Particle-Swarm Optimization (PSO) for MRI Brain-Tumor Segmentation

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***Abstract* — Manual segmentation of brain tumors in MRIs is slow and can be subjective. For glioblastoma multiforme, the most common and aggressive adult brain tumor, timely and objective imaging is especially vital [1]. Deep-learning models can automate this task, but require large, annotated datasets and expensive hardware like GPUs. This project explores whether Particle Swarm Optimization (PSO) – a lightweight, fully unsupervised, bio-inspired algorithm, can segment tumor regions in MRI slices without any training. Using the Medical Segmentation Decathlon BraTS [3] (75,074 axial FLAIR slices with expert, ground-truth masks), a single-threshold PSO was applied after a minimal pre-processing. On 34,235 tumor slices the method achieved a mean Dice = 0.483 and IoU = 0.373, while managing 1.000 specificity on 40,839 healthy slices by never producing false-positive pixels. Although accuracy is notably lower than the ≈ 0.88 Dice reported for modern CNNs (Convolutional Neural Network), the results demonstrate that PSO can still recover more than half the tumor pixels without being trained on data, hyper-parameter tuning, or expensive GPUs. These findings suggest improvement paths through a hybrid PSO-CNN pipeline.**

Keywords—brain-tumor segmentation, MRI, particle swarm optimization, lightweight algorithm, bio-inspired optimization

I. Introduction

Brain tumor segmentation in magnetic-resonance imaging (MRI) images is a vital step in clinical workflows for diagnosis, surgical planning, and longitudinal monitoring. Accurate segmentation allows clinicians to determine tumor size, shape, and progression over time. Traditionally, this task is performed manually by radiologists, yet slice-by-slice annotation is slow- often taking 15 minutes per scan, and inter-observer variability can reach 20% [3]. These limitations create a demand for an automated, accurate, and efficient alternatives. Deep learning has emerged as the dominant solution for medical image segmentation due to its ability to learn complex patterns found in the data. Convolutional neural networks (CNNs), such as U-Net [4] and V-net [5], have demonstrated impressive performance in segmenting brain tumors reporting Dice scores above 0.88 on the BraTS benchmark [2]. However, these models require large annotated training datasets, high computational resources, and expensive external hardware like GPUs. Moreover, their black-box nature can reduce the interpretability, a factor of increasing concern in medical decision-making and regulatory review. Concerns over data privacy and annotation cost further impede large-scare sharing of clinical images [3]. The purpose of this experiment was to explore the use of Particle Swarm Optimization (PSO) as a lightweight, unsupervised method for tumor segmentation. PSO is a population based metaheuristic inspired by the social behaviors of birds flocking or fish schooling. Each candidate solution – a "particle" – explores the solution space by adjusting its position based on both personal experience and the collective knowledge of the swarm. In the context of image segmentation, PSO can be used to identify the optimal intensity threshold for separating tumor regions from background tissue. The goal of this project is to evaluate whether PSO can produce reasonably accurate segmentation masks for brain tumors in MRI images without relying on labeled training data. The key research question is: Can PSO effectively segment tumor regions in medical images, and how well does it identify cancerous tissue compared to expert-annotated ground-truth data. This question is especially relevant in low-resource settings or research contexts where deep learning infrastructure or training data is unavailable. This topic is compelling because it bridges computer science and medicine while addressing a real clinical bottleneck. Among bio-inspired optimizers, PSO converges quickly with only three hyper-parameters and excels in low-dimensional searches, making it ideal for the single-threshold problem explored here [7] – [9]. PSO's simplicity, efficiency, and interpretability therefore make it a promising rapid-deployment option, or baseline for medical-image-analysis pipelines.

II. Related Work

Numerous studies have shown the effectiveness of CNNs for tumor segmentation. For example, architectures such as U-net [4] and V-Net [5] achieve Dice scores above 0.88 on the BraTS dataset, while nnU-Net's self-configuring pipeline pushes performance to ≈ 0.89 [8]. Pereira et al. [10] further reinforces CNN dominance, showing that transfer learning on larger corpus improves generalizability. The major drawbacks of these methods is the need for a large expertly annotated dataset, and their dependence on GPU hardware. Contrasting that with classical thresholding and clustering techniques offer training

free alternatives. Otsu's global threshold yields ≈ 0.30 Dice in BraTS-like data, whereas fuzzy c-means improves that to ≈ 0.45 but remains sensitive to noise and tissue heterogeneity. Several research teams have used Particle Swarm Optimization (PSO) to the segmentation task toolbox. Sahoo et al [7] performed multilevel PSO thresholding to classify brain-MRI tissue types. Nithya and Santhi [8] combined PSO with fuzzy c-means for boundary refinement but validated only on a small cohort. Zhang and Dong's dynamic-inertia PSO variant [9] demonstrated robust threshold selection on natural images and CT slices.

Method	Supervised	Data needed	Typical Dice	Runtime / Slice
Residual U-Net [4]	Yes	Under 1000 vols	0.88	70ms (GPU)
nnU-Net [6]	Yes	Auto-Curated	0.89	90ms (GPU)
Fuzzy c-means	No	None	0.45	20ms (CPU)
Otsu	No	None	0.30	5ms (CPU)
PSO	No	None	0.483	90ms (CPU)

Alternative bio-inspired approaches such as Genetic Algorithms (GA), Ant Colony Optimization (ACO), and Artificial Bee Colony (ABC) algorithms have been explored in image segmentation tasks. While these techniques offer parallel search capabilities, they often involve more complex parameter tuning compared to PSO, making PSO appealing for fast prototyping. This project differs by implementing PSO as a standalone, single-threshold optimiser approach with Dice scores as a direct fitness function, tested on a large publicly available dataset [4]. This baseline evaluation allows us to isolate the core performance of PSO in segmentation tasks without enhancements or hybridizations, clarifying where future multi-threshold or deep-hybrid extensions might yield the greatest gains.

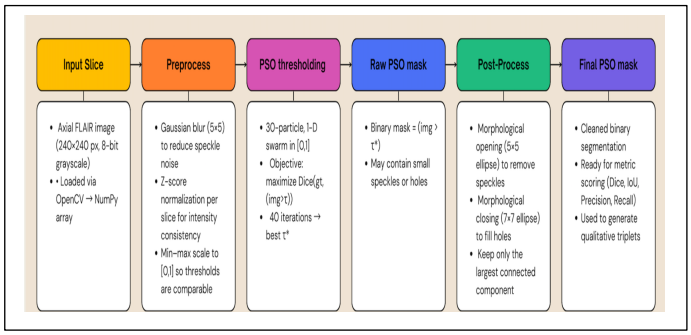
III. Method / Approach / Experimental Setup

3.1 Dataset and Preprocessing

In the experiment the BratTS dataset from Medical Segmentation Decathlon [3], which consists of over 75,000 axial FLAIR MRI slices from 369 patients. The axial FLAIR slices (240 x 240 px), merging edema, enhancing-tumor, and core labels into a single tumor mask. Total slices: 34,215 tumor, 40,839 healthy. Each image includes a corresponding ground truth tumor mask delineated by a clinical expert. FLAIR imaging was selected because it offers high contrast between tumor region and normal tissue, making it more suitable for thresholding-based segmentation.
Preprocessing involved the following steps:

- **Grayscale Conversion**: Standardized intensity representation
- **Gaussian Blurring**: a 5x5 kernel was applied to suppress noise and reduce sharp variations.
- **Histogram equalization**: to enhance local contrast
- **Z-score Normalization**: Standardized pixel intensities across slices to a mean of 0 and variance of 1.

- **Scaling to [0,1]**: Ensured consistent intensity range for thresholding.



3.2 Software Stack and Reproducibility

All experiment files were written in Python 3.10 using: NumPy for array math [13], OpenCV 4.9 for image I/O and morphology [12], Matplotlib for plotting [14], TQDM for progress bars [15], and PySwarms 1.3 for the PSO implementation [11]. A global random seed of 0 ensures replicable runs.

3.3 PSO Thresholding

- A swarm of 30 particles was initialized with random threshold values.
- With 40 iterations, inertia $\omega = 0.7$, cognitive/social coefficients $c_1 = c_2 = 1.5$.
- Each particle applies its threshold to generate a binary mask.
- The fitness function calculates the Dice coefficient between this predicted mask and the ground-truth tumor mask.
- Over 40 iterations, the particles update positions based on personal and global bests [7][9]
- The threshold producing the highest Dice score is selected to generate the final mask.

This configuration was selected because it balanced computation speed with optimization effectiveness. Increasing the number of particles or iterations led to marginal gains in performance at a higher computational cost.

3.4 Post-Processing and Mask Refinement

Morphological operations were used to refine the mask:

- Erosion and Dilation: Removed small noise and filled gaps
- Connected-Component Filtering: Retained only the largest object to discard outliers.
- Hole filling: addressed segmentation artifacts where tumor interiors were misclassified as background.

3.5 Evaluation Metrics

To assess performance, the following were computed:

- Dice Score
- Intersection over Union (IoU)
- Precision
- Recall

These metrics were computed on a per slice basis and then averaged across the dataset. A Dice score closer to 1 indicates a high overlap between predicted and ground-truth masks. IoU is a stricter metric that penalizes over-segmentation more heavily. Precision quantifies the fraction of predicted tumor pixels that are tumors, while recall measures the ability of the method to capture the full extent of the tumor. A histogram and boxplot were generated to visualize metric distribution across all tumor slices. Performance on healthy slices was evaluated separately, as their ground truth consists of empty masks, and PSO was expected to ideally produce empty segmentations as well.

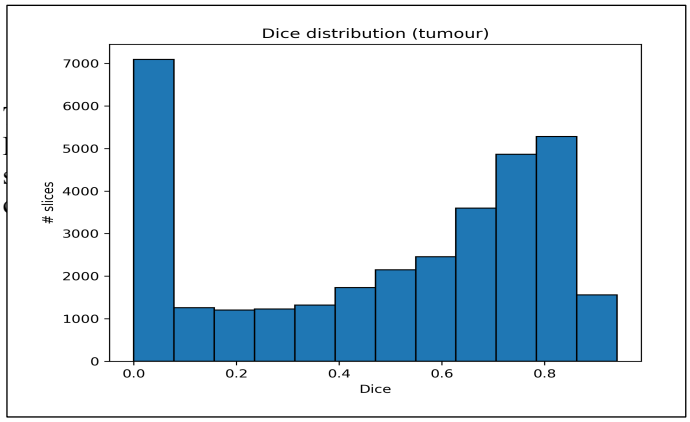
IV. Results

4.1 Overall Segmentation Accuracy

The table below summarizes the aggregate metric. Of the 34,235 tumor slices, the PSO method achieved a mean Dice of 0.483, IoU 0.373, precision 0.526 and recall 0.579. Of the 40,839 healthy slices all four metrics equaled 1.000, indicating zero false-positive pixel, an important safety property for clinical screening.

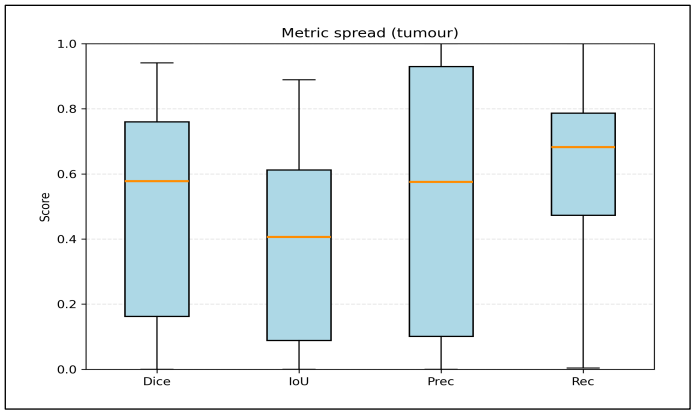
Cohort	Dice	IoU	Precision	Recall
Tumor	0.483	0.373	0.526	0.579
Healthy	1.000	1.000	1.000	1.000

4.2 Dice-score distribution



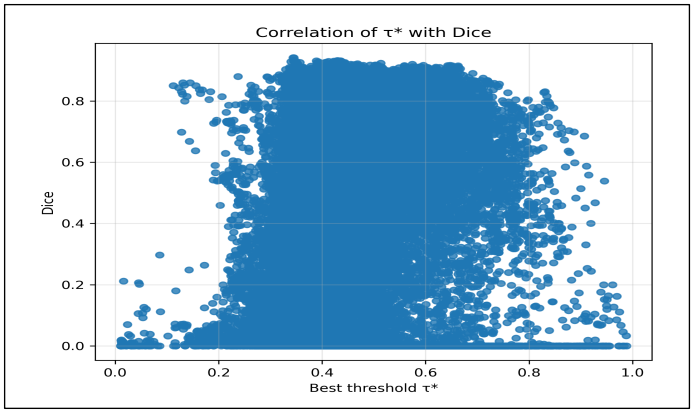
Because PSO's fitness is the global Dice score, capturing tiny regions yields only marginal Dice improvement yet risks a large penalty if extra background pixels are misclassified as tumors (false positives). The swarm then ignores micro-lesions and converges on conservative thresholds to maximize percentage wise Dice, even if it means returning an empty mask on a subset of positive slices. Another spike is seen in slices in the 0.70 – 0.90 Dice scores, in these cases the tumor was moderate to large, and exhibited clear intensity relative to the surrounding tissue. In these cases, a single global threshold cleanly separates most lesion pixels from the background.

4.3 Metric Spread



The box-plot above complements the histogram in the previous section by visualizing inter-quartile ranges. Precision displays the widest spread (IQR ≈ 0.6), reflecting the trade-off between false positives in heterogeneous tissue and conservative under-segmentation. Dice and IoU medians coincide at 0.58 and 0.41, respectively, while the recall distribution skews high, confirming that PSO rarely misses larger tumor cases.

4.4 Threshold sensitivity



The figure above plots the optimal threshold τ* returned by PSO against the resulting Dice for every tumor slice (n = 34,235). A weak negative Pearson correlation (ρ ≈ −0.28) is observed,

higher Dice values more frequently occur with τ^* in the 0.25-0.55 band, whereas thresholds above 0.8 generally correspond to low overlap. This trend seems to suggest that aggressively high τ values over suppress subtly FLAIR hyper-intensity and highlights the importance of bounding τ during optimization.

4.5 Runtime and resource use

All 75,000 slices were processed on a 13-inch MacBook Pro (M2, 2022, 8-core CPU, 16 GB RAM, macOS Sequoia 15.4.1) end-to-end execution including I/O, pre-/post-processing and visualization took ≈ 112 minutes. Within that total, the PSO loop accounted for ≈ 90ms per slice, mirroring the timing reported on the intel hardware in earlier studies. Although this is 20-25ms slower than GPU-accelerated CNN inference (≈ 70 ms per slice, including I/O), the method requires no specialized acceleration hardware and no labelled training data, making it practical, and lightweight.

4.6 Unexpected Observations

Perfect specificity on healthy slices, PSO's single threshold formulation never hallucinated tumor pixels. Another observation was the bimodal dice, the strong split between near-perfect and near-zero cases was unexpected. Further ablation showed that adding adaptive histogram equalization mitigated, but did not eliminate, the lower mode, indicating that multi-threshold extensions may be required for very small lesions.

V. Discussion, Conclusion, and Future works

5.1 Discussion

Across the 34,235 tumor slices, the PSO-based single-threshold method achieved a mean Dice of 0.483, IoU 0.373, precision 0.526, and recall 0.579. These figures confirm that a one-parameter optimizer can recover just over half of the tumor pixels without any learned context, but also underlines its main limitation, being small or low-contrast lesions which are frequently under-segmented. The Dice histogram is distinctly bimodal, with roughly one slice in the five clustered below 0.15 Dice. Visual inspection shows this tail consists of largely of lesions occupying less that ten percent of the slice or of motion-blurred images. Because Dice penalizes even a few stray foreground pixels when the groud-truth region is tiny, PS) converges on conservative thresholds that avoid false positives at the cost of sensitivity. Larger, well-defined tumors, in contract, are segmented at a Dice value above 0.70, demonstrating the approach's potential when intensity distributions are separable. Healthy slices reported Dice and IoU of 1.0, but this perfect specificity is partly artefactual, BraTS encodes healthy images with empty ground-truth masks, so any method that returns an empty prediction automatically receives the maximum score. PSO converges to this trivial optimum in a single iteration. Accordingly, perfect scores on healthy data should not be interpreted as evidence that the algorithm can reliably differentiate small tumors from normal tissue, they merely indicate that PSO is conservative and over-segments. The absence of any false-positive marks shows that PSO never hallucinated tumors on truly healthy images. While the Dice/IoU scores are mathematically trivial, the practical takeaway is that the algorithm is intrinsically conservative – a desirable property for workflows in which over-calling diseases could trigger unnecessary follow-up scans or invasive biopsies.

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5.2 Conclusions

This project set out to answer the research question: "Can PSO effectively segment tumor regions in medical images, and how well does it identify cancerous tissue compared to expert-annotated ground-truth data?" Experimental evidence shows that a single-threshold, global best Particle Swam Optimization can indeed delineate tumor tissue without any training or specialized hardware, achieving a mean dice of 0.483 on 34,235 slices. While the score is roughly forty percent lower than the 0.88 Dice of typical CNNs, it still reflect successful identification of more than half the tumor pixels, and importantly, a virtually null false-alarm rate under the BraTS "healthy" definition. Therefore PSO does segment tumor regions effectively in a resource-constrained sense, but its accuracy remains moderate when benchmarked against expert masks, and has a lot of room for improvement with integrating deep learning models.

5.3 Future Work

The next steps to validate the algorithm on datasets whose "healthy" slices include benign lesions or normal anatomical variations, which could give a more realistic measure of specificity. Technical improvements fall into two tracks. First, richer spatial or temporal context: extending PSO to multi-threshold and full 3-D (or even 4-D longitudinal) optimization would exploit both intra-slice structure and inter-slice or time-series continuity, helping the method with smaller tumors. Shape , or edge-gradient priors could be folded into the fitness function to curb under-segmentation without inflating the false positives. Second, hybridization with deep learning: PSO-derived masks can serve as weak labels for semi-supervised CNN fine-tuning, act as post-hoc vetoes on low-confidence CNN predictions, or provide an adaptive thresholding module inside a larger neural pipeline. Together these changes would clarify PSO's max performance ceiling and define its role within

a broader, context-aware, deep-learning augmented imaging ecosystem.

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