel Meta-nnUNet architecture that integrates MAML into the nnUNet framework, as depicted in Figure 2. This proposed architecture significantly improves segmentation performance by leveraging the MAML approach, allowing the model to rapidly adapt to new tasks with limited data. The figure illustrates the detailed architecture, highlighting how MAML is incorporated into the encoder and decoder paths of the nnUNet, enhancing its ability to generalize across different medical image segmentation tasks.

nnUNet architecture

The nnUNet architecture follows a U-shaped structure consisting of an encoder, a bottleneck, and a decoder. It is designed to capture global and local input medical images' features.

Encoder: the encoder consists of a series of convolutional layers followed by max-pooling operations. The convolutional layers are activated using the Rectified Linear Unit (ReLU) function:

$$x_{l+1} = \text{MaxPool}(\text{ReLU}(\text{Conv}(x_l, W_l)))$$

where x_l represents the input to the l -th layer, and W_l denotes the weights of the convolutional layer.

Bottleneck: the bottleneck layer sits between the encoder and decoder, capturing the most abstract features. It consists of convolutional layers without pooling, ensuring that the full spatial resolution is maintained while focusing on deeper features.

Decoder: the decoder upsamples the feature maps back to the original image resolution. This is achieved through transposed convolutions:

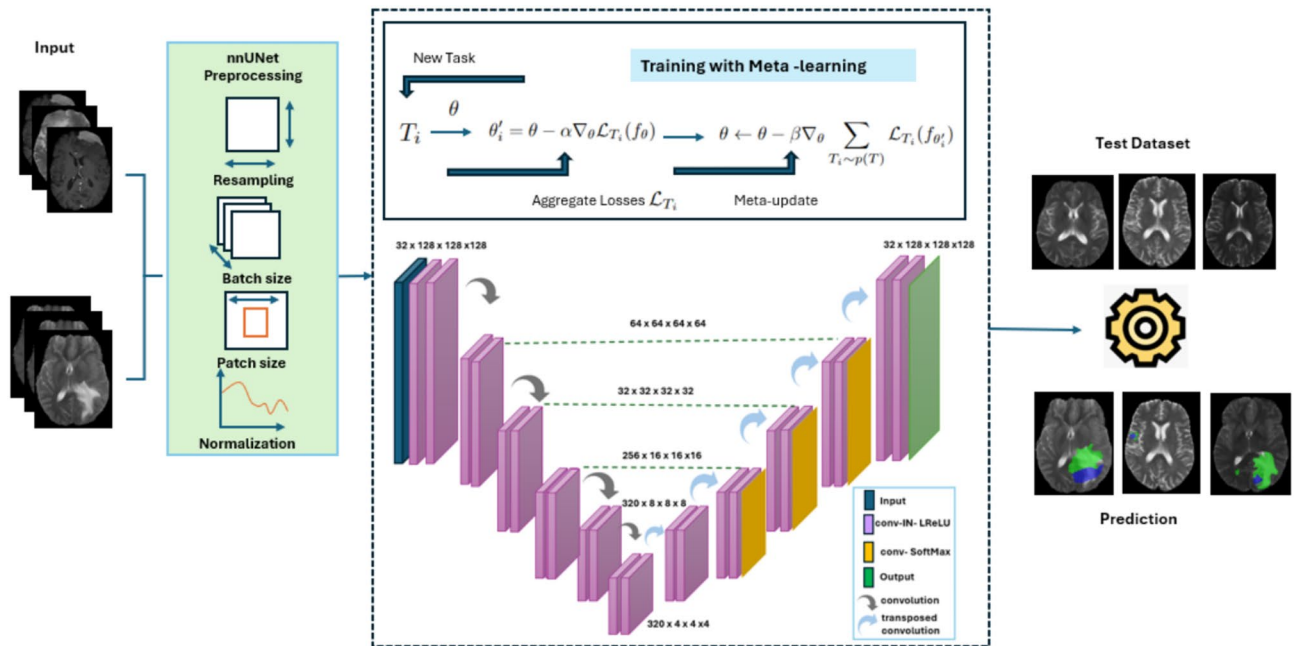


Fig. 2. The proposed Meta-nnUNet architecture, integrating Model-Agnostic Meta-Learning (MAML) into the nnUNet framework for enhanced segmentation performance.

$$x_{l-1} = \text{ReLU}(\text{ConvTranspose}(x_l, W_l))$$

Skip connections are used between the encoder and decoder's corresponding layers to preserve spatial information, facilitating more precise segmentation.

Output layer: the final output layer uses a softmax activation function to generate the segmentation masks for each class:

$$P(\text{class } c) = \frac{\exp(z_c)}{\sum_{c'} \exp(z_{c'})}$$

where z_c is the output of the final convolutional layer for class c .

Meta-learning with MAML

To enhance the model's generalization capability across different tumor types, such as meningioma and metastasis, we incorporated Model-Agnostic Meta-Learning (MAML) into the nnUNet architecture. MAML is designed to enable quick adaptation to new tasks with minimal data.

Inner loop (task-specific update): for each task T_i , the model parameters θ are updated using task-specific gradients:

$$\theta'_i = \theta - \alpha \nabla_{\theta} \mathcal{L}_{T_i}(f_{\theta})$$

where $\mathcal{L}_{T_i}$ is the loss function for task T_i , and α is the learning rate in the inner loop.

Outer loop (meta-update): the meta-parameters θ are updated by aggregating the losses computed with the updated task-specific parameters θ'_i :

$$\theta \leftarrow \theta - \beta \nabla_{\theta} \sum_{T_i \sim p(T)} \mathcal{L}_{T_i}(f_{\theta'_i})$$

where β is the learning rate in the outer loop.

This approach allows the model to leverage knowledge from the source task (glioma) and adapt quickly to the target tasks (meningioma and metastasis), achieving high segmentation accuracy even with limited labeled data.

Loss functions: focal Tversky loss

Given the variability in class distributions, particularly with underrepresented regions like Edema (ED) in meningioma and Enhancing Tumor (ET) in metastasis, we employed the Focal Tversky Loss (FTL) to address the challenges posed by class imbalance.

Tversky index: The Tversky Index, which balances the trade-off between false positives and false negatives, is defined as:

Metric	WT	Non-enhancing tumor	Enhancing tumor
Dice	0.8621 ± 0.2413	0.8550 ± 0.1611	0.9405 ± 0.0772
Sensitivity	0.8979 ± 0.1673	0.8793 ± 0.2346	0.8819 ± 0.1880
Specificity	0.9987 ± 0.0012	0.9987 ± 0.0014	0.9998 ± 0.0002

Table 1. Segmentation performance for meningioma cases.

Metric	WT	Non-enhancing tumor	Enhancing tumor
Dice	0.8141 ± 0.0562	0.8391 ± 0.0717	0.8428 ± 0.0639
Sensitivity	0.8929 ± 0.1156	0.8578 ± 0.1495	0.8406 ± 0.1398
Specificity	0.9995 ± 0.0006	0.9995 ± 0.0005	0.9998 ± 0.0002

Table 2. Segmentation performance for metastasis cases.

$$\text{Tversky Index} = \frac{|A \cap B|}{|A \cap B| + \alpha|A \setminus B| + \beta|B \setminus A|}$$

where A is the set of ground truth voxels, B is the set of predicted voxels, and α and β control the weighting of false positives and false negatives. By default, α and β are set to 0.5, providing a balanced approach to penalizing false positives and false negatives.

Focal Tversky loss (FTL): The Focal Tversky Loss is a modification of the Tversky Index, designed to focus on hard-to-classify regions by applying a focusing parameter γ . The FTL is defined as:

$$\text{FTL} = (1 - \text{Tversky Index})^\gamma$$

where γ is typically set to 2.0 to increase the focus on complex cases (i.e., those with lower predicted probabilities). This loss function is beneficial when there is a significant class imbalance, as it emphasizes the contribution of minority classes, improving the model's sensitivity to underrepresented regions.

Implementation in training: During training, FTL was applied across the model to ensure that the network could effectively learn to segment regions with varying degrees of representation in the dataset. FTL allows the model to adapt to the specific challenges of the task, such as the small or difficult-to-classify regions present in medical imaging data.

Learning rate scheduling

To ensure effective training, we employed a learning rate scheduling strategy:

Learning rate scheduling: The learning rate was adjusted dynamically during training using a polynomial decay schedule:

$$\text{lr} = \text{initial_lr} \times \left(1 - \frac{\text{epoch}}{\text{max_num_epochs}}\right)^{0.9}$$

This approach ensures that the learning rate decreases smoothly as the training progresses, allowing the model to make finer adjustments to the parameters in later stages.

Training duration: Instead of applying early stopping, we set the maximum number of epochs to 300. This approach ensures that the model undergoes a comprehensive training process, allowing sufficient time for convergence while preventing premature termination. These settings allowed the model to effectively learn from the glioma dataset and adapt to the meningioma and metastasis datasets, demonstrating its versatility and robustness across different tumor types.

Results

The proposed model was evaluated on meningioma and metastasis cases using the Dice coefficient, Sensitivity, and Specificity metrics. The results are summarized in Tables 1 and 2.

Metrics

We evaluate segmentation for three tumour sub-regions: *Whole Tumor (WT)*, *Non-Enhancing Tumor (NET; necrotic/non-enhancing core)*, and *Enhancing Tumor (ET)*. Each region is treated as a one-vs-background mask.

Let P be the predicted binary mask and G the ground-truth mask. With voxel counts of true positives (TP), false positives (FP), false negatives (FN), and true negatives (TN), we report:

Dice coefficient (Sørensen–dice / F1 for sets)

$$\text{Dice}(P, G) = \frac{2|P \cap G|}{|P| + |G|} = \frac{2 \text{ TP}}{2 \text{ TP} + \text{FP} + \text{FN}}, \quad (1)$$

which measures volumetric overlap (range [0, 1]; higher is better).

Sensitivity (recall / true positive rate).

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}}, \quad (2)$$

the proportion of tumour voxels correctly detected.

Specificity (true negative rate).

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}, \quad (3)$$

the proportion of background voxels correctly identified as non-tumour. Because background typically dominates, specificity is interpreted alongside Dice.

Meningioma cases

Table 1 presents the model's performance on meningioma cases. The model achieved a Dice coefficient of 0.8621 ± 0.2413 for Whole Tumor (WT), 0.8550 ± 0.1611 for Non-Enhancing Tumor, and 0.9405 ± 0.0772 for Enhancing Tumor (ET). These results indicate strong segmentation performance, particularly in the WT and ET regions. However, the Non-Enhancing Tumor region exhibited more variability, as reflected in its slightly lower and more inconsistent Dice score.

The sensitivity metrics were 0.8979 ± 0.1673 for WT, 0.8793 ± 0.2346 for non-enhancing Tumor, and 0.8819 ± 0.1880 for ET, demonstrating the model's ability to correctly identify tumor regions. The WT and ET regions showed better detection accuracy than the non-enhancing Tumor regions.

Specificity scores were consistently high across all regions: 0.9987 ± 0.0012 for WT, 0.9987 ± 0.0014 for Non-Enhancing Tumor, and 0.9998 ± 0.0002 for ET. These values highlight the model's precision in differentiating tumor and non-tumor tissues.

Metastasis cases

Table 2 presents the model's performance for metastasis cases. The model achieved a Dice coefficient of 0.8141 ± 0.0562 for Whole Tumor (WT), 0.8391 ± 0.0717 for Non-Enhancing Tumor, and 0.8428 ± 0.0639 for Enhancing Tumor (ET). These results suggest strong segmentation performance across all regions, with satisfactory performance in the Non-Enhancing Tumor and ET regions.

Sensitivity metrics were 0.8929 ± 0.1156 for WT, 0.8578 ± 0.1495 for Non-Enhancing Tumor, and 0.8406 ± 0.1398 for ET, indicating that the model could accurately identify tumor regions. WT showed slightly better detection than the other regions.

Specificity scores were very high across all regions: 0.9995 ± 0.0006 for WT, 0.9995 ± 0.0005 for Non-Enhancing Tumor, and 0.9998 ± 0.0002 for ET. These values reflect the model's ability to differentiate between tumor and non-tumor tissues precisely, confirming the reliability of the model's segmentation performance for metastasis cases.

The results suggest that the meta-transfer learning approach effectively segments metastasis tumors, providing a solid foundation for further research.

Comparative analysis of learning strategies

In the domain of brain tumor segmentation, research has predominantly centered on gliomas, leaving other tumor types, such as meningiomas and metastases, relatively underexplored. Despite their clinical significance, non-glioma cases have received limited investigation, and meta-transfer learning (MTL) studies in these areas are scarce. Additionally, the methodologies used in existing studies often vary greatly, making it challenging to compare results across studies. Recognizing this gap, we developed a strategy to systematically evaluate the performance of nnUNet for meningioma and metastasis cases, utilizing three distinct variants of the baseline model. Our primary focus is to investigate the performance of meta-transfer learning on small datasets compared to direct transfer learning and other settings. We do not address the impact of full dataset utilization in this study, but we plan to explore it in future work.

The paper Meta-Transfer Learning for Few-Shot Meningioma Segmentation by Yan et al. (ISBI 2024)²³ served as a key inspiration for our work. This study presents a meta-learning framework utilizing a 3D U-Net architecture with CNN Transformer modules and the Reptile meta-learning algorithm to segment meningiomas from small datasets. Their results highlight the effectiveness of few-shot learning for meningioma segmentation, demonstrating how meta-learning can improve generalization with limited data. Building upon their approach, we designed our comparative analysis to explore how meta-transfer learning performs on meningioma and metastasis cases under data-scarce conditions, aligning with the few-shot learning paradigm presented in their work.

We designed three experimental settings based on transfer learning (TL) and meta-transfer learning (MTL) principles to conduct this evaluation. In the first setting, we employed TL by fine-tuning the nnUNet model, which had been pre-trained on the BraTS 2020 glioma dataset, using 320 meningioma cases and 88 metastasis

Methods	Dice	Jaccard	Sensitivity	Specificity
nnUNet TL	0.90 ± 0.11	0.84 ± 0.15	0.88 ± 0.11	0.998 ± 0.0006
nnUNet pretrained	0.81 ± 0.23	0.73 ± 0.25	0.84 ± 0.24	0.997 ± 0.0005
nnUNet MTL (ours)	0.86 ± 0.24	0.74 ± 0.26	0.87 ± 0.25	0.997 ± 0.0006

Table 3. Performance comparison of meningioma cases for whole tumor segmentation using three different settings.

Methods	Dice	Jaccard	Sensitivity	Specificity
nnUNet TL	0.88 ± 0.11	0.80 ± 0.15	0.89 ± 0.11	0.9995 ± 0.0005
nnUNet pretrained	0.74 ± 0.26	0.65 ± 0.28	0.71 ± 0.28	0.9997 ± 0.0004
nnUNet MTL (ours)	0.81 ± 0.23	0.72 ± 0.24	0.82 ± 0.24	0.9995 ± 0.0006

Table 4. Performance comparison for metastasis cases (whole tumor segmentation).

cases for training and validation. This approach, which served as our upper bound, allowed the model to adapt to the specific characteristics of each tumor type in a fully supervised manner. In contrast, the second setting, regarded as the lower bound, directly tests the meningioma and metastasis test cases on the pre-trained nnUNet model without fine-tuning, offering insight into the model’s performance when no task-specific learning is applied.

In the third setting, we introduced our proposed MTL approach, designed to create a unified model capable of segmenting metastases and meningiomas. For this meta-learning strategy, we reduced the training dataset to just 15.6% for meningioma cases (50 out of 320 samples) and 56.8% for metastasis cases (50 out of 88 samples) compared to the fully-supervised TL setting. We also limited the training to 300 epochs, which is only 30% of the 1000 epochs used in the TL setting. This significant reduction in data and training duration highlights the strength of meta-learning in efficiently learning generalized features across different tumor types with minimal supervision while maintaining competitive performance.

Tables 3 and 4 present the performance comparisons of these three different settings for meningioma and metastasis cases, respectively, based on metrics such as dice, Jaccard, sensitivity, and specificity. For meningioma segmentation (Table 3), the TL variant achieved the highest dice score of 0.90 ± 0.11 , while our proposed MTL approach followed closely with a score of 0.86 ± 0.24 . The pre-trained model without fine-tuning showed the lowest performance, underscoring the importance of task-specific adaptation. Similarly, for the segmentation of metastases (Table 4), the TL approach again outperformed the others with a dice score of 0.88 ± 0.11 , while the MTL approach achieved a score of 0.81 ± 0.23 .

These results demonstrate that, while TL offers slightly superior performance for task-specific learning, the MTL approach provides a robust and generalized solution, especially when faced with limited data. The unified MTL model efficiently combines knowledge from both types of tumors, enhancing generalizability and reducing the need for extensive data and training epochs. This scalability and adaptability make MTL a promising framework for brain tumor segmentation in real-world clinical scenarios where multiple tumor types may be encountered and data availability may be limited.

Ablation study: impact of training epochs and FTL in meta-transfer learning

To examine the influence of training duration and loss function choice on meta-learning performance, we conducted an ablation study using Average Global Foreground Dice scores across 50 epochs for both meningioma and metastasis segmentation tasks. Figure 3 presents the comparative results for models trained with and without Focal Tversky Loss (FTL).

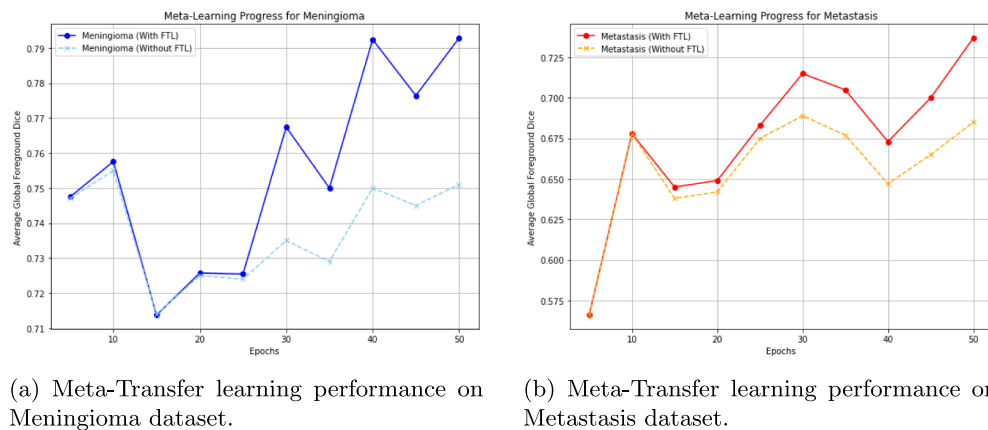
Models show comparable performance in early epochs in the case of meningioma (Fig. 3a). However, beyond epoch 15, the model trained with FTL consistently outperforms its counterpart, reaching above 0.79 Dice by epoch 50. In contrast, the model without FTL plateaus at approximately 0.75, highlighting the advantage of using FTL in later training phases.

A similar trend is observed for metastasis (Fig. 3b). Although both models perform similarly up to around epoch 10, the FTL-based model steadily improves and stabilizes near 0.73. Meanwhile, the model without FTL exhibits slower progression and begins to flatten beyond epoch 30.

These results demonstrate the dual advantage of prolonged training and the integration of FTL in meta-learning. Extended training allows for better generalization, while FTL improves segmentation accuracy, particularly in handling class imbalance. Together, they improve model adaptability in data-limited clinical scenarios.

Conclusion

This study presents an innovative approach to brain tumor segmentation by incorporating meta-transfer learning into the nnUNet framework. Our method has shown satisfactory results, particularly in segmenting underexplored tumor types such as meningiomas and metastases, often overlooked in glioma-focused research. By leveraging a pretrained network with limited labeled data, we successfully unified the model for multiple



(a) Meta-Transfer learning performance on Meningioma dataset. (b) Meta-Transfer learning performance on Metastasis dataset.

Fig. 3. Comparison of MTL dice scores across epochs for two tumor types, with and without focal Tversky loss (FTL).

tumor regions. Adapting Model-Agnostic Meta-Learning (MAML) as a form of transfer learning has proven effective in enhancing the model's generalization across different tumor types. This unified segmentation model improves accuracy and broadens the applicability of the nnUNet framework to various types of brain tumors, offering valuable insight for medical image analysis.

Future directions

While this study has established a strong foundation for using meta-transfer learning in brain tumor segmentation, there are several avenues for future research. One potential direction is to explore the application of this approach in a deeper way to other types of tumors or medical imaging modalities, which may present different challenges in data availability and heterogeneity. Additionally, integrating advanced techniques, such as attention mechanisms or transformer-based models within the meta-learning framework, could be investigated to further enhance the model's ability to capture complex patterns in medical images. Finally, extending this work to include a wider range of clinical scenarios and validating the approach in real-world clinical settings will be crucial to translating these advances into practical tools for healthcare professionals.

Data availability

The data that support the findings of this study are openly available in the BraTS 2023 Meningioma and Metastasis dataset <https://www.synapse.org/#!Synapse:syn51271053> and the BraTS 2020 Tumor dataset at <https://www.med.upenn.edu/cbica/brats2020/>

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Author contributions

M.T. conceived the study, performed data curation, developed the methodology and software, provided resources, created visualizations, conducted formal analysis, supervised the project, and wrote the original draft, including review and editing. A.D.I. contributed to supervision, validation, and investigation. S.L. provided supervision, methodology support, resources, and formal analysis and contributed to the investigation. All authors reviewed and approved the final manuscript.

Declarations

Competing interests

The authors declare no competing interests.

Additional information

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