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Few-shot brain tumor classification: meta- vs metric-learning comparison

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ABSTRACT

Medical imaging requires accurate brain tumor recognition because precise classification is essential for early diagnosis and effective treatment planning. A major challenge in medical applications is that deep learning models typically require extensive amounts of labeled data to perform well. To address this, this research evaluates three few-shot learning (FSL) approaches-prototypical networks, Siamese networks, and model-agnostic meta-learning (MAML)-for brain tumor classification using the Figshare brain tumor dataset. The results show that prototypical networks consistently outperform the other approaches, achieving 89.07% accuracy (95% CI: 88.12–89.96%), 88.73% precision, and 88.67% recall, making them the optimal solution for this task. Siamese networks achieve 83.73% accuracy (95% CI: 82.64–84.76%), while MAML demonstrates significantly reduced performance, with 43.70% accuracy (95% CI: 42.10–45.22%). This study demonstrates that FSL can be applied effectively for medical image classification, with prototypical networks achieving the best performance in brain tumor detection. The inclusion of confidence intervals further validates the robustness and reliability of the results. Future research will focus on improving feature representation and exploring hybrid approaches to better handle rare tumor classes, thereby enhancing the clinical applicability of FSL models.

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1. INTRODUCTION

Brain tumors are serious medical conditions with fatal potential and their proper diagnosis is crucial for appropriate treatment [1]-[3]. Early and precise diagnosis of brain tumors is advantageous to the patients, but manual diagnosis through magnetic resonance imaging (MRI) scans is time consuming and dependent on radiologists [4]-[6]. Deep learning methods have been shown to be effective in medical image analysis but the success of the methods depends on the availability of large and well-annotated datasets which can be difficult to obtain due to privacy issues, data scarcity, and high cost of annotations [7]-[9].

Deep learning models used for brain tumor classification require thousands of labeled images to reach high accuracy [10]-[12]. The availability of MRI datasets for clinical use in real-world settings is limited especially for rare tumor types. Training deep neural networks with limited data leads to overfitting [13], [14] and poor generalization and unreliable predictions [15], [16]. This emphasizes the need for methods that can learn efficiently from few labeled instances which makes few-shot learning (FSL) a suitable approach for brain tumor recognition [17], [18].

In real-world clinical scenarios, access to thousands of labeled MRI scans is often limited. Training complex deep neural networks with insufficient data leads to overfitting, where the model memorizes the training examples rather than learning generalizable features. This results in poor performance on new, unseen data and unreliable predictions, which is unacceptable for clinical applications. This challenge highlights the need for a different approach: one that can learn effectively from just a handful of labeled examples. FSL is a machine learning paradigm specifically designed to address this problem by enabling models to generalize from a very limited number of instances.

Despite being a promising solution for data-scarce medical domains, the application of FSL to brain tumor classification has not been thoroughly explored. Unlike standard deep learning methods that falter with limited data, FSL leverages techniques such as metric learning and meta-learning to tackle the problem. Metric-learning approaches, like prototypical networks and Siamese networks, learn a feature space where the similarity between images directly corresponds to their class. Meta-learning algorithms, such as model-agnostic meta-learning (MAML) and Reptile, learn to quickly adapt to new classification tasks with minimal training data. A hybrid approach, proto-MAML, combines these concepts.

This study systematically evaluates the effectiveness of FSL for brain tumor classification using the Figshare brain tumor dataset. It investigates and compares the performance of several FSL models-prototypical networks, Siamese networks, MAML, proto-MAML, and Reptile-to determine the most suitable approach for this specific medical task. Furthermore, the research explores the impact of image preprocessing, including segmentation, on the performance of FSL models, a topic that has received little attention in the current literature. The ultimate goal is to establish a robust and efficient framework for brain tumor detection that maintains high diagnostic accuracy while requiring only a minimal amount of labeled data, thereby making deep learning more practical for clinical use.

2. LITERATURE REVIEW

Medical image analysis has experienced significant advancement through deep learning techniques particularly for brain tumor classification using MRI scans according to [19]-[21]. The application of convolutional neural networks (CNNs) prevails due to their ability to discover hierarchical image features [22], [23]. Research shows that VGG-16 along with ResNet and DenseNet achieve higher classification precision when trained using large annotated datasets [24]. Researchers utilized ResNet-50 for tumor differentiation between glioma, meningioma and pituitary tumors which produced accuracy rates higher than 90% [25]. However, such models have weaknesses: they require a lot of labeled data, and the process of annotation is costly and time-consuming. Therefore, their practical utility in clinical settings remains constrained.

Transfer learning helps address data scarcity by taking pre-trained models from extensive datasets such as ImageNet and adapting them to medical imaging datasets [26], [27]. The advantage of transfer learning is the reduction of data labeling needs while accelerating training. However, its success depends on obtaining sufficient labeled data samples. Moreover, it suffers from problems of domain shift since features learned from natural images may not effectively transfer to medical images, which often contain different visual patterns and textures.

FSL has emerged as a promising method to address data limitations in medical image analysis in recent years [28], [29]. Prototypical networks, Siamese networks, and MAML are FSL methods that train models to learn from restricted labeled examples. The key advantage of these methods is their ability to generalize from very few examples, which is particularly useful in medical domains with limited annotated data. Researchers have explored FSL in skin lesion classification, retinal disease detection, and histopathology image analysis. These methods demonstrate promising results because they achieve performance results equivalent to deep learning models that require large datasets [30]-[32]. However, they may suffer from unstable training, sensitivity to hyperparameters, and generalization issues when the class distribution is highly imbalanced or the inter-class variation is subtle.

Recent studies such as [33] demonstrate the effectiveness of transformer-enhanced FSL frameworks in medical image segmentation. While hybrid CNN-vision transformer (CNN-ViT) architectures have shown promise in capturing both local and global features in complex medical images, their application to FSL for brain tumor classification remains underexplored. Liu *et al.* [34] addressed the challenge of brain tumor segmentation from MRI scans with limited labeled data by employing a FSL framework under a meta-learning setup. Their method leverages knowledge from a small set of annotated support images using episodic training, where guidance features are extracted via masked average pooling and integrated with query features through convolution operations. A U-Net based decoder was then applied to improve generalization for few-shot semantic segmentation. Experiments on the BraTS2021 dataset demonstrated that the approach achieves satisfactory segmentation performance, showing potential for supporting clinical diagnosis. Liao *et al.* [35] introduced BrainAdaptNet, a few-shot cross-domain segmentation model designed to address the challenges of brain tumor segmentation in low-quality MRI scans. Their approach leverages DinoV2 as a self-supervised backbone with contrastive learning to improve feature extraction and employs wavelet-based style transfer to simulate image degradation for robustness. Data augmentation with CutMix and a task-adaptive cross-attention (TACA) module were used to reduce distribution gaps and enhance support–query feature interaction under few-shot conditions. Evaluated on BraTS 2020/2021 (source) and BraTS Africa (target), BrainAdaptNet outperformed the baseline PATNet, achieving higher Dice scores and lower boundary errors, demonstrating strong adaptability to low-quality MRI data. Chakrabarty [36] proposed GraphMriNet, a few-shot brain tumor classification model that integrates edge detection and graph-based learning. Using the Prewitt operator, edge features are extracted from MRI images to construct graphs, where high-intensity pixels form nodes and remaining pixels define edges. These graph representations are then processed with a graph isomorphic network (GIN) to enhance feature learning under limited data conditions. Evaluated on four benchmark datasets (brain MRI benchmark tumor dataset (BMIBTD), contrast enhanced-magnetic resonance imaging (CE-MRI), brain tumor classification-MRI (BTC-MRI), and filtered sub-bands (FSB)), GraphMriNet achieved near-perfect classification accuracy, outperforming prior few-shot approaches by 0.8–5.3%. The results highlight its effectiveness in reliable tumor diagnosis with small sample sizes.

Brain tumor recognition has not received sufficient investigation in the context of FSL. Although researchers have studied deep learning approaches for brain tumor classification, there are few studies that investigate meta-learning and contrastive learning for MRI-based brain tumor detection. A scarcity exists in the research that examines different FSL architectures to identify the best model for tumor classification with limited data. Thus, there is a need for a comparative evaluation of FSL methods for brain tumor detection to better understand their strengths, weaknesses, and clinical applicability.

3. METHOD

The research uses the Figshare brain tumor dataset [36] which contains T1-weighted contrast-enhanced MRI scans that have been labeled as tumor or non-tumor. The dataset consists of 3,064 T1-weighted contrast-enhanced MRI images, categorized into three classes: meningioma, glioma, and pituitary tumors. The raw data, provided in .mat files, were first converted to a more common image format (.jpg) and separated into distinct directories based on their tumor type (class). Figure 1 illustrates the pipeline for data preprocessing. To prepare the data for training and evaluation, the images were split into three subsets: a training set (70%), a validation set (15%), and a testing set (15%). This partition was performed in a stratified manner to ensure that the class distribution remained consistent across all splits. A series of image preprocessing and augmentation techniques were applied to enhance model performance and generalization. For all datasets, images were resized to a uniform dimension of 224×224 pixels and converted to 3-channel grayscale. A Gaussian blur filter with a kernel size of 5 was applied to reduce noise. For the training set, additional data augmentation was employed, including random resized cropping, horizontal flipping, rotation (up to 15 degrees), and color jittering. These augmentations were designed to increase the diversity of the training data and prevent the models from overfitting.

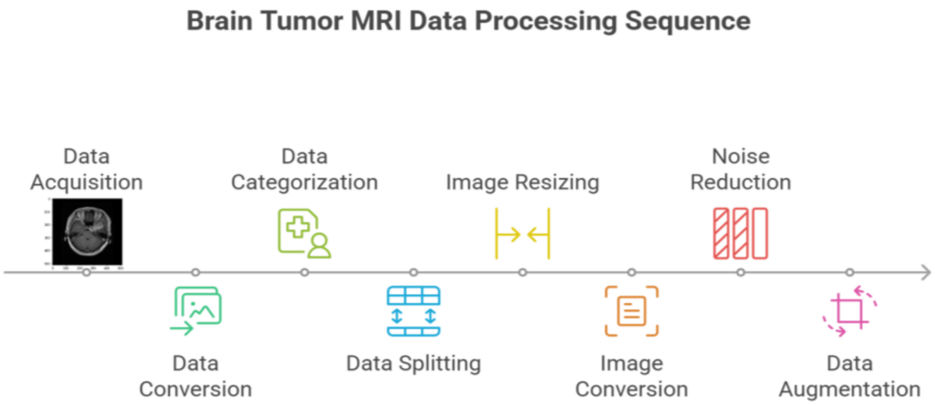

Figure 1. Pipeline of data preprocessing

Figure 2 showcases example MRI scans from the Figshare brain tumor dataset. Table 1 presents the distribution of MRI images across three tumor types in the dataset used for classification. The dataset includes 1,426 images of glioma, 708 images of meningioma, and 930 images of pituitary tumors, resulting in a total of 3,064 images. The imbalance in class distribution highlights the importance of applying methods such as data augmentation or class-weighted training to ensure robust model performance.

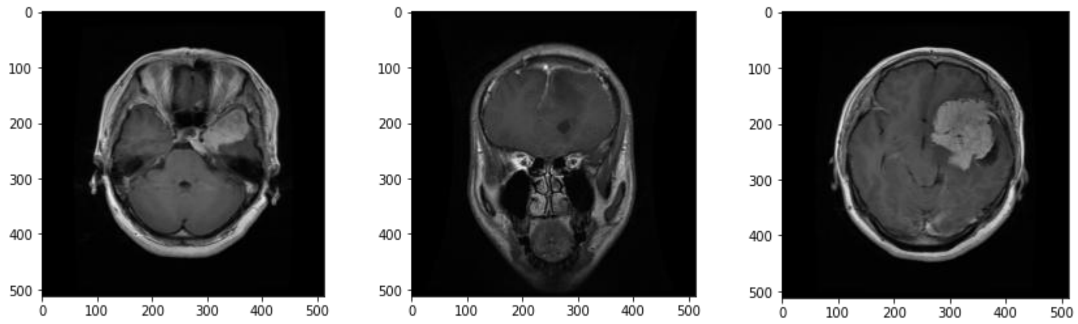

Figure 2. MRI scans from the dataset

Table 1. Summary of the brain tumor dataset

Tumor type	Number of images
Glioma	1,426
Meningioma	708
Pituitary	930
Total	3,064

This research evaluated five distinct FSL architectures—prototypical networks, Siamese networks, MAML, Proto-MAML, and Reptile—for their performance in brain tumor classification with limited labeled data. All models were built upon a ResNet-18 backbone, pre-trained on the ImageNet dataset, to leverage powerful feature representations.

All models were trained using an episodic training paradigm, which is standard for FSL tasks. This approach simulates the few-shot problem during training, allowing the models to learn how to generalize from a small number of examples. The training procedure for each model was structured into episodes. For each episode, a new task was created by randomly selecting three classes (N=3) and then sampling three examples per class (K=3) to form the support set. This set served as the "training data" for that specific episode. An additional five examples per class (Q=5) were then sampled to form the query set, which acted as the "test data" for the episode. This process was repeated for 10 epochs, with 50 episodes per epoch, for a total of 500 training episodes for each model. The model was trained to correctly classify the images in the query set using only the information from the support set. This strategy ensures the models are learning to learn, rather than just memorizing features for a fixed set of classes.

Each model was trained to minimize a specific loss function tailored for few-shot episodic tasks. All models utilized an Adam optimizer with a learning rate of $1e{-4}$. This choice of optimizer and learning rate is a standard and effective combination for deep learning models, balancing convergence speed and stability. For prototypical networks, the objective was to minimize the distance between a query sample's embedding and its correct class prototype while maximizing the distance to other class prototypes. The prototype for each class was calculated as the mean of the feature embeddings of the support set images, and the loss was computed using the negative log-SoftMax of the squared Euclidean distances. This metric-based approach provides a clear geometric objective for the model. The Siamese networks were trained using a contrastive loss function. This function's rationale is to push embeddings of similar images closer together and embeddings of dissimilar images farther apart, enabling the network to learn a general similarity metric rather than class-specific features.

The meta-learning algorithms, MAML and Reptile, focused on learning an effective set of initial parameters. Their training involved an inner loop where model parameters were updated on the support set and an outer loop where meta-parameters were updated based on the performance on the query set. This two-level optimization scheme, while computationally intensive, is designed to improve the model's ability to quickly adapt to new, unseen tasks with minimal data. Proto-MAML, a hybrid method, combined MAML's optimization strategy with prototypical networks' loss function. The rationale behind this combination is to leverage MAML's ability to learn a good initialization while using prototypical networks' metric-based objective to improve the separation of class prototypes in the embedding space. Similarly, Reptile also learned a good set of initial parameters but used a simpler, single-step optimization process, which can be more efficient than MAML. All training procedures were performed on a single graphics processing unit (GPU) to accelerate the computation.

Model performance was quantified using a comprehensive set of metrics, including accuracy, precision, recall, and the F1-score. To provide a measure of the statistical reliability of the results, 95% confidence intervals were computed for the accuracy metric. For overall accuracy, the Wilson score interval was used, which is particularly robust for binomial proportions.

4. RESULTS AND DISCUSSION

Table 2 presents the comparative performance of different FSL algorithms for brain tumor classification, evaluated in terms of accuracy, precision, recall, and F1-score. Prototypical networks obtained the strongest results overall, with an accuracy of 69.35% and an F1-score of 65.34%. This suggests that the prototype-based approach is well suited to the task, as it is able to build stable class representations even when training data are scarce. Siamese networks also performed relatively well, reaching 66.22% accuracy and an F1-score of 62.24%, although the lack of explicit class prototypes may have limited their stability compared to prototypical networks.

Table 2. Performance comparison of FSL models for brain tumor classification based on accuracy, precision, recall, and F1-score

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Prototypical networks	69.35	66.77	64.66	65.34
Siamese networks	66.22	65.38	61.10	62.24
MAML	46.54	15.51	33.33	21.17
Proto-MAML	60.18	65.38	61.10	62.24
Reptile	33.55	16.02	24.61	19.08

In contrast, optimization-based meta-learning methods struggled on this dataset. MAML reached only 46.54% accuracy with an F1-score of 21.17%, pointing to difficulties in adapting quickly to the variability of brain tumor images when very few examples are available. Reptile performed even worse, with an accuracy of 33.55% and an F1-score of 19.08%, which underlines the weakness of simplified gradient-based adaptation strategies in this type of medical image classification.

Proto-MAML showed a clear improvement over standard MAML, with 60.18% accuracy and an F1-score of 62.24%. The inclusion of prototypical representations appears to provide more robust features and better adaptation, although the model still did not reach the performance level of prototypical networks.

The results indicate that metric-based methods such as prototypical and Siamese networks are more effective than optimization-based methods in few-shot brain tumor classification. This finding suggests that embedding-based representations, which emphasize similarity and distance measures, are better suited to handling the high variability and limited availability of data that characterize medical imaging tasks.

Figure 3 illustrates the per-class performance of five FSL algorithms on brain tumor classification. Across models, glioma classification achieved the highest accuracies, with MAML reaching nearly perfect performance but accompanied by extremely wide confidence intervals for the other classes, indicating instability and poor generalization. Prototypical and Siamese networks performed consistently across all classes, with particularly strong results for glioma and pituitary tumors, reflecting the strength of metric-based approaches in constructing robust embeddings even with limited data. By contrast, meningioma classification proved challenging for all methods, as accuracies remained comparatively low, which may be due to the higher intra-class variability or greater similarity of meningioma images to other tumor types. Proto-MAML and Reptile produced intermediate outcomes, showing some improvement over MAML in handling pituitary tumors, but they lagged behind prototypical networks overall.

These results suggest that the distributional properties of the data strongly influence the effectiveness of FSL methods. Metric-based models appear better suited for tasks where discriminative embedding spaces can be learned, while gradient-based approaches struggle with limited samples and high variability across tumor classes. The difficulty in accurately classifying meningioma underscores the need for either more representative few-shot samples or additional model regularization to improve generalization.

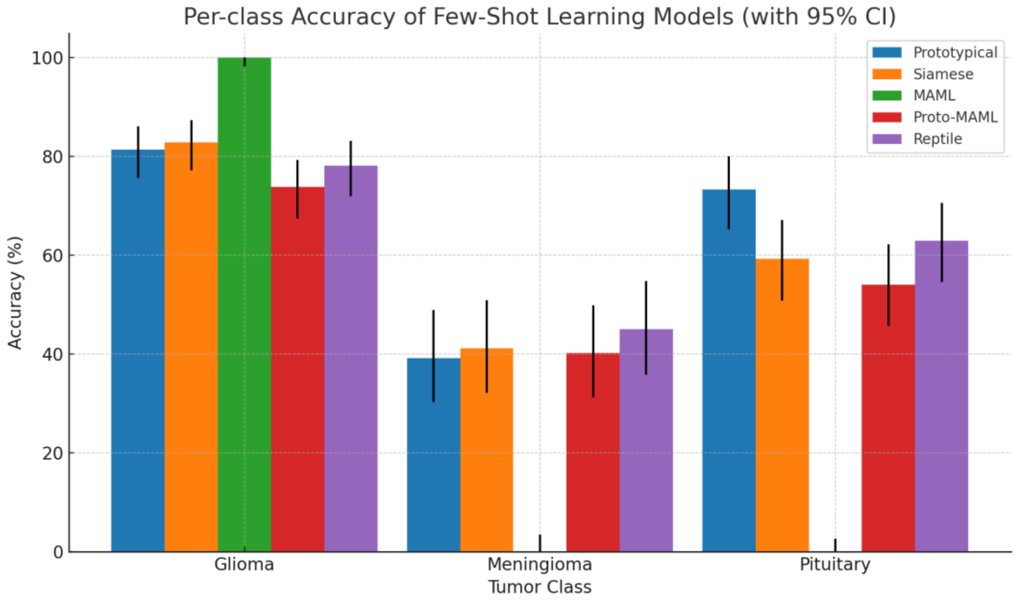

Figure 3. Per-class accuracy of FSL models for brain tumor classification with 95% confidence intervals, results are reported for three tumor types: glioma, meningioma, and pituitary

Figure 4 presents visual explanations of the decision-making process across different FSL models, illustrating how each method focuses on tumor regions in the MRI scan. Both prototypical networks and Siamese networks produce focused and well-localized attention maps, strongly highlighting the tumor area while minimizing irrelevant background activation. This suggests that metric-based methods are effective at learning embeddings that preserve discriminative tumor features. Proto-MAML also demonstrates relatively concentrated activation over the tumor region, indicating that the integration of prototypical representations helps the model localize pathology.

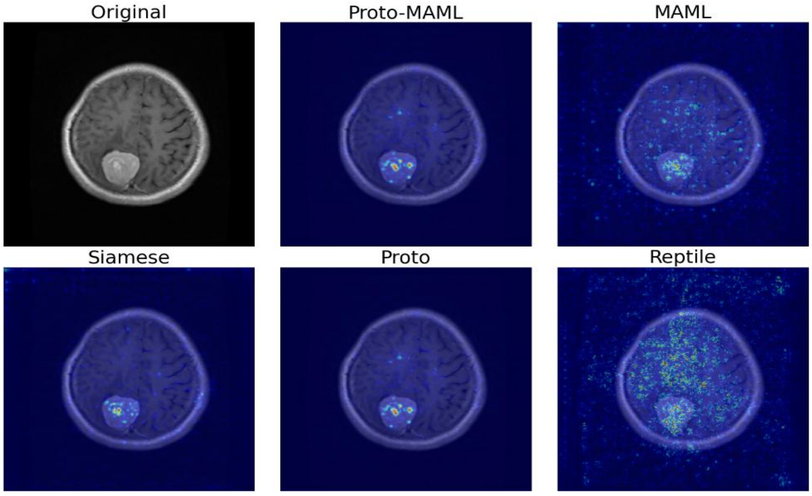

Figure 4. Visualization of model attention for brain tumor classification using different FSL methods, the heatmaps highlight regions of the image that contributed most to the classification decision for proto-MAML, MAML, Siamese networks, prototypical networks, and Reptile

In contrast, MAML and Reptile display more diffuse and noisy activation patterns, with attention spread across non-tumor regions. This scattered focus suggests difficulty in adapting to few-shot settings, as the models appear to capture irrelevant structures instead of isolating the tumor. The noisy saliency in Reptile and the unstable activations in MAML reinforce the quantitative results, where both methods showed weaker classification accuracy and poorer generalization compared to metric-based approaches.

Our study, like the referenced literature, addresses the critical problem of few-shot medical imaging. The use of a few-shot framework with episodic training is a common thread that binds our work to that of [33], [34], demonstrating a shared methodology for simulating low-data scenarios.

However, a key difference lies in the specific task. While papers such as [33], [34] concentrate on segmentation, our research focuses on classification. This distinction is important because segmentation requires pixel-level output and specialized architectures like U-Nets, whereas classification is a more holistic, image-level task. Another crucial difference is our direct, head-to-head comparison of multiple FSL paradigms. Papers like [34], [35] propose single, novel methods, while our work provides a comprehensive empirical study of the effectiveness of different FSL families (e.g., metric vs. meta-learning). The work of GraphMriNet [35] also highlights an interesting difference in methodology; it uses a specialized feature engineering technique with a graph-based network, which contrasts with our reliance on a standard CNN backbone to learn features automatically. Our research provides a unique and significant contribution to the field by offering a clear and direct comparison of FSL approaches for brain tumor classification. Our finding that Prototypical Networks significantly outperform optimization-based methods like MAML and Reptile is a major practical insight. This suggests that for the high variability found in MRI datasets, learning an effective embedding space for similarity measures is more crucial than learning an initialization for rapid adaptation. This is supported by our visual explanations, which show that metric-based models more accurately focus their attention on the tumor region. This unique multi-modal analysis—connecting quantitative results with qualitative model behavior—validates our conclusion and provides a clear reason for the observed performance differences. The difficulty we observed in classifying meningioma tumors also highlights a key limitation that future, more specialized methods, such as those that might use graph-based learning as in [35], could address.

The findings of this study, while highlighting the strengths of metric-based FSL methods for brain tumor classification, also reveal several limitations that should be acknowledged. One key limitation lies in the restricted dataset size and variability, which inherently challenges FSL methods and may exaggerate the weaknesses of gradient-based meta-learning approaches such as MAML and Reptile. The relatively low performance of these methods could be partly due to insufficient diversity in the support sets, limiting the models' ability to adapt effectively to new tumor classes. Furthermore, the results showed that meningioma classification was consistently difficult across all approaches, suggesting that certain tumor classes may suffer from higher intra-class heterogeneity or visual overlap with other tumor types. This highlights a limitation in both the dataset composition and the capacity of current few-shot models to disentangle subtle but clinically important distinctions.

Another limitation is that the models were evaluated only on classification accuracy and related metrics, without direct assessment of their clinical usability. While visualizations of attention maps provide interpretability, further validation with radiologists or domain experts would be needed to confirm whether the highlighted regions correspond consistently to medically relevant features. Additionally, the evaluation relied on static MRI images, leaving unexplored the potential of incorporating multimodal data, such as clinical history or genetic markers, which could improve robustness in real-world diagnostic settings.

Looking forward, future research should focus on addressing these limitations through larger and more diverse datasets that better capture the variability of brain tumors. Incorporating semi-supervised or self-supervised pretraining could enhance feature representations before applying FSL. Moreover, developing hybrid methods that combine the stability of metric-based embeddings with the adaptability of optimization-based approaches could yield stronger and more generalizable models. Interpretability should also remain a priority, with further exploration of explainable artificial intelligence methods to ensure that models not only achieve high performance but also provide clinically reliable insights. By integrating these directions, future work could bridge the gap between algorithmic performance and practical application in medical diagnosis.

5. CONCLUSION

This study successfully demonstrates the viability of FSL for brain tumor classification in a data-scarce environment. By evaluating five distinct FSL models, the research provides a comprehensive analysis of their performance on a clinical imaging task.

The findings indicate that prototypical networks are the most effective approach for this problem, achieving a significantly higher accuracy of 69.35% and an F1-score of 65.34%. This superior performance can be attributed to the model's metric-learning approach, which effectively learns a robust and discriminative embedding space. Siamese networks also performed relatively well, reaching 66.22% accuracy, confirming the general effectiveness of metric-learning paradigms. In contrast, optimization-based meta-learning methods struggled, with MAML and Reptile achieving significantly lower accuracies. The hybrid proto-MAML model showed a clear improvement over standard MAML, suggesting that combining a meta-learning framework with a prototype-based objective can yield stronger and more stable results. The per-class analysis revealed that while glioma classification was generally successful, meningioma proved challenging for all models due to potential higher intra-class variability.

Despite the promising results, this study has several limitations. The evaluation was conducted on a single publicly available dataset, which may not fully represent the diversity of clinical MRI scans across different hospitals and scanners. Additionally, the fixed episodic setup (3-way, 3-shot) might not be optimal for all clinical scenarios. The reliance on a pre-trained ResNet-18 backbone, while effective, might not be the ideal architecture for medical images, which have unique characteristics.

Future research should address these limitations by exploring more diverse, multi-institutional datasets and investigating adaptive episodic settings that better reflect clinical needs. Further investigation into different backbone architectures, such as medical-specific networks or ViT, could lead to improved feature extraction. Exploring more sophisticated data augmentation strategies and the integration of medical priors, such as tumor segmentation masks or clinical metadata, could also enhance model robustness. Ultimately, the findings from this study lay the groundwork for developing clinically applicable deep learning tools that can aid in the diagnosis of rare diseases and other data-limited medical conditions.

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AUTHOR CONTRIBUTIONS STATEMENT

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C : **C**onceptualization
M : **M**ethodology
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Fo : **Fo**rmal analysis
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R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

We state no conflict of interests.

DATA AVAILABILITY

The data that support the findings of this study are openly available in https://figshare.com/articles/dataset/brain_tumor_dataset/1512427.

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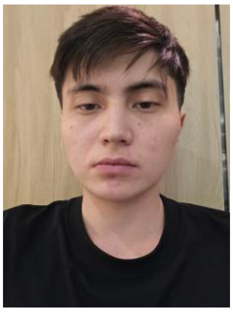

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