

A Systematic Review Of State-Of-Art Methods Of Convolutional Neural Network Based MRI Brain Tumor Classification (2015-2025): Optimization, Augmentation, Performance Analysis, Datasets, Research Challenges, And Future Scope

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ABSTRACT

Brain tumor detection and classification using magnetic resonance imaging (MRI) are essential components of modern diagnostic workflows, with convolutional neural networks (CNNs) demonstrating strong effectiveness due to their superior feature extraction and classification capabilities. However, existing research remains fragmented, showing inconsistencies in datasets, augmentation strategies, hyperparameter tuning methods, and evaluation metrics. This systematic literature review (SLR) synthesizes evidence from 132 peer-reviewed studies published between January 2015 and June 2025, following the PRISMA framework and categorizing the selected works into custom CNN architectures ($n = 60$) and transfer learning approaches using pretrained models ($n = 72$). The review addresses five research questions focusing on frequently used MRI datasets for binary and multi-class classification, commonly adopted augmentation methods, hyperparameter optimization strategies including manual, heuristic, and advanced approaches, the most widely used pretrained CNN models, and the performance metrics employed for evaluating classification effectiveness. The findings highlight key limitations such as reliance on non-clinical homogeneous datasets, underrepresentation of rare tumor subtypes, limited exploration of advanced augmentation methods, inadequate documentation of hyperparameter search spaces, and inconsistent evaluation practices. To advance the field, future research should prioritize clinically diverse datasets, adopt improved augmentation techniques such as GAN-based synthesis and domain adaptation, and incorporate systematic hyperparameter optimization strategies, including Bayesian optimization with well-defined search spaces. This SLR provides a unified synthesis of current knowledge, identifies methodological gaps, and offers clear directions for developing robust, generalizable, and clinically reliable CNN-based diagnostic models.

Keywords: Convolutional Neural Network, MRI, Hyperparameters, Brain tumor, Detection, Classification.

1 Introduction

According to the American Cancer Society's Cancer statistics 2025, more than 2 million new cancer cases (excluding non-melanoma skin cancers) and over 618,000 cancer-related deaths are projected in the United States in 2025 [1]. Specifically, for brain and other nervous system cancers, the Surveillance, Epidemiology, and End Results (SEER) Program estimates around 24,820 new cases and approximately 18,330 deaths in 2025, accounting for about 1.2% of all new cancer cases [2]. The age-adjusted incidence rate for brain and nervous system cancers is reported as 6.1 per 100,000 persons per year, while the mortality rate is 4.4 per 100,000 persons per year, based on population data from 2018–2022 (incidence) and 2019–2023 (mortality) [2]. These figures underscore the continued public health burden posed by brain tumors in the U.S. and highlight the importance of advancing diagnostic and treatment strategies for improved outcomes. According to the World Health Organization (WHO) classification of Central Nervous System (CNS) tumors, brain tumors are broadly categorized into benign (non-cancerous) and malignant (cancerous) types, with further stratification into primary and secondary tumors. Primary tumors originate within the brain and include gliomas, meningiomas,

pituitary tumors, and others, whereas secondary (metastatic) tumors spread to the brain from cancers in other organs such as the lung, breast, or liver. WHO also grades malignant brain tumors into four grades (I-IV) based on histological and molecular characteristics, where Grade I represents slow-growing, less aggressive tumors, and Grade IV (e.g., glioblastoma multiforme) represents highly aggressive, fast-growing, and life-threatening tumors. This grading system helps guide prognosis and treatment planning, making it the global standard for tumor classification [3, 4].

Clinically, diagnosing a brain tumor is challenging due to variations in its size, location, growth rate, and pathology. A brain tumor can be diagnosed by two approaches either intrusive or non-intrusive. The biopsy comes under the intrusive approach where a slit is done to gather a tumor sample for assessment. It is contemplated as the benchmark for cancer diagnosis in which the pathologists detect several aspects of cells of the tumor sample beneath a microscope to approve malignancy. The physical check-up of the brain and body scanning using imaging modalities comes under non-intrusive approaches. The various techniques for brain imaging are PET (Positron Emission Tomography), CT (Computed Tomography), MRI, SPECT (Single-Photon Emission CT), and MRS (Magnetic Resonance Spectroscopy). These imaging modalities help medical practitioners or radiologists to observe disease progression, locate brain disorders, and in surgical planning [5]. Out of the above-stated techniques, MRI is examined as the best one by radiologists or clinicians. MRIs use strong magnets to generate a magnetic field that causes protons in the body to align with it. MRI offers a sensitive appearance of the brain, vascular anatomy, and spinal cord. It can also display the brain structure in all orientations (axial, sagittal, and coronal). Over other methods, MRI has advantages like low radiation, high contrast features, the absence of beam-hardening artifacts, and a sense of nervous disease easily [6, 7].

Due to the increased effect and mortality rate of the brain tumor in all age groups, it is essential to diagnose it as early as possible. Earlier, the tumor had been diagnosed manually by radiologists and clinicians, which has become time-consuming and ineffective as the number of patients has increased. Deep learning, which is the subdomain of machine learning, uses fully automatized CNNs which give good outcomes in image recognition and classification [8, 9]. No doubt, that CNNs give a high classification rate as compared to machine learning techniques but increasing classification accuracy is still a hot research topic in deep learning. There are so many parameters which give their impact on classification accuracy of CNN and it is crucial to accurately detect and classify the malignancies as they provide essential information for doctors to map out treatment options and monitor the progression of the disease. The primary goal of this Systematic Literature Review (SLR) is to frame some research questions on these parameters for enhancing the classification accuracy of brain tumors of MRI images.

Despite substantial progress, existing research exhibits significant variability in experimental setups, methodological choices, and reported results. This fragmentation makes it challenging to draw comprehensive conclusions about the most effective practices for brain tumor detection and classification. Therefore, it is essential to conduct a SLR to critically examine the full range of methods employed, from dataset preparation and augmentation techniques to model selection, hyperparameter optimization, and performance evaluation to identify prevailing trends, highlight research gaps, and establish a solid foundation for the development of an optimized CNN framework.

The roadmap for conducting this SLR, is enabling researchers to systematically collect, analyze, and synthesize information from existing studies. The framework starts with the Introduction, where the purpose and objectives of the review are outlined and sets a foundational understanding of the study's novelty and significance. The Methodology

section is central to ensuring the rigor and reproducibility of the SLR. It includes a detailed workflow for identifying, filtering, and selecting relevant articles, framing precise and impactful research questions, and formulating a robust search strategy to retrieve scholarly work. Selection criteria are meticulously defined to ensure only high-quality and pertinent studies are reviewed. The selected articles are then summarized comprehensively to provide an overview of the existing knowledge landscape.

The Overview and Analysis of Selected Studies section involves comprehensively summarized selected studies and detailed analysis of each framed Research Question (RQ), systematically addressing the key aspects of the review. This helps derive insights and patterns from the reviewed literature. Each RQ focuses on specific dimensions of the research domain, ensuring a thorough understanding of the topic. In the Research Gaps & Future Scope section, the findings from the RQs are synthesized to uncover gaps in the current knowledge base. This opens the new avenues for future research directions, ensuring the field's progression and innovation. The process culminates in the Conclusions, which encapsulates the review's overall contributions, the implications of the findings, and a succinct summary of the study.

2 Methodology

2.1 Basic Workflow of Selected Articles

CNNs have revolutionized computer vision by enabling automatic extraction of hierarchical features from medical images, making them highly suitable for tasks such as brain tumor detection and classification. However, the success of CNN-based frameworks in this domain depends not only on the network architecture and hyperparameter choices but also on the entire pipeline as shown in Figure 1, used during model development. This pipeline includes the selection of appropriate MRI datasets, preprocessing and augmentation strategies to increase dataset diversity, tuning methods to optimize CNN parameters, choice of models, whether custom-designed CNNs or pretrained networks and the evaluation metrics used to assess performance.

Each component of this procedure plays a critical role in determining the accuracy, robustness, and clinical applicability of the developed model. For instance, datasets differ widely in class distribution, imaging protocols, and annotation quality, which can significantly impact model performance. Augmentation techniques, including flipping, rotation, scaling, and brightness adjustments, are essential for enhancing model generalization but vary in effectiveness across studies. Moreover, the choice between using a custom CNN architecture or leveraging transfer learning with pretrained CNNs can influence the balance between model complexity, training time, and diagnostic accuracy. Hyperparameter tuning methods, ranging from manual selection to advanced optimization algorithms, directly affect convergence speed and final performance. Finally, inconsistent use of evaluation metrics such as accuracy, sensitivity, specificity, precision, recall and F1 score complicates the comparison of findings across different studies.

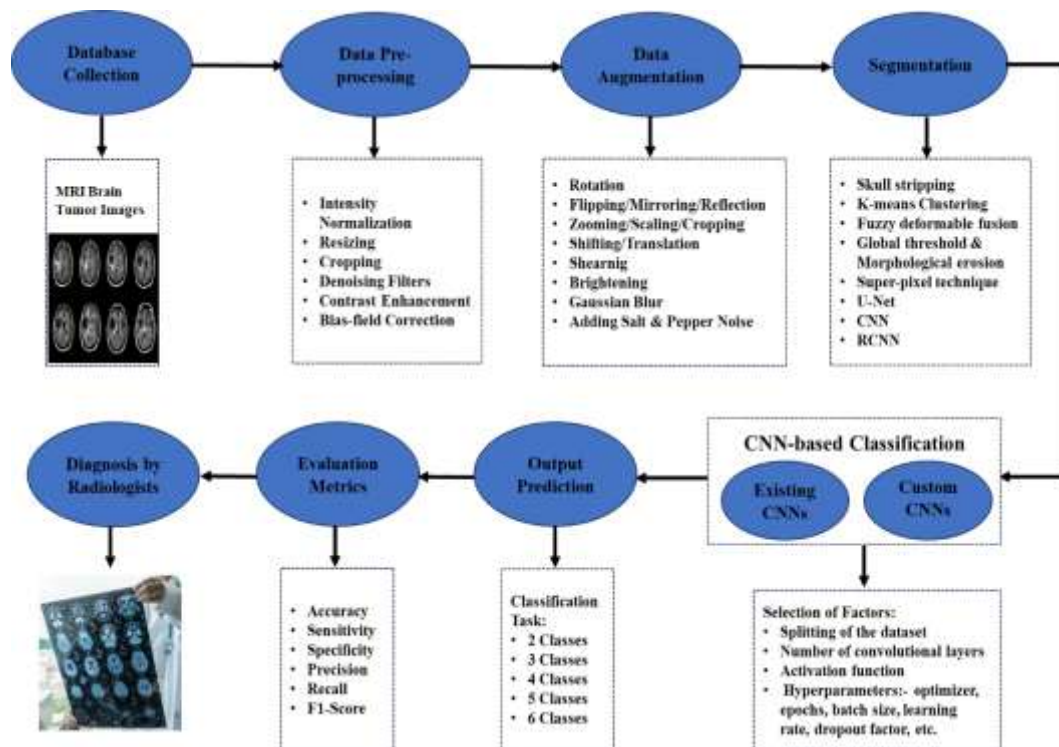


Fig. 1. Provides a structured representation of the end-to-end workflow for MRI brain tumor classification, emphasizing the integration of image pre-processing, augmentation, segmentation, and CNN-based classification.

2.2 Systematic Review Protocol

A systematic review protocol is a detailed roadmap for a systematic review. It outlines the entire process, from defining the research question to data analysis and interpretation. Creating a protocol ensures transparency, reproducibility and rigour in our review. This systematic review will investigate the entire workflow involved in the detection and classification of brain tumors using CNNs. Specifically, it will examine studies published between January 2015 and June 2025, focusing on key components such as datasets used, preprocessing and augmentation techniques, model types (custom or pretrained CNNs), hyperparameter tuning methods, optimization strategies, and performance evaluation metrics. By systematically reviewing these aspects, the study will provide a comprehensive understanding of the current state of research, identify critical research gaps across the CNN-based detection and classification pipeline, and offer valuable insights to guide future work toward more effective, accurate, and clinically applicable CNN-based frameworks.

2.2.1 Research Questions

Framing the research question is a fundamental step in conducting a systematic literature review (SLR) as it defines the scope, focus and direction of the entire process. A well-crafted research question helps establish clear boundaries for the review, ensuring that only relevant studies are included while avoiding unrelated or tangential research. Additionally, the research question ensures rigor by aligning the review with its objectives and maintaining focus throughout the process. It provides a framework for evaluating, organizing and analyzing the findings, facilitating the synthesis of results and drawing meaningful conclusions. Moreover, a clear research question enhances transparency and reproducibility, enabling others to understand and replicate the review.

By identifying existing knowledge gaps, the research question also ensures that the review addresses critical areas and contributes to advancing the field. Ultimately, it supports evidence-based decision-making by providing actionable insights, making it an essential foundation for a high-quality systematic literature review. The following research questions are framed to explore the trends, methods and gaps in the literature related to the use of CNNs for MRI brain tumor classification.

RQ1: What datasets are most frequently used in the selected studies and how are they applied across binary and multi-class classification tasks?

- The goal is to understand the diversity and relevance of datasets in supporting these classification tasks, highlighting their suitability and adaptability for different levels of classification complexity and helps to identify gaps in dataset usage, such as underrepresentation in specific classification categories, guiding future research in dataset development and application

RQ2: What data augmentation techniques are employed, how frequently are they used and which are most commonly applied?

- The aim of this research question is to analyze the role of data augmentation techniques in the reviewed studies on MRI brain tumor classification. It helps to identify the most commonly used augmentation methods, evaluate their prevalence and understand their impact on improving model performance and generalization. This analysis can guide future research by highlighting effective augmentation strategies and revealing gaps or underutilized techniques in the field.

RQ3: What techniques are used for the tuning of hyperparameters in the selected studies and what are the corresponding search spaces in studies that apply manual tuning or optimization methods?

- The goal of this RQ is to systematically identify and analyze the hyperparameters tuning methods discussed in the reviewed studies. This RQ aims to provide insights into best practices for hyperparameter selection and tuning, guiding future research and practical applications in the domain.

2.2.2 Search Strategy

To effectively extract important material while eliminating irrelevant studies using a carefully thought-out search strategy, an orderly research study is necessary. For this systematic review, only papers that offered new methods for deep learning-based brain tumor categorization and detection were taken into consideration. We searched the digital archives of Elsevier, ACM, IEEE, Springer, MDPI, Wiley, and MICCAI from January 2015 to June 2025, for publications that met our requirements. The search strings used regarding repositories, which included primary, secondary and supplementary keywords, are shown in Table 1. The total results generated from these databases are 132 articles.

Table 1: Research Protocol for Systematic Literature Review

Research Protocol	Description
Digital archives	In the present study, digital libraries such as Elsevier, ACM, IEEE, Springer, MDPI, Wiley, and MICCAI are considered for research papers, articles conference papers, and research reports.
Language	English only

Search Fields	Keywords, Articles' Titles, or Abstract
Search Terms	“deep learning” OR “CNN” OR “deep model” OR “artificial intelligence” AND “Glioma” OR “brain tumor” OR “brain cancer” OR “grading” OR “malignancy” AND “classification” OR “detection” OR “diagnosis” AND “MRI” OR “Magnetic Resonance” OR “MR images” OR “radiology” IN Title or Abstract

2.2.3 Selection Criterion

The criteria used for the selection procedure were based on PRISMA (Preferred Reporting Items for Systematic Review and Meta-Analysis) using a three-phase identification, screening, and eligibility procedure using number of inclusion-exclusion standards. The articles have the following inclusion process:

- Be an original study that was published in a journal with peer review with full-text access
- Articles having datasets of MRI images of brain tumors
- Articles having CNN-based classification algorithms

The exclusion process was:

- Book or book chapter
- Unclear description of the dataset
- Review articles
- Unpublished paper
- Classification related to ML techniques
- Classification with other deep networks like Artificial Neural Networks (ANNs), Feed-Forward Networks (FFNs), Generative Adversarial Networks (GANs), Autoencoders (AEs), Recurrent Neural Network (RNN), Deep Boltzmann Machine (DBM), Restricted Boltzmann Machine (RBM)
- Duplicate research articles
- Articles related to segmentation only
- Not peer-reviewed
- Retracted articles
- Articles have not been given the classification accuracy

The PRISMA [10] flow chart outlines the systematic process of identifying, screening, and including articles for analysis in the systematic literature review, as shown in Figure 2. Initially, 1,527 articles were identified through database searches. Out of these, 48 articles were excluded for being non-English, leaving 1,479 articles eligible for title or abstract evaluation. During this phase, 195 duplicate articles were removed, resulting in 1,284 articles for further consideration. Subsequently, 344 articles were excluded as they did not include the dataset of MRI brain tumors.

In the eligibility phase, 940 articles underwent full-text evaluation, during which 808 articles were excluded based on several criteria. Specifically, 196 articles were excluded for focusing on machine learning techniques instead of deep learning, 223 for using other deep networks like ANNs, GANs, or AEs etc., 129 for being segmentation studies, 37 for being books or book chapters, and 53 due to unclear dataset descriptions. Additional

exclusions included 93 review articles, 26 retracted articles, 18 articles without classification accuracies, 20 unpublished articles, and 10 non-peer-reviewed articles.

Ultimately, 132 articles were incorporated in the final analysis, categorized into two groups: 60 studies on MRI brain tumor classification using custom CNNs, 72 studies utilizing transfer learning-based existing CNNs. This structured approach highlights the rigorous methodology employed to ensure the inclusion of relevant and high-quality studies in the review.

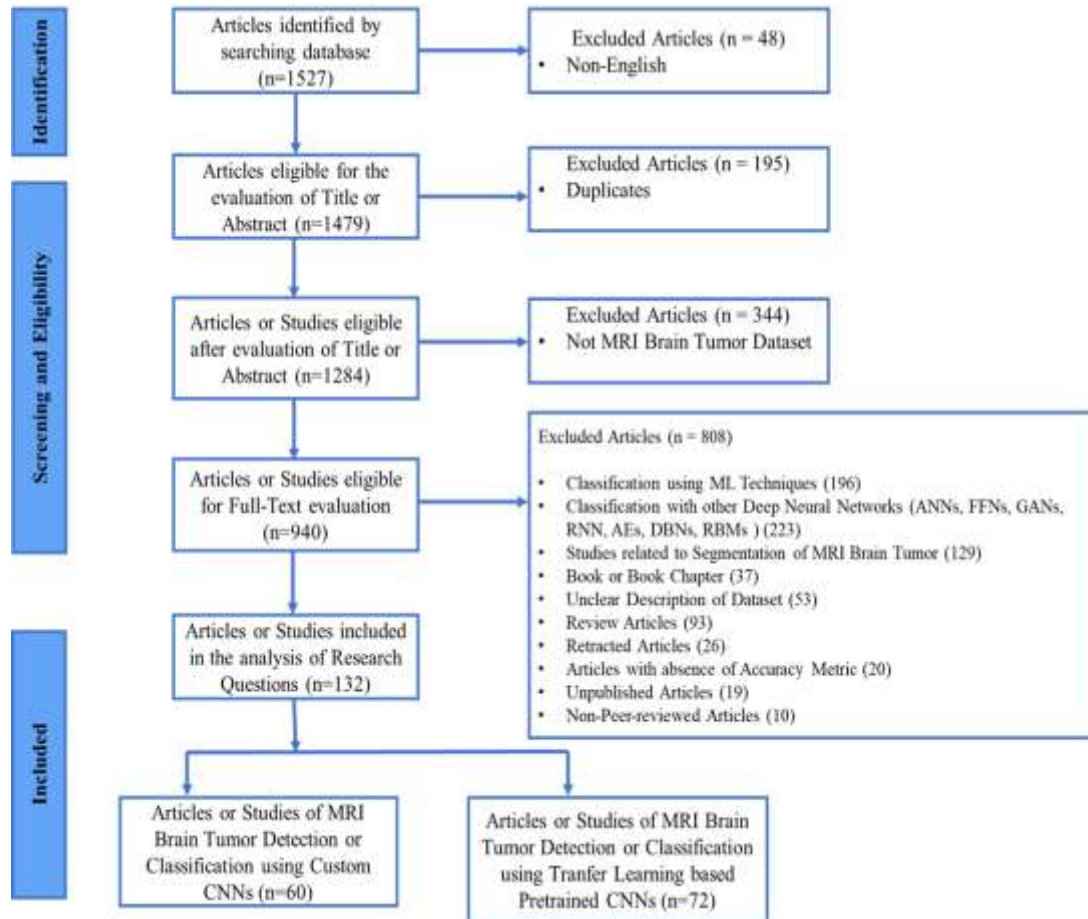


Fig.2. PRISMA A diagram of systematic literature search. n: Number of articles.

3 Overview and Analysis of Selected Studies

A comprehensive overview of 132 research articles has been formulated, summarizing the performance enhancement strategies in CNN-based classification of MRI brain tumors and suggesting directions for future research in this domain. Among the reviewed articles, 60 studies employed custom CNN architectures and 72 studies utilized pre-trained models with transfer learning techniques for detection and classification of brain tumor. The yearly distribution of selected studies from 2015 to 2024, as shown in Figure 3, indicates a clear upward trajectory in research activity over the years, with notable fluctuations in recent times. From 2015 to 2016, no studies were recorded, followed by a gradual initiation phase in 2017 (1 study) and 2018 (2 studies). The growth trend became more noticeable from 2019 (5 studies) to 2020 (9 studies), after which there was a sharp surge in publications, reaching 25 studies in 2021. This momentum continued into 2022 (32 studies) and peaked in 2023 with 38 studies, reflecting the heightened research interest and advancements in convolutional neural networks during this period.

Figure 4 provides a more detailed breakdown, comparing the yearly number of studies using Custom CNNs and Pretrained CNNs from 2015 to 2024. From 2015 to 2016, no studies were published in either category. The earliest adoption occurred in 2017 with a single Custom CNN study. Between 2018 and 2020, the adoption of both approaches gradually increased, with Pretrained CNNs starting to gain prominence from 2019 onwards. A significant rise is observed from 2020 to 2023, with both methods peaking in 2023, Custom CNNs at 18 studies and Pretrained CNNs slightly ahead at 20 studies. The year 2024 shows a drop for both approaches (Custom CNNs: 9; Pretrained CNNs: 7), mirroring the overall decline. Across the decade, Pretrained CNNs generally maintained a slight numerical advantage over Custom CNNs, reflecting a growing inclination toward transfer learning and leveraging existing deep learning architectures.

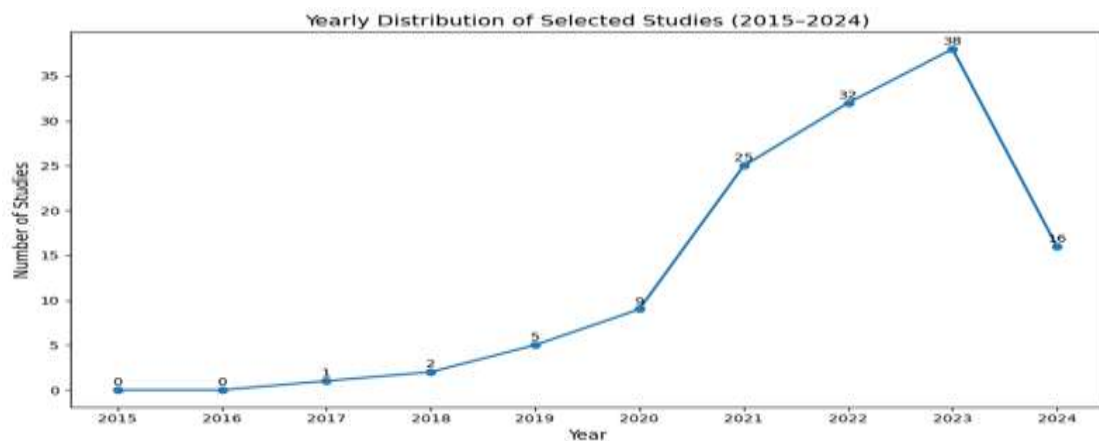


Fig. 3. Year-wise distribution of selected studies from 2015 – 2024.

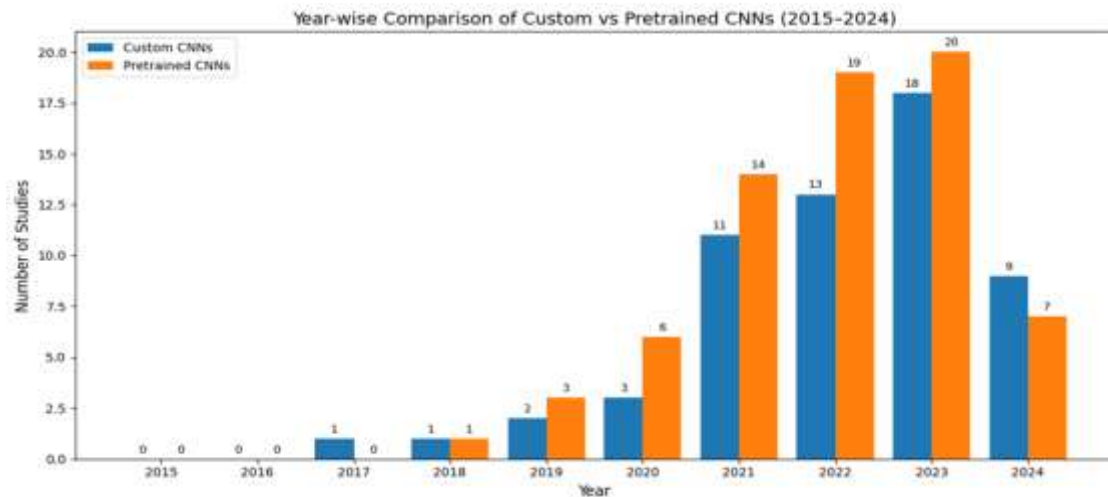


Fig. 4. Year-wise trends in Custom vs Pretrained CNN usage (2015-2024).

3.1 Analysis of RQ1: What datasets are most frequently used in the selected studies and how are they applied across binary and multi-class classification tasks?

Descriptive Analysis: The Table 2 presents the datasets used in various CNN-based brain tumor classification studies, along with the class labels, number of studies per dataset and the total number of studies. Among the datasets, the Figshare Dataset is the most frequently used, appearing in 47 studies, followed by the Kaggle Dataset with a total of 73 studies across different class combinations. The BraTS dataset is used in 10 studies, mainly for tumor vs. non-tumor and glioma subtype classification tasks.

The TCIA dataset, particularly its REMBRANDT subset, is used in 8 studies, while the RIDER subset appears in 1 study. Radiopedia and MICCAI and RSNA datasets are rarely used, each appearing in 1 study. Combined datasets are also employed in 5 studies, indicating an interest in leveraging multiple sources to improve classification robustness. These combined datasets often merge data from REMBRANDT, MIRIAD, BRAINS, BraTS, TCGA-LGG, Figshare, and IXI. The class distributions vary greatly across datasets, ranging from simple binary classifications (e.g., tumor vs. non-tumor) to multi-class problems involving different tumor types and grades (e.g., HGG vs. LGG, Grade II–IV gliomas, meningioma vs. glioma vs. pituitary). The Other (Private) Datasets category includes 3 studies using proprietary data, indicating some reliance on institution-specific collections. Overall, the table shows a preference for publicly available datasets such as Figshare, Kaggle, and BraTS, but also highlights diversity in class labeling and dataset combinations, which can complicate direct comparisons between studies.

Figure 5 demonstrate that most studies use only one dataset, with 104 studies depending on a single source. Using two datasets is less common, seen in 16 studies. Using more than two datasets is rare, only 4 studies use 3 datasets, and just 1 study each uses 4, 6, or 7 datasets. In some cases, researchers combine datasets from different sources, seen in 5 studies, mainly to increase sample size or cover more tumor types.

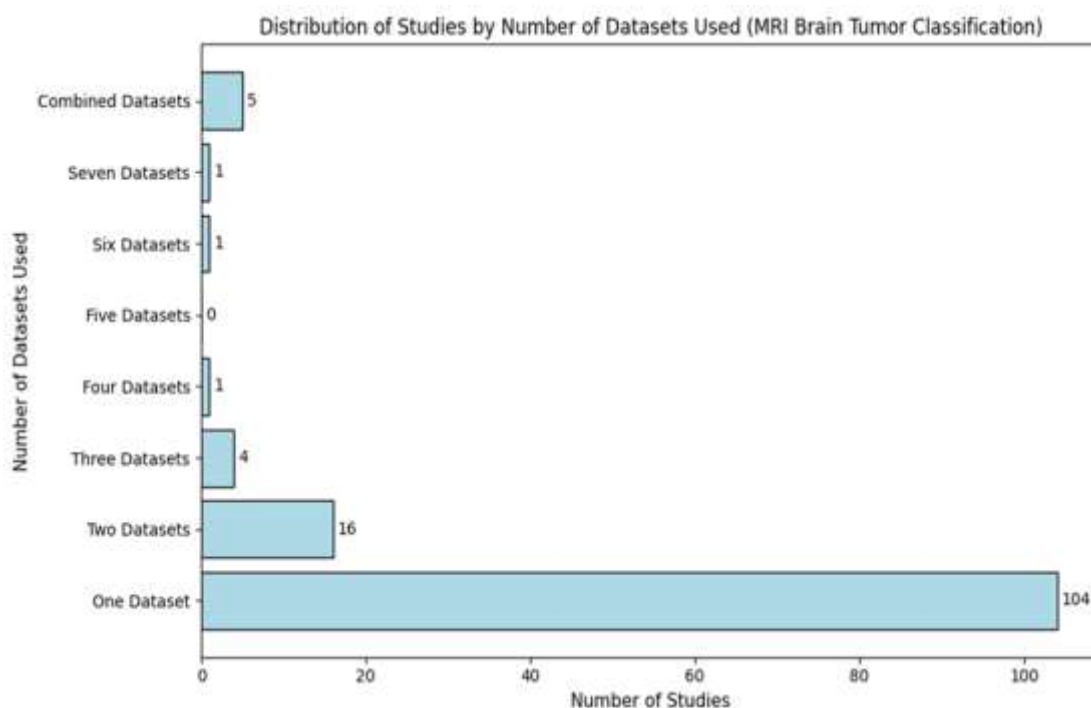


Fig. 5. Distribution of selected studies by number of datasets.

Table 2: Datasets utilized in selected studies.

Dataset Name		Total No. of Studies
BraTS		10
Figshare Dataset		47
Kaggle Dataset		73
TCIA (REMBRANDT and RIDER)		9
Radiopedia		1
MICCAI and RSNA		1
Combine d Datasets	REMBRANDT + MIRIAD + BRAINS; Radiopedia + BraTS 2015; RIDER + REMBRANDT + TCGA-LGG + Figshare; MICCAI + RSNA	4
Other		3

BraTS: Brain Tumor Segmentation, ISLeS: Ischemic Stroke Lesion Segmentation, HGG: High-Grade Glioma, LGG: Low-Grade Glioma, GBM: Glioblastoma Multiforme, EP: Ependymoma, MB: Medulloblastoma, OLI: Oligodendroglioma, REMBRANDT: Repository of Molecular Brain Neoplasms Data, BRAINS: Brain Images of Normal Subjects, MIRIAD: Minimal Interval Resonance Imaging in Alzheimer's Disease, MICCAI: Medical Image Computing and Computer-assisted Intervention Society, RSNA: Radiological Society of North America, RIDER: Reference Image Database to Evaluate Response, AST: Astrocytoma

Thematic Analysis: MRI brain tumor classification research demonstrates a strong bias toward certain datasets, particularly Figshare and Kaggle, which dominate the literature. The Figshare dataset, despite class imbalance, shows a bias toward the glioma tumor type (Meningioma: 708 images, Glioma: 1426, Pituitary: 930) [20, 24, 30, 32, 48, 53, 73, 79, 87]. Similarly, Kaggle datasets show varying scales of imbalance but remain widely adopted. For example, the Kaggle dataset by Navoneel et al. contains 155 tumor and 98 normal images [27, 46, 86, 106], while the S. Bhuvaji dataset has 937 meningioma, 926 glioma, 901 pituitary, and 500 normal images, with a bias toward the normal class [29, 33, 34, 41, 45, 59]. This repeated reliance on a narrow set of datasets raises concerns about model generalizability and the risk of overfitting to dataset-specific features.

In contrast, the TCIA dataset, used in only nine studies [14, 21, 31, 43, 62, 68, 76, 105, 127], holds significant clinical value because it contains high-quality, standardized MRI scans often accompanied by detailed clinical annotations, such as tumor grade, subtype, and patient outcomes. This makes it particularly valuable not only for tumor detection but also for accurate grading, which is critical in guiding treatment decisions and predicting prognosis. Combined datasets, though representing a smaller share of research, provide a pathway toward improved variability and real-world applicability, yet their use remains underexplored relative to single-dataset approaches [11, 12, 26, 54].

The trend in Figure 5 shows that brain tumor classification studies [13, 15 - 18, 34, 36, 49] often relies on a single dataset, which can make models less generalizable and more tuned to specific dataset features. While combining multiple datasets can improve diversity and performance, it is still rarely done, likely due to challenges like differences in image formats, labeling styles, or quality across sources. Expanding the use of multiple or combined datasets could make models more robust and better suited for real clinical situations.

Many studies on MRI brain tumor analysis also focus on a single stage of diagnosis, such as detection or basic classification, without implementing a complete diagnostic pipeline. Few studies [21, 26, 31, 43, 68] focus on the grading of the tumor but not the comprehensive approach, which would involve first detecting the presence of a tumor, then classifying it into a general type, followed by sub-classification of malignant tumors

into their specific histological types, and finally grading the tumor to assess its severity and guide treatment planning. The lack of such end-to-end diagnostic frameworks limits the clinical utility of current models, as they do not fully replicate the multi-step decision-making process followed in real-world neuro-oncology practice.

3.2 Analysis of RQ2: What data augmentation techniques are employed, how frequently are they used and which are most commonly applied?

DL models require large and diverse datasets to achieve high performance and generalizability. However, in medical imaging, particularly MRI brain tumor classification, data scarcity is a major challenge due to the limited availability of annotated scans, high imaging costs, privacy concerns, and the rarity of certain tumor types [143, 144]. Small datasets often lead to overfitting, where models memorize training data instead of learning general patterns, resulting in poor performance on unseen cases. To address this, data augmentation has emerged as a crucial strategy for enhancing DL model training without the need for additional data collection.

Descriptive Analysis: Out of the 132 studies reviewed, 73 studies applied data augmentation techniques to improve the performance of CNN-based MRI brain tumor classification models. This highlights the widespread recognition of augmentation as an essential step in medical imaging deep learning workflows. The heatmap in Figure 6 converts the frequencies into percentages, allowing for direct comparison across datasets despite the differing study counts. Overall, Rotation and Flipping/Mirroring/Reflection emerge as the most dominant techniques in all datasets, with percentages exceeding 66% in every case and reaching over 90% for Figshare's Rotation usage. Zooming/Scaling and Shifting/Translation are moderately used, with values typically between 28% and 51% except in TCIA, where they are notably lower. Color Transformation and Shearing show selective adoption, with moderate use in datasets such as Kaggle and BraTS. In contrast, techniques like Cropping and Gaussian Blur have consistently low adoption rates, remaining under 20% across all datasets. TCIA shows a distinct pattern with unusually high usage of Salt & Pepper Noise (66.7%), while this technique remains marginal elsewhere. These trends suggest that while certain augmentations like rotation and flipping are universally favored for their effectiveness and low risk of distorting key image features, others are applied more selectively, influenced by dataset characteristics, study objectives, and the need to preserve critical medical image details.

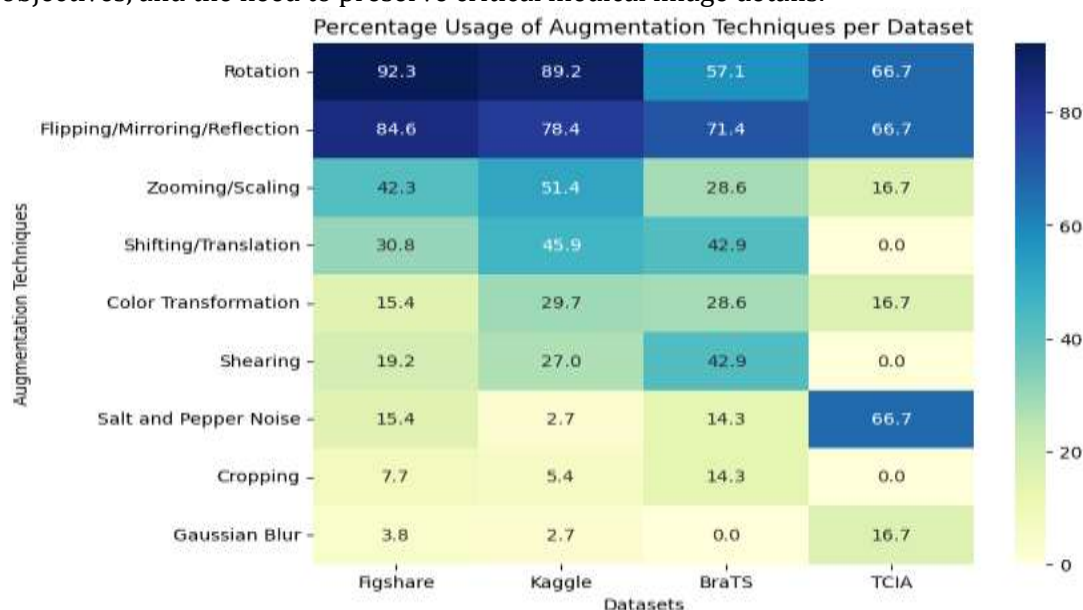


Fig. 6. Heatmap Representation of Augmentation Technique usage in Different Datasets.

Thematic Analysis: The choice of augmentation techniques in MRI brain tumor classification studies appears to be strongly influenced by the nature of the data and the need to preserve critical diagnostic features. Support for the preference of geometric transformations comes from studies like [145], who found that 90° and 180° rotations were most effective for augmentation on TCIA glioma data. Another study [146] showed that cyclic shifting, rotation, and flipping significantly improved tumor grading models, reinforcing their role in preserving diagnostic features. Hence, techniques, such as Rotation and Flipping/Mirroring/Reflection, are consistently and widely adopted across all datasets, with usage rates exceeding 66% and reaching above 90% in Figshare and Kaggle. Their dominance indicates that researchers view them as essential, low-risk strategies for enhancing model robustness while preserving the semantic integrity of medical images. Geometric transformations such as rotation, flipping, zooming and shifting dominate the field because they enhance model generalization without altering tumor shape, texture, or intensity in ways that could mislead the model. These methods also mimic natural variations in patient positioning and scanning conditions, making them clinically relevant.

In contrast, techniques like color transformation, noise addition, cropping, and blurring are used sparingly (<20%) in [17, 21, 22, 31, 43, 71, 76, 80, 84, 93, 99, 111, 118, 119, 129, 142], reflecting caution in modifying medical images where subtle pixel-level details can be diagnostically important. The relatively low adoption of these more aggressive or detail-altering augmentations suggests a lack of systematic exploration of their potential benefits in specific contexts. But can appear prominently in special cases such as the 66.7% usage of Salt & Pepper Noise in TCIA, suggesting dataset-specific needs or experimental objectives. This pattern reveals a methodological gap: augmentation strategies are often selected heuristically based on dataset type rather than being optimized for the specific diagnostic task, highlighting the need for adaptive and data-driven augmentation selection methods.

3.3 Analysis of RQ3: What techniques are used for the tuning of hyperparameters in the selected studies and what are the corresponding search spaces in studies that apply manual tuning or optimization methods?

Hyperparameters play a crucial role in the performance of CNNs, as they directly influence model learning dynamics, convergence rate, generalization ability, and final classification accuracy. Parameters such as learning rate, batch size, number of filters, kernel size, dropout rate, optimizer type, and activation functions determine how effectively a CNN can learn discriminative features from MRI brain tumor images. An inappropriate choice of hyperparameters can lead to underfitting, overfitting, slow convergence, or suboptimal performance, making their careful selection a critical step in model development for medical image analysis.

Descriptive Analysis: The Table 3 presents a detailed overview of hyperparameter configurations, their dimensionalities, and the tuning methods used across 10 studies involving custom CNN architectures. Each study specifies a range of hyperparameters within its search space, categorized as either discrete, continuous, or hybrid. The dimensionality column indicates the number of independent hyperparameters considered, while the search space size shows the total possible combinations, which in some cases is infinite due to the inclusion of continuous parameters. For instance, studies with hybrid search spaces combining discrete and continuous variables, such as studies [22, 30], report infinite search space sizes. In contrast, purely discrete configurations,

such as studies [26, 68], provide exact counts of possible configurations, ranging from thousands to hundreds of thousands. Hyperparameter tuning methods vary between Bayesian Optimization and Grid Search, with Bayesian Optimization typically applied to hybrid or infinite spaces, while Grid Search is used for finite discrete spaces.

Table 3: Summary of Hyperparameter Search Spaces, Dimensionality, and Tuning Methods in Selected CNN Studies.

Reference and Year	Model	Search Space	Type	Dimensionality and Configuration	Hyperparameter Tuning Method
[22] 2021	Custom CNN	Dropout Percentages [0, 0.5]	Continuous	dimensionality = 5 Search-space size = infinite (Hybrid Search-space)	Bayesian
		Conv2D Filters [16, 32, 64, 128, 256, 512]	Discrete		
		Conv2D Kernel Size (x, x) [2, 3, 4, 5]	Discrete		
		Max Pooling Size (x, x) [2, 3, 4, 5]	Discrete		
		Dense Filter [16, 32, 64, 128, 256, 512, 1024, 2048, 4096]	Discrete		
[26] 2021	Custom CNN	Number of convolution and max pooling layers [1, 2, 3, 4]	Discrete	dimensionality = 9 Search-space size = 716,800	Grid
		Number of FC layers [1, 2, 3, 4]	Discrete		
		Number of filters [16, 24, 32, 48, 64, 96, 128]	Discrete		
		Filter size [3, 4, 5, 6, 7]	Discrete		
		Activation function [ELU, SELU, ReLU, Leaky ReLU]	Discrete		
		Mini-Batch Size [4, 8, 16, 32, 64]	Discrete		
		Momentum [0.80, 0.85, 0.9, 0.95]	Discrete		
		Learning Rate [0.0001, 0.0005, 0.001, 0.005]	Discrete		
		l2 Regularization [0.0001, 0.0005, 0.001, 0.005]	Discrete		
[30] 2022	Custom CNN	Activation function [ReLU, ELU, Sigmoid, SELU, Tanh]	Discrete	dimensionality = 5 Search-space size = infinite (Hybrid Search-space)	Bayesian
		Batch size [1 to 128]	Continuous		
		Dropout rate [0.1 to 0.5]	Continuous		
		Number of dense nodes [32 to 1024]	Continuous		
		Gradient descent optimizer [Adam, Nadam, AdaMax, RMSProp, SGD]	Discrete		
		Convolutional layer size [5, 7, 9, 11]	Discrete	dimensionality = 6	Bayesian
		Kernel size [3x3, 5x5]	Discrete		

[59] 2023	Custom CNN	Filters size [min value =16, max value =256, step =16]	Continuous	Search-space size = 3,072 (Hybrid Search-space)	
		Dropout-rate [0.0, 0.2, 0.3, 0.4, 0.5, 0.6]	Discrete		
		Optimizer [Adam, SGD with Nesterov]	Discrete		
		Learning rate [0.001, 0.0001]	Discrete		
[68] 2024	Custom CNN	Layers of maximum pooling and CNN [1, 2, 3, 4]	Discrete	dimensionality = 6 Search-space size = 829,440	Grid Search
		Layers that are completely connected [1, 2, 3, 4]	Discrete		
		Nnumber of flters [8, 16, 24, 32, 48, 64, 96, 128, 256]	Discrete		
		Intensity of fltration [3, 4, 5, 6, 7]	Discrete		
		Activation [ReLU, ELU, Leaky ReLU]	Discrete		
		Size of minibatch [4, 6, 16, 24, 32, 64]	Discrete		
		Rate of change [0.78, 0.77, 0.95, 0.96]	Discrete		
		Rate of learning [0.0002, 0.00043, 0.002, 0.004]	Discrete		
		R2-regularization [0.0002, 0.00043, 0.002, 0.004]	Discrete		
[108] 2022	Incep ResNetV3	-	-	-	Grey wolf
[110] 2022	GoogLeNet	-	-	-	Grid
[112] 2022	VGG16	-	-	-	Grid
[126] 2023	EfficientNet B3	Number of convolutional + max pooling layers [2, 3, 4, 5, 6]	Discrete	dimensionality = 6 Search-space size = 600	Genetic
		Number of fully connected + dropout layers [1, 2, 3]	Discrete		
		Activation functions [Elu, softmax]	Discrete		
		Feedforward optimizer [Nadam]	Discrete		
		Learning rate [1e-4, 1e-5, 1e-8, 3e-4, 5e-5]	Discrete		
		Dropout rate [0.2, 0.3, 0.4, 0.5]	Discrete		
[134] 2024	EfficientNet B4	Units [64, 128]	Discrete	dimensionality = 5 Search-space size = 192	Bayesian
		Dropout Rate [0.2, 0.3, 0.4, 0.5]	Discrete		
		Optimizer [Adam, SGD, RMSprop, Adagrad]	Discrete		
		Learning rate [0.01, 0.001, 0.0001]	Discrete		
		Batch size [16, 32]	Discrete		

Thematic Analysis: The analysis of hyperparameter tuning practices shows that most CNN-based studies do not perform systematic tuning. More than 70% of the studies in the dataset do not apply any tuning at all. This may be due to a lack of awareness about the importance of hyperparameters for model performance or because of constraints such as high computational cost and limited time. Manual tuning is more common than optimization methods but still accounts for fewer than one fifth of the studies. Although relatively more common, manual tuning relies heavily on researcher intuition, making it time consuming, prone to bias, and unsuitable for exploring large search spaces. Optimization methods, although capable of exploring complex and large search spaces more effectively, are used in only a small proportion of the studies. This pattern suggests a methodological gap and highlights an opportunity for future research to apply automated and systematic tuning strategies to improve the accuracy and generalizability of CNN models.

Table 3 shows how different studies tune hyperparameters for custom CNNs, focusing on the type of parameters, the size of the search space, and the methods used for optimization. A clear pattern is that studies [22, 30, 59, 134] with large or hybrid search spaces (mixing discrete and continuous parameters) usually use Bayesian Optimization, as it is better for handling large or infinite possibilities efficiently. In contrast, studies with only discrete parameters often use Grid Search, which checks every possible option but is more time-consuming. The number of parameters explored (dimensionality) varies widely, from as few as five to as many as nine, showing differences in how complex or flexible the models are. Common hyperparameters include layer counts, filter sizes, activation functions, and learning rates, though the exact choices differ between studies. It is also important to note that studies [108, 110, 112] do not mention their search space, which makes it harder to compare their methods directly with others. Overall, the table shows two main approaches: precision-focused optimization for large spaces and exhaustive search for smaller, well-defined spaces.

4 Research Gaps and Future Scope

4.1 Dataset Standardization

4.1.1 Limited use of Clinically Rich Datasets

Most studies on MRI brain tumor classification rely heavily on the Figshare and Kaggle datasets, whereas the TCIA dataset, which offers high-quality MRI scans along with detailed clinical annotations such as tumor grade, subtype, and patient outcomes, which can help in treatment planning, is rarely utilized [14, 21, 31, 43, 62, 68, 76, 105, 127]. This limited use of diverse datasets increases the risk of models' overfitting to dataset-specific characteristics rather than learning generalizable tumor features, which can reduce their performance when applied to unseen clinical data.

4.1.2 Focus on Simpler Classification Tasks

Most research on MRI brain tumor classification focuses on tasks involving only two to four classes, as large and well-balanced datasets covering many tumor types are difficult to obtain. More detailed multi-class classification, including rare tumor types, has the potential to support clinicians in making more accurate and specific diagnoses, yet such studies remain uncommon in the literature [21, 25, 26, 68, 138, 141].

4.1.3 Focus on Single Dataset Training

Many studies in MRI brain tumor classification train and test models using the same dataset, while the use of multiple datasets or cross-dataset evaluation, which could

improve model reliability and generalizability, is still rare [21, 28, 58, 68]. This limited adoption is often due to differences in dataset formats, labeling styles, and image quality, which create challenges for integration and harmonization.

4.1.4 Lack of Comprehensive Tumor Diagnosis

Current studies often address only one stage of MRI brain tumor analysis, such as detection or basic classification, without progressing to sub-classification of malignant types and grading. This absence of complete, multi-stage diagnostic pipelines reduces the clinical applicability of these models in replicating real-world decision-making.

Future research should prioritize the use of clinically rich and diverse datasets like TCIA, explore more complex multi-class classification including rare tumor types, adopt multi-dataset training and cross-dataset evaluation for improved generalizability, and develop complete multi-stage diagnostic pipelines that progress from detection to subtype classification and grading for greater clinical applicability.

4.2 Specific Augmentation

4.2.1 Limited evaluation of augmentation effects on diagnostic integrity

A few studies [28, 100, 114] applied augmentation while assessing whether the transformations preserved diagnostically relevant features, whereas many others [15 - 18, 25, 36, 49, 98] did so without systematically evaluating the potential impact on tumor morphology or the risk of misleading radiological interpretation.

4.2.2 Lack of Dataset-Specific Augmentation Adaptation

Most of the reviewed studies [14, 31, 43, 44, 56, 84, 113, 118, 138] applied identical augmentation techniques across different datasets without modification, regardless of variations in imaging modality, resolution, acquisition parameters, or tumor presentation. Only one study [21] tailored different augmentation settings to the different datasets. This indicates a research gap in dataset-specific augmentation strategies, where adaptive methods could potentially enhance feature preservation and model robustness.

4.2.3 Lack of Parameter Sensitivity in Common Augmentation Techniques

While rotation, flipping, and zooming are among the most commonly employed augmentation techniques in the reviewed studies, there is a notable absence of systematic investigation into the sensitivity of these methods to parameter settings. In most cases, studies applied fixed values for augmentation parameters (e.g., rotation angles, flip orientation, zoom ranges) without evaluating how variations in these values might affect the spatial localization, orientation, or scale of the tumor region. Since excessive rotation, zoom, or flipping can alter the perceived position or shape of the tumor, inappropriate parameter selection may distort key diagnostic features, potentially leading to degraded model performance. No study in the review explicitly examined optimal parameter ranges for these transformations in the context of preserving tumor integrity.

4.2.4 Lack of integration with advanced augmentation methods

No study integrated advanced approaches such as GAN-based synthetic data generation or domain adaptation with classical augmentations under clinical guidance.

Future work should focus on applying dataset-specific optimized augmentation techniques using optimization methods to adapt transformations based on imaging modality and tumor characteristics. This includes evaluating the diagnostic integrity of augmentations, systematically tuning parameter ranges, and integrating advanced

approaches such as GAN-based synthesis or domain adaptation under clinical guidance to enhance feature preservation and model robustness.

4.3 Hyperparameters Optimization

4.3.1 Lack of systematic hyperparameter tuning

Over 70% of CNN-based brain tumor classification studies do not perform any hyperparameter tuning, potentially limiting model performance and generalizability.

4.3.2 Over-reliance on manual tuning

Manual tuning is more common than optimization methods but still rare and dependent on researcher intuition, which is time-consuming, prone to bias, and unsuitable for large search spaces.

4.3.3 Limited adoption of advanced optimization methods

Bayesian Optimization and other automated strategies are used in only a small fraction of studies, despite their ability to efficiently explore large and hybrid parameter spaces.

4.3.4 Insufficient reporting of search space details

Some studies [108, 110, 112] fail to specify the dimensionality or boundaries of their search spaces, making reproducibility and fair comparison difficult.

4.3.5 Narrow focus on discrete parameters

Some studies [26, 68, 129, 134] restrict tuning to discrete parameter choices, neglecting continuous or hybrid parameter spaces that could yield better performance.

Future research should prioritize dataset-specific hyperparameter tuning using advanced optimization methods such as Bayesian Optimization to improve performance and generalizability. Clearly defining and reporting search space boundaries, including continuous, discrete i.e. hybrid parameters, will enhance reproducibility and allow fair comparisons across studies. This approach can ensure more robust and adaptable CNN models for brain tumor classification.

5 Conclusions

This systematic literature review (January 2015 – June 2025) comprehensively analyzed 132 peer-reviewed studies on MRI brain tumor classification, categorized into 60 studies employing custom CNN architectures and 72 studies leveraging transfer learning with existing pretrained CNNs, following the PRISMA framework. The review addressed five research questions based on datasets used, data augmentation techniques applied, methods for hyperparameter tuning, transfer learning-based CNNs applied and the evaluation metrics. This review identifies critical gaps and future directions in MRI brain tumor detection and classification after analysing the research questions. Future research should prioritize the use of clinically rich and diverse datasets like TCIA, explore multi-class classification including rare tumor types, adopt multi-dataset training with cross-dataset evaluation, and develop complete multi-stage diagnostic pipelines for improved clinical applicability. Dataset-specific optimized augmentation techniques, tuned through advanced optimization methods, should be applied with careful consideration of diagnostic integrity, integrating approaches like GAN-based synthesis or domain adaptation for enhanced feature preservation. Hyperparameter tuning should be dataset-specific, leveraging methods such as Bayesian Optimization with clearly defined search spaces to improve reproducibility and adaptability. While pretrained CNNs show strong

potential, future work should diversify architectures, explore lightweight and domain-specific models, and integrate multi-modal data. Standardized evaluation protocols using a core set of metrics (accuracy, recall, precision, specificity, F1-score) and advanced measures (AUC-ROC, MCC, confidence intervals) are essential to ensure robust, clinically relevant, and comparable results across studies.

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