

# An artificial intelligence framework and its bias for brain tumor segmentation: A narrative review

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## Highlights

- •  
PRISMA search strategy and statistical distributions for brain tumor segmentation (BTS).
- •  
Comparison between different AI models, its qualitative and quantitative analysis.
- •  
Ranking Score Method for Risk-of-bias (RoB) estimation in AI.
- •  
Usage of 32 AI attributes for mean score computation and cutoff determination.
- •  
Primary and secondary recommendations for lowering the RoB in AI for BTS.

## Abstract

### Background

Artificial intelligence (AI) has become a prominent technique for medical diagnosis and represents an essential role in detecting brain tumors. Although AI-based models are widely used in brain lesion segmentation (BLS), understanding their effectiveness is challenging due to their complexity and diversity. Several reviews on brain tumor

segmentation are available, but none of them describe a link between the threats due to risk-of-bias (RoB) in AI and its architectures. In our review, we focused on linking RoB and different AI-based architectural Cluster in popular DL framework. Further, due to variance in these designs and input data types in medical imaging, it is necessary to present a narrative review considering all facets of BLS.

## Approach

The proposed study uses a PRISMA strategy based on 75 relevant studies found by searching PubMed, Scopus, and Google Scholar. Based on the architectural evolution, DL studies were subsequently categorized into four classes: convolutional neural network (CNN)-based, encoder-decoder (ED)-based, transfer learning (TL)-based, and hybrid DL (HDL)-based architectures. These studies were then analyzed considering 32 AI attributes, with clusters including AI architecture, imaging modalities, hyper-parameters, performance evaluation metrics, and clinical evaluation. Then, after these studies were scored for all attributes, a composite score was computed, normalized, and ranked. Thereafter, a bias cutoff (AP(ai)Bias 1.0, AtheroPoint, Roseville, CA, USA) was established to detect low-, moderate- and high-bias studies.

## Conclusion

The four classes of architectures, from best-to worst-performing, are TL > ED > CNN > HDL. ED-based models had the lowest AI bias for BLS. This study presents a set of three primary and six secondary recommendations for lowering the RoB.

## Introduction

According to data collected by Global Cancer Statistics in 2020 [1], brain tumors represent one of the most life-threatening cancers and the 21st most common type of cancer worldwide. Moreover, nearly 90% of primary central nervous system (CNS) tumors are brain tumors [2]. Brain tumors also have a significant financial impact, as treatments incur a mean cost of  $\$2788 \pm 3719$  [3], which can vary depending on the imaging technique used. It is estimated that it costs \$62,602 to extend a brain tumor patient's life by 16.3 months [3] when employing modern treatment techniques. Due to

this financial burden, the death rate of brain tumor patients increases daily; the five-year average survival rate of the patients is 72.5% [4].

Medical imaging is considered one of the most promising and fastest ways to diagnose brain tumors. Magnetic resonance imaging (MRI) and computed tomography (CT) are typically employed for brain scans [5]. MRI scans are among the most preferred methods for diagnosing brain tumors [6], as they provide more precise and detailed pictures than CT scans. MRI can also provide better images of soft tissue than CT and is useful for tissue characterization. Different MR images, such as T1-weighted, post-contrast T1-weighted (T1ce), T2-weighted, and fluid-attenuated inversion recovery (FLAIR) protocols [7] provide complementary information that helps segment the brain tumor and its surrounding tissues. The visual output of the different MRI modalities along with the segmented tumor regions, namely, necrosis, enhancing, and edema types [8] is shown in Fig. 1. The three tumor regions used in the practical clinical application are: (i) the necrosis region (consisting of non-enhancing and enhancing part of tumor), (ii) the enhancing region (consisting of enhancing part of the whole tumor), and (iii) the peritumoral edema region (consisting of edema region of the whole tumor)". Glioma, which develops from glial cells, is one of the most common malignant tumors [9]. It is categorized into low-grade glioma (LGG), which grows slowly, and high-grade glioma (HGG), which is highly malignant and potentially life-threatening. HGG is untreatable in some cases, even when advanced imaging, radiotherapy, and surgical techniques are employed. HGG segmentation is a challenging task [10,11] due to cell mutations, irregular growth in multiple tissues, and the complex and diverse nature of HGG. Treatment is also challenging because tumor characteristics vary from patient to patient; therefore, it can be difficult to use a large number of scans and volumes when attempting to visualize and quantify lesions. These images also contain various artifacts [12], such as irregularities, pixel variations, and inhomogeneity, which are acquired through the use of different scanners. Therefore, an accurate and fast brain tumor segmentation (BTS) method is needed to handle binary (high and low) and multiple types of risk classes (e.g., low, mild, moderate, and high), thus promoting early diagnosis and cost-effective treatment.

Artificial intelligence (AI) has become a prominent solution for medical diagnoses and is essential to detecting brain tumors. Generation-wise segmentation technologies are depicted in Fig. 2. The first generation of brain lesion segmentation (BLS) was primarily

characterized by the conventional method [13,14]. The second and third generations mainly consisted of machine learning (ML)-based [10,15] and DL-based AI technologies. ML and DL differ in terms of how they derive features from instances. ML classification models often emerge as independent analytical learning models and obtain precise predictions using features that have been extracted. ML technology has been shown to be useful for tissue characterization in medical imaging applications [16]. The performance of ML methods [17,18] depends solely on the radiologist or researcher and their expertise in selecting the most compelling features, which results in biased methods.

Therefore, researchers have become interested in AI-based deep learning (DL) models [19] that utilize various statistical knowledge layers and convolutional operations to obtain features and employ predictions [20,21]. DL-driven medical image analyses can change the current roles of radiologists and clinicians, allowing them to devote less time to screening medical images and concentrate more on making diagnoses and treatment decisions. Therefore, although DL techniques are more expensive than other techniques in terms of space and computation time, they produce exact predictions when implemented in a widespread dataset.

After continuing an active on BLS for some past years, we observed that, to date, no review article on BLS has connected the latest AI technologies with the tumor imaging paradigm. This motivates us to present a systematic review on BLS using the latest AI technology of the deep learning paradigm. In this review, we discussed and presented a detailed statistical analysis of BLS in DL technology with respect to (i) DL-based AI architectures, (ii) model hyper-parameters, (iii) imaging modalities, (iv) clinical validation, and (v) scientific validation. Our finding from this analysis drives us towards the main contribution of the proposed review, which is to classify the DL-based segmentation model into four different categories (i.e., CNN-based, ED-based, TL-based, HDL-based) and then perform a depth-wise bias analysis of these models for a BLS task. However, it is observed that there exists a bias in DL models for BLS, where the performance is very high but clinically there are not reliable or the model did not perform scientific or clinical validations or did not undergo hyper-parameterization to optimize the AI models. For evaluating the bias in these studies, we employ an AP(ai)Bias 1.0 (AtheroPoint, Roseville, CA, USA), which is based in essence on a ranking score method (RSM) [22]. Using the 32 AI-based attributes, we grade the

attributes (using an AI expert with minimum of 10 years of experience), estimate the final score, normalize it, and then rank these studies to determine the low-bias and moderate-bias cutoffs. These bias studies are then linked to the AI architectures providing recommendations for improving the AI system design. The proposed narrative review selected the 75 best publications using the PRISMA model described in section 2. This review presents (i) a statistical distribution of AI attributes in BLS for different DL architectures, (ii) AI architectures for tumor segmentation with a detailed explanation of four DL architecture classes, and (iii) a comprehensive risk-of-bias (RoB) analysis based on 32 different AI attributes such as dataset partitioning, activation function; statistical analysis, and clinical validation.

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The rest of this paper is organized as follows: Section 2 briefly describes the PRISMA model and statistical distributions; section 3 depicts the detailed classification of the DL architecture, along with its pros and cons. Then, in section 4, the RoB analysis is carried out—based on the analysis, a few recommendations are made to improve the bias of the studies. Finally, a critical discussion is presented in section 5.

## **Section snippets**

### **PRISMA model design**

An extensive search was carried out on PubMed, Google Scholar, and Scopus. The keywords used for selecting studies were “brain tumor segmentation,” “deep learning in brain tumor segmentation,” “AI-based BLS,” “machine learning in brain tumor segmentation,” “CNN in brain tumor/lesion extraction,” “transfer learning in brain tumor/lesion extraction,” and “multiclass brain tumor classification.” Fig. 3 shows the PRISMA model consisting of the brain tumor articles used in this study.

A total of

## **AI architecture for brain tumor segmentation**

In the previous section, research trends in BTS and its importance, different BTS algorithms, its statistics in terms of hyper-parameters, and AI attributes were discussed. However, these parameters are used in every DL-based model to tune its performance, and we have to focus on the internal structure of the DL-based model, which greatly affects its design and implementation in research. Hence, this section presents a brief outline of different generations of segmentation techniques used in

## **Risk-of-bias estimation and recommendations**

We have seen a detailed layout of different DL-based architecture, along with their performances and the AI attributes used in each of these models. However, each model essentially performs convolutional operations to extract the features. Pre-processing and over-fitting are also considered in each model to maximize the performance. To perform a detailed study on the behavior of the models used by different authors, we compute the bias studies of all articles and analyze them to make some

## **Critical discussion**

The proposed study presented a narrative review for BTS using AI-based DL. Hence the review starts by describing the search strategy using the PRISMA model, followed by the statistical analysis of AI attributes. The review included 75 DL-based qualitative articles on BLS. DL-based studies on BLS continue to gain the interest of researchers; however, to the best of our knowledge, no review has focused on the architectural evolution of DL while aiming to understand the AI bias for BLS. Therefore,

## **Conclusion**

DL is the most recent efficient AI technique in BTS due to its automatic feature extraction. We reviewed articles that employed four different DL architectural models (i.e., CNN-based, ED-based, TL-based, and HDL-based) utilizing a certain operation performed in each model for BLS. A statistical depth analysis was carried out. The

results were displayed as pie charts and bar charts showing the distributions of different parameters such as image modalities, optimizers, activation function,

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## Citation Excerpt :

In order to improve the generalization capabilities of deep models, it suggests prospective research approaches for synthesizing high-quality artificial brain tumor cases. Das et al (Das et al., 2022). employed a PRISMA methodology to classify 75 pertinent research works into four categories, namely convolutional neural network (CNN), encoder-decoder (ED), transfer learning (TL), and hybrid DL (HDL)-based architectures.

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