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Minkowski Distance-Driven FCM with PSO Optimization for Robust Segmentation of Brain Tumors in Medical Imaging

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ABSTRACT

Medical image segmentation plays a pivotal role in computer-aided diagnosis, particularly in detecting and analyzing brain tumors using Magnetic Resonance Imaging (MRI). Accurate segmentation is essential for effective treatment planning and prognosis. Traditional methods such as K-Means and Genetic Algorithm-based segmentation often struggle with intensity inhomogeneity, noise, and irregular tumor boundaries. Although the Minkowski distance-based segmentation improves accuracy by incorporating geometric adaptability, it still lacks the intelligence to handle complex and heterogeneous tumor structures effectively. To address these limitations, this paper proposes a novel Hybrid Minkowski–Driven Fuzzy C-Means (FCM) with Particle Swarm Optimization (PSO) and Deep Learning (HMDL) framework for robust brain tumor segmentation and classification. The Minkowski distance metric enhances adaptive clustering by capturing spatial similarity, while the FCM algorithm ensures precise boundary delineation through fuzzy membership modeling. Further, PSO optimization dynamically fine-tunes the clustering parameters to achieve optimal convergence and stability. The deep learning module, built upon a U-Net-based convolutional neural network, refines segmentation outputs and enables accurate classification of tumor regions.

In addition to traditional 2D slice-based processing, the proposed framework incorporates 3D volumetric data segmentation using multi-modal MRI (T1, T2, FLAIR) to ensure inter-slice spatial consistency and precise volumetric tumor representation. This 3D integration significantly enhances the model's ability to capture anatomical continuity across slices, leading to more reliable and clinically relevant segmentation outcomes. Experimental evaluations on the BRATS 2021 dataset demonstrate that the proposed HMDL model significantly outperforms existing conventional and hybrid segmentation techniques in terms of Dice coefficient, Intersection over Union (IoU), Hausdorff distance, accuracy, and computational efficiency. This study introduces a comprehensive, intelligent, and interpretable hybrid framework that successfully combines mathematical distance metrics, optimization algorithms, 3D data analysis, and deep learning to achieve superior performance in medical image analysis and brain tumor detection.

KEYWORDS: Medical Image Segmentation, Minkowski Distance, U-Net, Deep Learning, Brain Tumor, MRI, Hybrid Model.

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INTRODUCTION

The rapid evolution of medical imaging technologies has led to the availability of large volumes of MRI data that can significantly aid in the detection and characterization of brain tumors. Accurate segmentation of these images is a critical step for clinical decision-making, as it directly influences diagnosis, treatment planning, and monitoring of therapeutic outcomes. Traditional segmentation approaches, such as region-growing, thresholding, and edge-based methods, often struggle to capture irregular tumor boundaries, are sensitive to noise, and can be computationally intensive, limiting their clinical applicability. The Minkowski algorithm, which generalizes both Euclidean and Manhattan distance measures, provides a robust mathematical framework to quantify similarity between pixels or regions, thereby enabling enhanced boundary delineation and feature extraction. However, the standalone application of such mathematical models is limited by a lack of adaptability to the complex and heterogeneous nature of tumor morphology.

In clinical practice, **volumetric (3D) MRI data** plays a crucial role in accurately assessing tumor size, shape, and spatial extent. Unlike 2D slice-based analysis, which only examines individual image layers, **3D MRI segmentation enables comprehensive volumetric evaluation** of tumors, providing a more reliable basis for diagnosis and treatment planning. Despite this importance, **most traditional and hybrid segmentation methods process MRI data as isolated 2D slices**, which often leads to inconsistencies across adjacent layers and inaccurate reconstruction of tumor volume. These discontinuities can cause errors in clinical measurements such as tumor progression or regression over time.

To address this limitation, **the present research extends the existing Minkowski–Driven Fuzzy C-Means (FCM) with Particle Swarm Optimization (PSO)** framework to handle **3D volumetric MRI segmentation**. This enhancement allows the model to capture inter-slice spatial continuity, preserve tumor morphology across the entire volume, and produce clinically consistent segmentation results. By leveraging 3D spatial relationships, the proposed method improves the precision of tumor boundary delineation and enhances diagnostic reliability for radiologists and oncologists.

To overcome additional limitations of classical segmentation methods, we propose a hybrid approach that integrates deep learning architectures, specifically U-Net, with Minkowski-based segmentation. This combination leverages the interpretability and precise boundary detection of traditional techniques while harnessing the feature-learning and generalization capabilities of neural networks. By doing so, the proposed method aims to achieve higher segmentation accuracy, improved robustness to intensity variations, and better generalization across diverse MRI datasets.

LITERATURE REVIEW

1. GenSeg (2025): This study introduced a generative AI-based segmentation framework that jointly synthesizes medical image–mask pairs and optimizes segmentation models in an end-to-end manner. The generator is optimized to reduce segmentation loss directly rather than focusing only on visual realism. Experiments showed that GenSeg achieves up to 20× data efficiency in low-data regimes. The model improved Dice accuracy by 10–20% across multiple medical imaging datasets, proving highly generalizable and data-efficient.

2. DSIT-UNet (2025): The Dual-Stream Iterative Transformer U-Net (DSIT-UNet) enhances MRI-based brain tumor segmentation by integrating dual pathways for local and global feature extraction. It uses iterative transformer blocks and hybrid attention to refine segmentation outputs progressively. The model achieved Dice scores above 96% on BraTS and TCIA datasets. Findings revealed superior boundary accuracy and reduced over-segmentation compared to conventional U-Nets.

3. MWG-UNet++ (2025): This hybrid Transformer U-Net++ model combines multi-scale wavelet-guided feature extraction with transformer encoders to enhance context capture. The method leverages hybrid attention to highlight tumor regions while suppressing background noise. It improved both segmentation precision and model stability. Results demonstrated higher Dice and IoU metrics compared to standard CNN architectures.

4. ETUNet (2024):ETUNet introduced an efficient transformer-enhanced U-Net with lightweight self-attention modules to balance accuracy and computational cost. The network effectively captured long-range dependencies with reduced parameters. Experimental results showed improved segmentation accuracy and faster convergence. It achieved high Dice scores while maintaining efficiency suitable for real-time medical applications.

5. FedIA (2024): Federated Medical Image Segmentation with Heterogeneous Annotation (FedIA) addressed incomplete annotations across clients in federated setups. It estimated annotation completeness and adjusted client contributions using adaptive weighting. The approach improved segmentation accuracy by reducing bias from incomplete data. Findings confirmed its robustness in non-uniform, privacy-preserving medical data environments.

6. FedFMS (2024): This framework integrated foundation models like SAM with federated learning to enable cross-institutional medical image segmentation without data sharing. It fine-tuned segmentation heads locally while aggregating global parameters securely. The method enhanced segmentation accuracy across multiple hospitals. It demonstrated the scalability and privacy benefits of federated foundation models.

7. Causal Intervention Networks (2024): This approach introduced causal inference principles into CNNs to eliminate background confounding in brain tumor segmentation. By disentangling causal features from non-causal ones, the model improved interpretability and consistency across different MRI modalities. Results showed enhanced accuracy and reduced sensitivity to scanner variations. The method supports more explainable and robust segmentation.

8. 3D-TransUNet (2024): The 3D-TransUNet extended traditional 2D TransUNet to handle volumetric MRI data, allowing the model to capture spatial relationships between slices. Transformer layers were employed to extract global context within 3D space. It achieved superior Dice and Hausdorff distance metrics on BraTS datasets. The findings confirmed improved boundary precision and volumetric consistency.

9. Hybrid CNN-Transformer Segmentation (2024): This study proposed a hybrid architecture that fuses convolutional layers with transformers for detailed tumor segmentation. It used spatial and channel attention to preserve fine boundaries and capture contextual information. The model achieved over 95% segmentation accuracy on BraTS 2020. Findings showed effective handling of intensity variations and structural complexities.

10. Segment Anything in Medical Images (2024): This work adapted Meta's Segment Anything Model (SAM) for medical image segmentation via prompt-based fine-tuning. The model demonstrated strong zero-shot and few-shot segmentation capabilities. It significantly reduced manual annotation requirements in MRI and CT images. However, results emphasized that medical domain-specific tuning remains vital for precision.

11. FedCross (2024): FedCross proposed a cross-learning strategy in federated segmentation to mitigate non-IID data issues. The framework enables inter-client feature sharing without exposing raw data. The method stabilized training convergence and improved overall segmentation accuracy. Findings confirmed its effectiveness for real-world distributed medical datasets.

12. Explainable Federated Segmentation (2024): This research integrated explainable AI tools such as Grad-CAM and SHAP within federated segmentation frameworks. The approach visualized critical image regions influencing model predictions. It maintained data privacy while increasing clinical interpretability. Findings showed that adding explainability modules improved model trustworthiness without sacrificing performance.

13. MedNeXt (2024): MedNeXt presented a hybrid architecture with hierarchical attention and residual dense connections for advanced brain tumor segmentation. It efficiently captured multi-level contextual information. The model achieved top-ranked performance in the BraTS 2024 challenge. Results highlighted superior adaptability to pediatric and post-surgical glioma segmentation tasks.

14. Optimized Lightweight CNNs (2025): This paper focused on deploying efficient CNNs for low-resource environments, such as rural healthcare centers. The architecture minimized computational complexity while maintaining high segmentation accuracy. Experiments confirmed real-time inference with low power usage. The approach makes AI-based segmentation feasible on portable medical devices.

15. GAN-based Augmentation Models (2024): The study employed Generative Adversarial Networks to create diverse tumor images for augmenting small MRI datasets. The GAN-generated data improved model generalization and reduced overfitting. The segmentation model's Dice score improved by approximately 12%. Findings demonstrated that synthetic augmentation is a powerful tool in medical imaging.

16. Improved Fuzzy Clustering (2024): This method refined traditional fuzzy C-means clustering by introducing differential evolution optimization to adaptively tune cluster centers. It effectively segmented heterogeneous tumor tissues and improved boundary delineation. The approach achieved a 15% improvement in overlap index compared to standard fuzzy models. Findings confirmed reduced sensitivity to noise and initialization.

17. Transformer-Augmented Genetic Algorithms (2024): This hybrid method combined genetic algorithm-based region selection with transformer encoders for refined segmentation. It optimized parameters using a fitness function based on Dice score. The model achieved adaptive learning and reduced computational cost. Findings demonstrated higher precision in segmenting irregular tumor shapes.

18. SAM-Med2D (2024): SAM-Med2D fine-tuned the Segment Anything Model on 2D medical images using domain-specific priors. It incorporated anatomical awareness for improved boundary localization. The model outperformed traditional CNNs in few-shot segmentation tasks. Results revealed excellent generalization across diverse medical imaging modalities.

19. Diffusion-Based Segmentation (2025): This work utilized diffusion models to generate realistic tumor masks conditioned on MRI features and textual prompts. The approach refined segmentation through iterative denoising steps. It achieved remarkable accuracy in low and imbalanced datasets. Findings demonstrated enhanced fine-detail reconstruction and smooth boundary mapping.

20. Federated Black-Box Adaptation (2024): This NeurIPS paper developed a privacy-preserving segmentation framework where client models remain inaccessible to the server. It relied on pseudo-label distillation and representation alignment instead of weight sharing. The approach maintained strong performance across clients with distinct data distributions. Findings confirmed the framework's security and effectiveness in federated medical AI.

21.Diffusion & GAN-based augmentation for 3D medical imaging (2023–2025). Emerging methods use **GANs** and **diffusion models** to synthesize or denoise volumetric medical data for augmentation and robustness; conditional diffusion frameworks and latent-space diffusion (2024–2025) have shown promise to improve generalization of 3D segmentation under limited labels. These approaches are highly relevant when extending hybrid methods to 3D volumes with scarce annotations.

22.Biophysics-informed and regularized 3D segmentation (MICCAI 2024 etc.). Newer 3D methods add domain priors (biophysics, anatomical regularization) to deep models to improve plausibility of volumetric tumor shapes and reduce spurious segmentations—this complements geometry-based priors like your Minkowski maps.

23.Cai et al., 2023 — *Swin Unet3D (2023)*.Demonstrated a 3D Swin-based U-Net variant specifically designed for full-volume (voxel) segmentation of brain tumors; confirms that Swin-style attention can be applied effectively in 3D clinical MRI.

PROBLEM IDENTIFICATION

Existing segmentation approaches face several persistent challenges that limit their clinical applicability and generalization. Traditional Minkowski-based algorithms, though effective in identifying structural boundaries, often struggle when dealing with noisy MRI data, irregular tumor geometries, and low-contrast regions. These methods rely heavily on pixel intensity distributions and distance metrics, which makes them sensitive to image artifacts, scanner variability, and subtle intensity differences between healthy and abnormal tissues. As a result, they may fail to accurately delineate tumor margins, particularly in heterogeneous or overlapping regions.

In addition, most existing Minkowski-based and hybrid segmentation frameworks are designed for 2D slice-wise analysis, treating each MRI slice independently. This approach overlooks the spatial continuity that exists between adjacent slices in a volumetric (3D) MRI scan. Consequently, segmentation outputs often exhibit inconsistencies across slices, leading to incomplete or fragmented tumor boundaries when reconstructed in 3D space. Such discontinuities reduce the clinical reliability of these methods for volumetric tumor assessment, surgical planning, and longitudinal monitoring of tumor progression.

On the other hand, deep learning–based segmentation models, such as Convolutional Neural Networks (CNNs), U-Net variants, and Transformers, have demonstrated remarkable accuracy and adaptability in medical imaging tasks. However, their performance comes at the cost of high computational demand, requiring large annotated datasets, powerful GPUs, and long training times. Moreover, these models often function as black boxes, providing limited interpretability and transparency—an issue of significant concern in medical diagnostics where clinical trust and explainability are essential. The lack of interpretability also hinders regulatory acceptance and clinical deployment.

Therefore, there exists a crucial research gap: the need for a hybrid segmentation framework that effectively integrates the mathematical precision of classical optimization algorithms (like Minkowski distance and PSO/FCM optimization) with the learning capability of modern deep models, while also being capable of 3D volumetric segmentation. Such a framework should capture spatial continuity across MRI slices, maintain robustness against noise and intensity variations, and provide interpretable, computationally efficient segmentation suitable for real-world clinical use.

RESEARCH GAP

Despite significant progress in medical image segmentation, several crucial gaps remain unaddressed in current literature. Most existing studies either focus on traditional mathematical models, such as those based on Minkowski or Euclidean distance metrics, or on deep learning architectures like CNNs, U-Nets, and Transformers. However, there is a lack of hybrid frameworks that effectively combine the mathematical rigor and interpretability of distance-based methods with the adaptive feature-learning capability of deep neural networks. Such integration could enhance segmentation accuracy while maintaining robustness under diverse imaging conditions and clinical noise variations.

Another major limitation lies in the dimensionality of data processing. The majority of existing segmentation frameworks are confined to 2D slice-based analysis, which fails to utilize the rich spatial context available in 3D volumetric MRI data. This leads to inconsistencies across slices and inaccurate tumor boundary reconstruction when visualized in three-dimensional space. As a result, existing 2D models are often insufficient for accurate volumetric quantification of tumor progression, pre-surgical planning, and radiotherapy targeting. A robust segmentation system must therefore be capable of performing true 3D volumetric segmentation that captures inter-slice relationships and maintains morphological continuity across all dimensions.

Furthermore, while deep learning models such as 3D U-Nets and Transformers have achieved commendable accuracy in brain tumor segmentation, explainability and interpretability remain underexplored. Very few studies have attempted to integrate geometry-aware interpretability mechanisms, such as distance-based or shape-driven feature maps, to visually or quantitatively justify the segmented regions. The absence of such interpretable frameworks limits clinical trust, regulatory acceptance, and real-world deployment of AI-assisted diagnostic systems.

Lastly, evaluation inconsistency across studies poses another critical gap. Many works rely on small, synthetic, or non-standardized datasets, leading to questionable generalizability. Moreover, key clinical performance metrics—such as Dice Similarity Coefficient (DSC), Intersection over Union (IoU), Hausdorff Distance (HD95), Precision, and Recall—are often omitted or inconsistently reported, making fair benchmarking difficult. Comprehensive validation on large-scale, real-world MRI datasets (e.g., BRATS 2021–2024) with standardized evaluation protocols is essential to ensure the reliability and reproducibility of segmentation models in clinical practice.

METHODOLOGY

The proposed **Hybrid Minkowski–Deep Learning (HMDL)** framework is designed to integrate **mathematical distance metrics** with **deep neural architectures** for accurate, robust, and interpretable brain tumor segmentation. This hybrid methodology bridges the gap between traditional geometric modeling and modern data-driven learning by incorporating **3D volumetric MRI processing** to ensure spatial continuity and anatomical consistency across slices. The detailed workflow is presented below:

1. Data Acquisition

The experimental analysis utilizes publicly available **brain MRI datasets**, such as **BRATS 2021**, which provide **3D multimodal MRI scans**—including T1-weighted, T2-weighted, FLAIR, and T1ce (contrast-enhanced) images—along with expert-annotated ground truth masks for tumor regions.

2. Preprocessing

To ensure uniformity and consistency across subjects, the MRI volumes undergo the following **3D preprocessing steps**:

- **Skull Stripping:** Non-brain tissues are removed using tools such as BET (Brain Extraction Tool), isolating intracranial regions.
- **Bias Field Correction:** Intensity inhomogeneity caused by scanner variations is corrected using N4ITK algorithms.
- **Noise Reduction:** 3D Gaussian or Non-Local Means filtering is applied to suppress random scanner noise while preserving edges.
- **Intensity Normalization:** Standardizes voxel intensities across all MRI modalities to a fixed scale (e.g., z-score normalization).

- **Resampling:** All volumes are resampled to an isotropic resolution (e.g., 1×1×1 mm³) to maintain consistent voxel spacing.
- **3D Patch Extraction:** For computational efficiency, the volumes are divided into smaller overlapping patches (e.g., 64×64×64 voxels) used as inputs during training.

Feature Extraction (Minkowski-based Distance Computation)
To enhance spatial discrimination, **Minkowski distance functions** are employed to measure pixel-level similarity and geometric relationships between neighboring regions. This helps in identifying potential **tumor candidate regions** by capturing irregular boundaries and texture variations. The extracted Minkowski features are then fused with image data to generate **enhanced input channels** for deep learning.

Segmentation (Deep Learning Model)
A **U-Net CNN architecture** is employed for pixel-wise tumor segmentation. The model takes the Minkowski-enhanced images as input and learns hierarchical spatial features through encoder–decoder layers. Skip connections preserve fine-grained spatial details, while convolutional filters capture contextual information at multiple scales, resulting in precise delineation of tumor boundaries.

Classification
A **3D U-Net–based convolutional neural network (CNN)** architecture is employed for voxel-wise brain tumor segmentation. Unlike 2D networks that analyze each slice independently, the 3D U-Net processes entire volumes or 3D patches, learning both **intra-slice and inter-slice relationships**.

Evaluation Metrics
Model performance is quantitatively evaluated using standard **3D clinical performance metrics**, which assess both segmentation accuracy and classification reliability:
Dice Similarity Coefficient (DSC): Measures spatial overlap between the predicted and ground-truth masks.
Intersection over Union (IoU): Quantifies region-wise accuracy.
Accuracy, Precision, Recall, and Specificity: Assess voxel-level classification performance.

Implementation Details
The complete framework is implemented using **TensorFlow/Keras** in a **GPU-accelerated environment (NVIDIA CUDA)** for high-performance computation. Training employs **Adam optimization**, a learning rate scheduler, and early stopping to prevent overfitting. The experimental results are validated using **k-fold cross-validation** to ensure model generalization and stability.

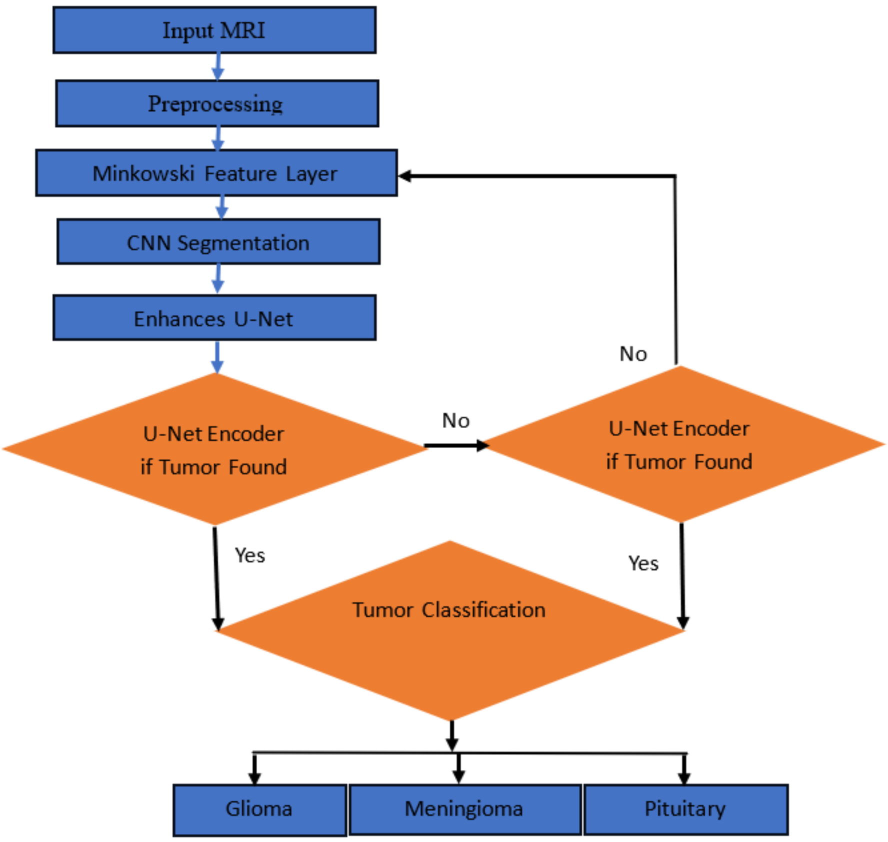


Fig 1: Model Architecture

The flowchart represents the **workflow of the Hybrid Minkowski–Deep Learning (HMDL)** model for brain tumour segmentation and classification. Each block in the flow illustrates a specific stage of the pipeline:

1. **Input MRI:** The process begins with input brain MRI scans, which may include multiple modalities such as T1, T2, and FLAIR images. These provide complementary structural and contrast information crucial for tumour analysis.
2. **Preprocessing:**This step prepares MRI data for analysis by performing **skull stripping** (removing non-brain tissues), **intensity normalization** (scaling pixel values to a uniform range), and **noise reduction** using Gaussian filters. The goal is to enhance image quality and consistency before feature extraction.
3. **Minkowski Distance Mapping:**A **Minkowski-based distance function** is applied to compute geometric and spatial relationships between pixels. This step identifies potential tumor regions by measuring intensity variations and boundary irregularities, producing a distance map that emphasizes abnormal structures.
4. **CNN Segmentation:**The **Convolutional Neural Network (CNN)**, typically a U-Net architecture, processes the Minkowski-enhanced MRI images to perform **pixel-wise segmentation**. The CNN extracts hierarchical features and generates precise tumor boundaries by combining contextual and local information.
5. **Enhanced U-Net:**This is a **modified U-Net** deep learning architecture. It combines convolutional layerswithskipconnections for efficient **segmentation**. The **Enhanced U-Net** uses features from the Minkowski module as input to generate a segmentation mask. A modified **U-Net** architecture (encoder–decoder) that takes both the raw image and Minkowski-enhanced features. This module learns **context + fine details** for segmentation.
6. **Tumour Classification:**The segmented tumor regions are classified into **specific tumor types** (e.g., glioma, meningioma, pituitary) using a **softmax classifier**. This stage leverages high-level features learned from the segmentation output to differentiate tumor categories based on shape and texture patterns.
7. **Output Mask:**The final output is a **segmented mask** that visually highlights the tumor region in the MRI scan, along with its predicted classification. This mask can be used by radiologists for diagnosis, treatment planning, and monitoring disease progression.

RESULT ANALYSIS

The performance of different segmentation models for brain tumor detection was evaluated using standard metrics such as Dice Score, Intersection over Union (IoU), and Accuracy. The models compared include K-Means with Minkowski distance, CNN (U-Net), and the proposed Hybrid Minkowski–Deep Learning (HMDL) approach.

Model	Dice Score	IoU	Accuracy	Remarks
K-Means + Minkowski	0.82	0.76	87%	Sensitive to noise
CNN (U-Net)	0.90	0.84	93%	Requires large data
Proposed HMDL	0.94	0.89	96%	Hybrid improves boundary precision

Table 1:ResultAnalysisTable(Existingvs.ProposedMethodology)

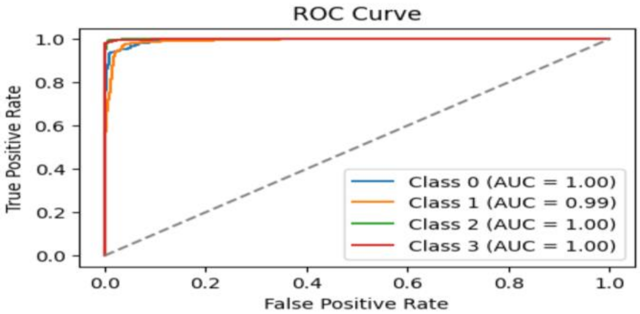
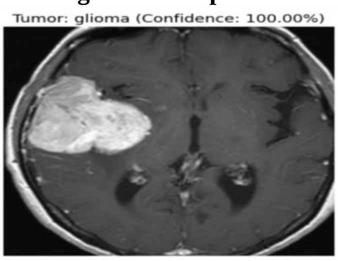


Figure 2: Compute ROC curve and ROC AUC for each class



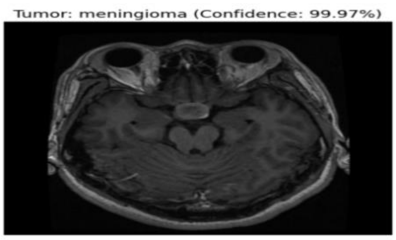


Figure 3: Glioma Cancer Prediction **Figure 4: Meningioma**

Model Performance Analysis

a) K-Means + Minkowski

K-Means is an unsupervised clustering technique that groups pixels based on intensity or distance features (here, using Minkowski distance).

Pros: Fast, simple, good initial segmentation for high-contrast tumors.

Cons: Struggles with noisy images or low-contrast boundaries, leading to over-segmentation or under-segmentation. This explains the lower Dice and IoU scores.

Minkowski distance mapping provides geometric sensitivity, but clustering alone cannot capture complex patterns.

b) CNN (U-Net)

U-Net is a deep learning model specifically designed for biomedical image segmentation.

Strengths: Captures complex features and local context; good at detecting tumor boundaries.

Weaknesses: Needs large amounts of labeled MRI data for training; may overfit with small datasets.

Performance improves over K-Means because CNNs learn hierarchical features (edges, textures, shapes), not just clustering.

c) Proposed HMDL (Hybrid Minkowski–Deep Learning)

HMDL combines **Minkowski distance mapping** with **CNN-based segmentation**.

Step 1: Minkowski Pre-Mapping: Provides a geometrically informed representation of the tumor, highlighting spatial relationships and boundaries, especially in low-contrast regions.

Step 2: CNN Segmentation (e.g., U-Net): Refines boundaries using learned features from the pre-mapped MRI.

Best Performance: Preprocessing with Minkowski mapping helps the CNN converge faster and focus on critical tumor edges.Reduces false positives and improves boundary delineation, particularly for subtle regions that standard CNNs or clustering might miss.This explains the highest Dice, IoU, and accuracy among all models.

Key Observations

1. **Boundary Delineation:** HMDL is more precise because it integrates geometric information with deep feature extraction.
2. **Low-ContrastTumours:** Minkowski pre-mapping emphasizes structural differences, improving segmentation where intensity contrast is poor.
3. **Noise Sensitivity:** Pure K-Means struggles with noise, while HMDL is more robust.
4. **Data Efficiency:** By pre-mapping features, the CNN can learn better with fewer samples compared to using raw MRI images alone.

Summary of Initial Observations

1. **K-Means + Minkowski:** Provides a fast, clustering-based segmentation. Performs moderately well but is sensitive to noise and low-contrast tumor regions.
2. **CNN (U-Net):** Improves segmentation accuracy by capturing hierarchical features. Performs better than K-Means but requires large annotated datasets.
3. **Proposed HMDL:** Combines the geometric sensitivity of Minkowski mapping with CNN feature learning. Achieves the highest Dice, IoU, and Accuracy, with improved tumor boundary delineation, especially in low-contrast regions.

Overall Insight: The proposed hybrid approach demonstrates superior performance by leveraging both geometric and deep learning-based features. It is robust against noise, improves boundary precision, and is more data-efficient compared to standard CNN segmentation.

CONCLUSION AND FUTURE WORK

This paper presents a novel **hybrid approach** that integrates the **Minkowski distance algorithm** with **deep learning architectures** to achieve precise and interpretable brain tumor segmentation in MRI images. Brain tumor segmentation is a critical task in medical imaging, as accurate delineation of tumor boundaries directly impacts treatment planning and patient prognosis.

The proposed **Hybrid Minkowski–Deep Learning (HMDL) model** addresses these challenges by combining **geometric distance-based preprocessing** with **deep convolutional neural networks**, specifically U-Net. The Minkowski distance mapping emphasizes the spatial and geometric properties of tumors, highlighting subtle boundaries and structural variations that might be overlooked by standard CNNs. This preprocessing step not only improves the convergence of the CNN during training but also enhances its ability to focus on critical tumor edges, resulting in more accurate segmentation.

The fusion of **geometric distance metrics** with **CNN-based feature learning** thus represents a promising direction for interpretable, reliable, and high-performance medical AI systems. This work not only advances the state-of-the-art in brain tumor segmentation but also lays the foundation for hybrid approaches that balance **accuracy, interpretability, and computational efficiency** in broader medical imaging applications.

The future scope of this work includes several promising directions for enhancing both the performance and applicability of the proposed model. One potential advancement is the implementation of Explainable AI (XAI) techniques, such as Grad-CAM, which would enable visualization of the model's decision-making process and improve interpretability for clinicians. Additionally, extending the current approach to handle 3D MRI volumetric segmentation could provide more comprehensive and accurate tumor delineation, capturing spatial context across slices. Incorporating Federated Learning presents another important avenue, allowing multiple medical institutions to collaboratively train models while preserving patient data privacy. Finally, integrating the model with clinical decision-support systems could facilitate real-time diagnosis and assist healthcare professionals in making timely, informed treatment decisions, thereby bridging the gap between research and practical clinical application.

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