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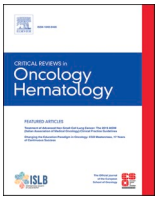

Advances of artificial intelligence in clinical application and scientific research of neuro-oncology: Current knowledge and future perspectives

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ABSTRACT

Brain tumors refer to the abnormal growths that occur within the brain's tissue, comprising both primary neoplasms and metastatic lesions. Timely detection, precise staging, suitable treatment, and standardized management are of significant clinical importance for extending the survival rates of brain tumor patients. Artificial intelligence (AI), a discipline within computer science, is leveraging its robust capacity for information identification and combination to revolutionize traditional paradigms of oncology care, offering substantial potential for precision medicine. This article provides an overview of the current applications of AI in brain tumors, encompassing the primary AI technologies, their working mechanisms and working workflow, the contributions of AI to brain tumor diagnosis and treatment, as well as the role of AI in brain tumor scientific research, particularly in drug innovation and revealing tumor microenvironment. Finally, the paper addresses the existing challenges, potential solutions, and the future application prospects. This review aims to enhance our understanding of the application of AI in brain tumors and provide valuable insights for forthcoming clinical applications and scientific inquiries.

1. Introduction

Brain tumors include primary tumors that originating from the central nervous system (CNS) and metastatic lesions arising from elsewhere in the body and spreading to the brain. In the United States, brain and other nervous system tumors are the leading causes of cancer-related deaths in men under 40 years of age and women under 20 years of age and are significant economic and social burdens (Siegel et al., 2022). Malignant primary brain tumors cause more than 250,000 deaths each year, with a five-year survival rate of approximately 36 % (Sung et al., 2021). Among all patients with primary malignant brain tumors, the median survival of patients with glioblastoma, the most common type of tumor, is less than 2 years (Lah et al., 2020; Tan et al., 2020). In addition, in patients with metastases originating from the primary lesion, the brain is considered the most common site, affecting approximately 23–28 % of this patient population (Lamba et al., 2021). Brain tumors have caused serious threats to human life and health. Therefore, early identification, accurate staging and appropriate treatment are considered to be highly clinically important.

Conventional diagnosis of brain tumors relies on traditional imaging techniques such as magnetic resonance imaging (MRI) and computed tomography (CT), followed by a clinicians' empirical interpretation. However, this process is highly susceptible to human interference and has significant potential for inaccuracies. These inaccuracies can occur in tumor segmentation, differentiation of tumor-like lesions, diagnosis of tumor types and stages, and differentiation of post-treatment changes, etc (Clarke and Chang, 2009; Fukuya et al., 2019; Huisman, 2009; Na et al., 2014; Wang et al., 2020). Moreover, advancements in medical technology have raised expectations for more precise clinical practices. There is now a growing demand for improved preoperative and intraoperative planning, refined precision in cancer treatment, and standardized patient management throughout the entire disease process. In scientific research, the development of novel drugs and delivery systems, the mapping of the tumor microenvironment (TME) landscape and the investigation of the underlying mechanisms of tumorigenesis and progression, are also matters of pressing urgency. The introduction and application of artificial intelligence (AI) in the field of neuro-oncology is bringing hope for the solution of the above needs, and bringing amazing technological innovations for the accurate diagnosis, precise treatment and scientific research of brain tumors.

AI is a branch of computer science in which computers or computer-controlled machines are used to perform tasks associated with human

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intelligence, such as reasoning, discovering meaning, generalizing, or learning from past experiences (Haug and Drazen, 2023; Wang et al., 2023). Based on the availability of high-dimensional datasets, progressively innovative algorithmic patterns, and their powerful ability to identify and combine information, AI techniques are gradually reshaping our established patterns of tumor diagnosis and treatment, holding great promise for the future of precision medicine (Bhinder et al., 2021; He et al., 2023). In recent years, AI-based technologies have also been widely applied in the scientific research and clinical management of brain tumors.

In this review, we provide an in-depth introduction to the fundamentals of AI techniques and offers a comprehensive overview of its current applications in neuro-oncology. Our research seeks to investigate how AI may bring new experiences to the precise, standardized, and whole-process management of brain tumors, and promote the scientific research. The current challenges, possible solutions and future prospects are discussed, with the anticipation of propelling the advancement of the discipline.

2. Artificial intelligence, machine learning, and deep learning

2.1. Overview of common concepts in AI field

AI is a branch of computer science originally defined as the use of machines to perform tasks associated with human intelligence, such as language recognition, visual perception, making decisions, and more. In simple terms, AI can be thought of as a programmed machine that recognizes and learns patterns and relationships between input and output data and is able to make decisions on entirely new input data based on the knowledge gained. In medicine, the application of AI includes two main branches as entity object and virtual component (Hamet and Tremblay, 2017). Entity objects are mainly various medical devices, robots, while virtual component is represented by two main branches as machine learning and deep learning. In Fig. 1, we delineate some pivotal concepts within AI realm, including artificial intelligence, machine learning, and deep learning, and elucidate the interconnections and distinctions among them.

Machine learning, a core branch of AI, enables computer systems to learn data and execute decisions without explicit programming (Deo, 2015; Greener et al., 2022). Predictions are made by finding patterns in existing data (Fig. 1A). Machine learning methods can be broadly categorized into supervised learning, unsupervised learning, semi-supervised learning and other different learning methods (Hashimoto et al., 2020). Supervised learning uses labeled data to train models that can predict outputs based on new inputs (Jiang et al., 2020; Lo Vercio et al., 2020) (Fig. 1B). Unsupervised learning deals with unlabeled data, aiming to discover underlying patterns and structures (Yang et al., 2023) (Fig. 1C). Semi-supervised learning, cross between supervised and unsupervised learning, combines a small amount of labeled data with a large amount of unlabeled data to improve model performance(Huynh et al., 2022; Yurt et al., 2022). It is particularly useful when labeled data is scarce or expensive to obtain. Common machine learning algorithms include linear regression, logistic regression, naive bayes, decision tree, random forest, k-nearest neighbor (KNN), k-means, support vector machine (SVM), etc.

Deep learning is a subset of machine learning that uses neural networks (NNs) with multiple layers to make predictions. These networks are inspired by the structure of the human brain and are capable of learning complex patterns from data (Bini, 2018; Castiglioni et al., 2021). The core of deep learning is NNs, which consist of layers of interconnected neurons. Each neuron receives multiple inputs and produces a single output, which is then passed to the next layer (Fig. 1D). This hierarchical structure allows deep learning models to learn features at multiple levels of abstraction, making them highly effective for processing complex and high-dimensional data. By increasing the number of layers in these networks, deep learning models can learn more complex and abstract features, leading to more accurate classification and prediction. This capability sets deep learning apart from traditional machine learning methods, making it particularly powerful for handling intricate data patterns. Common deep learning algorithms include multilayer perceptron (MLP), convolutional neural networks (CNNs), recurrent neural networks (RNNs), long short-term memory (LSTM), gated recurrent unit (GRU), deep residual networks (ResNet), etc.

2.2. Workflow of training AI models

After identifying the type of clinical problem and objective of the AI model (such as classification, clustering, or other tasks), the workflow for training and deploying an AI model can typically be broken down into the following key steps (Fig. 2):

2.2.1. Data collection and preprocessing

Data collection is crucial to AI model training. Advances in medical imaging and detection have led to the availability of diverse datasets, including traditional clinical data (radiology, pathology, electronic health records) and emerging omics data (genomics, transcriptomics, proteomics) (Subrahmanya et al., 2022). Multimodal datasets combining multiple data types can offer more comprehensive disease characterization (Acosta et al., 2022). Table 1 lists the common data types currently applied to AI technologies in brain tumors.

Subsequently, collected data needs to be preprocessed for the follow-up model training (Chahid et al., 2023). In the medical field, data preprocessing typically encompasses data cleaning, handling missing values, and standardization/normalization to enhance data quality (Chahid et al., 2023). Additionally, feature extraction and data augmentation are employed to boost the model's performance and interpretability. Each data type also has unique preprocessing requirements. For instance, image data often needs to be organized into multidimensional arrays or tensors (Salvi et al., 2021). Multimodal data requires temporal and spatial alignment and fusion to ensure consistency. Proper and correct preprocessing can transform the data into a format suitable for AI model training, thus improving the model accuracy.

2.2.2. Model selection

The selection of an appropriate AI model requires a comprehensive consideration of the objectives of the study, the nature of the data, the performance requirements of the model and so on. For example, deep learning models and SVMs can learn from medical data and predict the presence of diseases, which is suitable for the diagnosis of diseases (Din et al., 2022; Fathi et al., 2022; Resmini et al., 2021). Survival analysis can be used to predict the prognosis of disease. Cox proportional hazard regression model is the most widely used to predict survival, but it is limited by its linear nature (Ahmed et al., 2007; Prentice and Zhao, 2021). Incorporating Cox regression into deep learning can well enhance the effect of prognosis prediction (Ching et al., 2018; Katzman et al., 2018). In addition, machine learning algorithm models such as linear regression, decision trees, and random forests can be applied for continuous or discrete numerical data. And for image data such as medical radiological images, CNN is usually used.

2.2.3. Model training and evaluation

The pre-processed data is input into the selected algorithm for model training. The existing dataset is typically partitioned into a training set, a validation set, and a test set, with a standard allocation of 70 % for training, 15 % for validation, and 15 % for testing, and these proportions can be modified based on specific requirements. Choose an appropriate loss function to train the model with the training set, through continuous iteration to minimize the loss. Validation datasets are utilized to assess and verify and evaluate the training effects, adjusting parameters and architecture to enhance its performance.

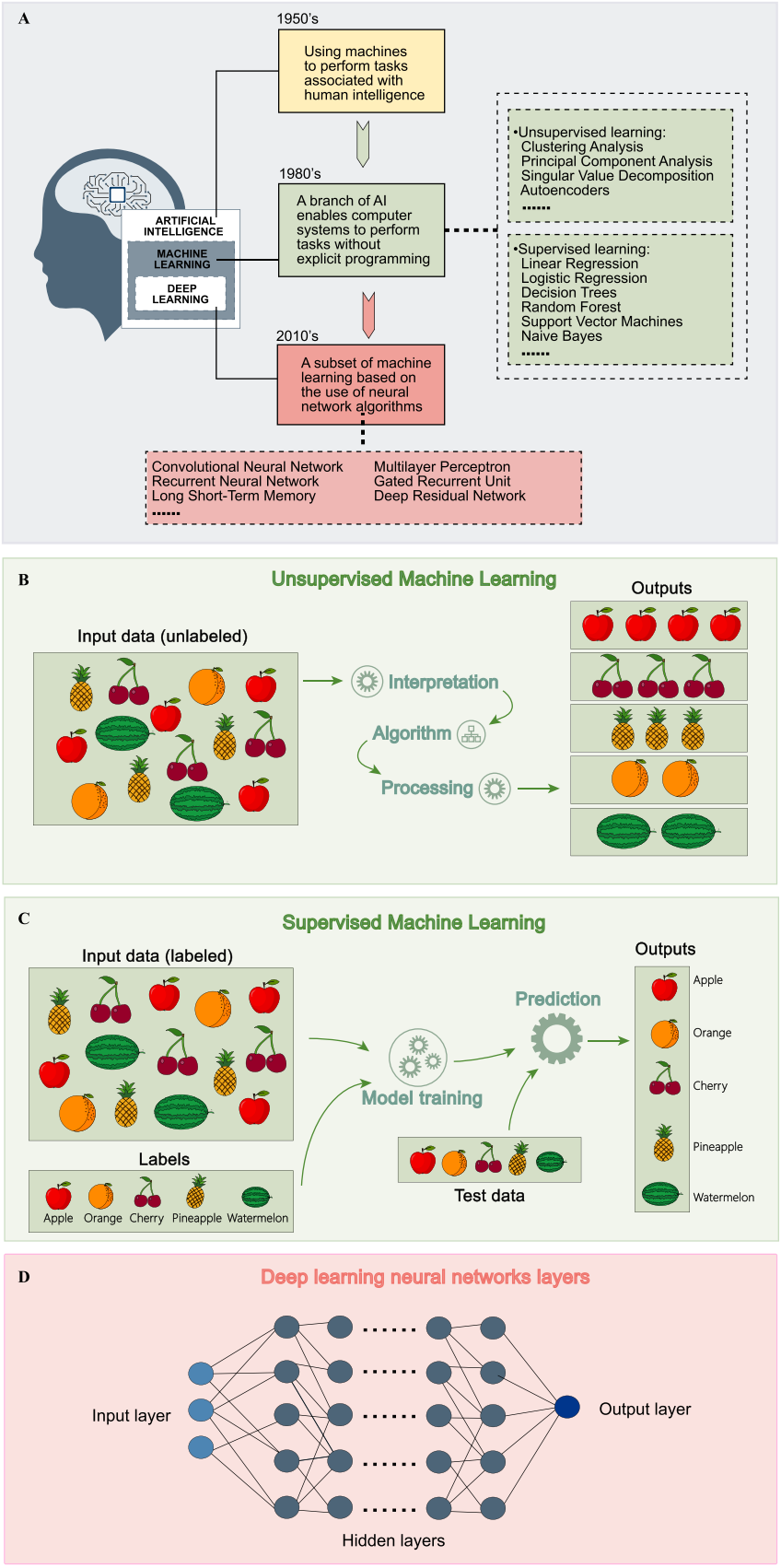

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Fig. 1. An overview of some concepts in the artificial intelligence (AI) field. (A) Concepts and common algorithms of AI, machine learning and deep learning.(B) The working paradigm of supervised machine learning. Supervised learning methods provide known input and output data so that a computer program can learn the mapping relationship between the input and output, and outputs can be predicted based on new inputs. (C) The working paradigm of unsupervised machine learning. Unsupervised learning deals with data without labeled responses, and the computer system needs to explore and discover underlying patterns and structures from these data. (D) The working paradigm of deep learning.

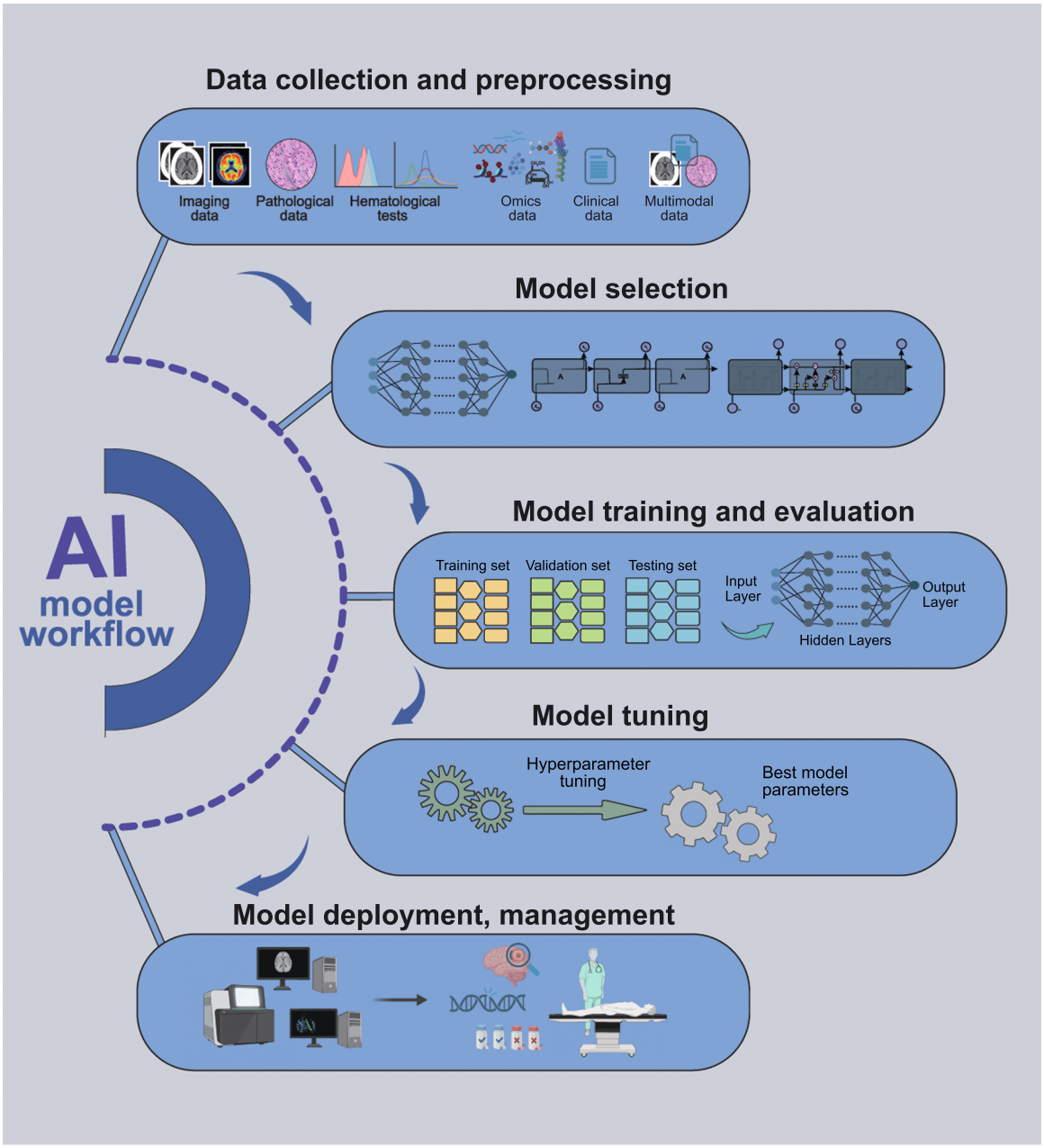

Fig. 2. Life-cycle of an AI model. The workflow for training and deploying an AI model can generally be broken down into the following key steps: (1) Data collection and preprocessing; (2) Model selection; (3) Model training and evaluation; (4) Molde tuning; (5) Model deployment and management.

2.2.4. Hyperparameter tuning

Unlike the model parameters learned from model training, hyperparameters are fixed parameters that are manually set before the training begins. Selecting the best combination of hyperparameters (such as number of layers, learning rate) to optimize the model performance is of great significance to improve the prediction accuracy and achieve the best performance of the model.

After training, the AI model can be deployed in a production environment, with continuous monitoring and feedback loops ensuring its ongoing performance and updates.

3. Application of AI in brain tumor diagnosis

The integration of AI in diagnosing brain tumors is swiftly progressing, marking several significant advancements. Below are insights into the most recent research findings and practical applications.

Table 1
Common data types applied to AI techniques for brain tumors.

Data type	Methods of data collection	Description	Reference
Radiographic imaging data	CT, MRI, PET, SPECT, etc.	Radiographic imaging data refers to the data obtained through radiographic imaging techniques, including CT, MRI, PET, etc., which are widely used in all aspects of the diagnosis and treatment of brain tumors	(Ko et al., 2021; Song et al., 2019; Zacharaki et al., 2009; Zahoor et al., 2022)
Histopathological data	Traditional examination of tissue samples	Traditional histopathology evaluates tissue sections through microscopy to obtain pathological data, which provides important information for the diagnosis, grading and treatment of brain tumors.	(Li et al., 2019; Liu et al., 2023; Nasrallah et al., 2023)
Terahertz data	Terahertz time-domain spectroscopy	Terahertz spectroscopy enables the analysis of biomolecular and conformational characteristics and has been applied for the detection, grading, and identification of molecular features of brain tumors.	(Gavdush et al., 2019; Meng et al., 2014; Wu et al., 2024)
Raman imaging data	Raman-based methods	Stimulated Raman histology is a swift, label-free, and cost-effective optical imaging technique that capitalizes on the natural vibrational attributes of molecules to create image contrast. It has been effectively utilized for the detection and grading of brain tumors.	(Hollon et al., 2023; Hollon and Orringer, 2021)
Omics data	Genomics: WGS, Sanger, NSG Epigenetics: WGBS, Chip-seq, ATAC-seq Transcriptomics: RNA-seq, scRNA-seq, SAGE Proteomics: MS, TMT, LFQ Metabolomics: GC-MS, LC-MS NMR	Omics data, when integrated with AI algorithms, offer a robust instrument for the precision treatment of brain tumors. comprehensively describe tumor status, understand disease characteristics, predict treatment response and prognosis, and provide patients with personalized treatment prescriptions.	(Chen et al., 2022; Yu et al., 2024; Zhang et al., 2024)
Hematology data	Liquid biopsy, traditional blood test, plasma degradation profiles	The results of various hematological tests can be used for early detection, diagnosis, differential diagnosis, molecular subtype identification and prognostic prediction of brain tumors.	(Eyraud et al., 2023; Herrgott et al., 2023; Podnar et al., 2019; Tsvetkov et al., 2021)
Clinical data	Records of patients' medical data	Records of clinical information including patient age, risk factors, adverse events, etc. can be used for patient care and management.	(Crabb et al., 2022; Oermann et al., 2013)
Multimodal data	Integration of different types of data	The integration of different types of data, such as neuroimaging, genomics, and clinical information, can provide a more comprehensive description of disease characteristics.	(Guo et al., 2023; Hollon et al., 2023; Juvekar et al., 2024)

3.1. Tumor screening and early detection

Early detection and diagnosis of brain tumors are crucial for timely treatment and improving patient outcomes, as the survival rate is negatively correlated with tumor stage. While biopsy is the gold standard for diagnosis, it is invasive and carries risks (Soomro et al., 2023). Non-invasive neuroimaging methods like CT and MRI are widely used but face challenges due to the complexity of tumor shapes and the need for expert interpretation. To address these challenges, AI-dependent detection models have been increasingly applied in clinical studies, showing promise in early screening and detection. Accurate image segmentation is key to precise diagnosis, and it can be achieved through traditional image processing, machine learning-based methods, and deep learning strategies (Soomro et al., 2023; Zhang et al., 2021). In Table 2, we list a summary of the primary methodologies for segmenting brain tumors, along with their respective strengths and limitations.

Traditional image segmentation encompasses a variety of techniques such as threshold-based, feature-based, contour-based and region-based methods. Each method has its own advantages and limitations, making them suitable for different types of images and specific applications. For instance, threshold-based methods segment images by identifying pixel intensity levels, working well for images with simple backgrounds (El-Hag et al., 2021; Jumiawi and El-Zaart, 2022; Kamireddy et al., 2024). Feature-based approaches differentiate tumors from normal tissues using characteristics such as texture, morphology, and intensity variations(Julesz, 1981; Xu et al., 2022). Contour-based segmentation is effective for tumors with clear boundaries but performs poorly with fuzzy edges (Comelli et al., 2019; Essadike et al., 2018). Region-growing techniques are ideal for segmenting regions with uniform properties (Letteboer et al., 2004; Mittal and Tayal, 2021; Sivakumar and Janakiraman, 2020). As technology advances, these traditional methods are increasingly being integrated with machine learning and deep learning, thereby enhancing the accuracy and efficiency of segmentation processes (El Kader et al., 2021; Md Ashafuddula and Islam, 2024).

Machine learning open up a new dimension in the screening and

Table 2
Primary methodologies for segmenting brain tumors.

Method		Advantages	Disadvantages	Reference
Traditional image processing techniques	Threshold-based method	simple in construction; fast in execution; flexible to use; easy to optimize	difficult to determine appropriate threshold value in complex images; sensitive to light and noise	(Jumiawi and El-Zaart, 2022; Kanmani and Marikkannu, 2018; Nowosielski et al., 2014)
	Feature-based method	intuitive and easy to understand; high computational efficiency; less require in data amount	rely on prior knowledge; challenge of feature selection	(Chaddad, 2015; Islam et al., 2013; Pei et al., 2020)
	Contour-based method	intuitive and easy to understand; better to keep the details	high calculation cost; limitation in dealing with complex scenes limitations of contour evolution	(He et al., 2007; Zhang et al., 2011)
	Region-based method	intuitive and easy to understand; better to keep the details	high calculation cost; may need to adjust the parameters manually	(Battalapalli et al., 2022; Biratu et al., 2021; Khosravanian et al., 2021)
Machine learning	Support Vector Machine	able to handle high-dimensional problems; able to learn from small sample sizes	consume a lot of memory and computation time when handling large number of samples	(Chen et al., 2021; Zhou et al., 2005)
	Random Forest	high accuracy; overfitting suppression; automatic feature selection; adaptability to various data types	sensitive to noise; poor model interpretability; high consumption of computational resources	(Kifle et al., 2023; Pereira et al., 2018; Zhou et al., 2024)
	K-Means	simplicity and ease of implementation of the algorithm; good clustering effects;	sensitive to the choice of initial cluster centers; sensitive to noise and outlier	(Abualhaj et al., 2017; Babu et al., 2021)
Deep learning	Convolutional Neural Network	automated feature extraction; multi-scale and multi-level feature learning; strong generalization ability	high demand for computational resources; high training costs; limited recognition capability for small targets and details	(Havaei et al., 2017; Pereira et al., 2016)
Ensembling method	Ensembling method	leverage the strengths of multiple models to enhance overall performance; effective in handling complex image scenes and backgrounds	high computational costs; potentially reduced model interpretability	(El-Hag et al., 2021; Li et al., 2019; Preethi and Aishwarya, 2021)

detection of brain tumors. Traditional machine learning methods significantly enhance the efficiency and accuracy of brain tumor detection by extracting image features—such as shape, grayscale, and texture—and putting them into classifiers like SVM, random forests, and KNN. Anwar and colleagues utilized an algorithm grounded in expectation maximization coupled with k-means clustering for the identification and extraction of tumor regions. Upon evaluation with the Brain Tumor Segmentation Challenge (BRATS) 2015 dataset, this technique achieved an average Dice coefficient of 0.92, indicative of its superior performance in tumor detection (Anwar et al., 2018). Rajan et al. developed an image segmentation algorithm that integrates k-means clustering with fuzzy c-means (KMFCM), and then employs SVM for image classification. This method adeptly identifies brain tumors with less execution time by efficient segmentation, precise edge detection, and intensity adjustment (Rajan and Sundar, 2019). In addition to KMFCM, a variety of algorithms based on fuzzy c-means (FCM) have also been developed and have exhibited good image processing effects, improving the accuracy and efficiency of brain tumor detection. Given the intricate data distribution typically found in MRI brain images, Bai and colleagues employed the concept of center-free to overcome the limitations of the FCM algorithms and proposed a novel clustering method called Intuitionistic center-free fuzzy c-means (ICFFCM). The method was refined by leveraging pixel-to-pixel similarities and pixel-to-cluster similarities, which made it better suited for capturing the complexities of MRI brain images while simultaneously improving their segmentation capabilities. Employing authentic brain MRI image datasets curated by BrainWeb, IBSR, and other researchers, a comparative analysis was conducted among ICFFCM, seven other clustering techniques and two standard voxel-based methods, specifically Statistical Parametric Mapping and FMRIB's Automated Segmentation Tool (Bai et al., 2019). The findings demonstrate that the ICFFCM method exhibits robustness and efficacy, surpassing the performance of the fuzzy-based clustering methods and attaining results on par with those of Statistical Parametric Mapping and FMRIB's Automated Segmentation Tool. Shree et al. proposed a machine learning method that used discrete wavelet transformation to capture wavelet coefficients and the gray-level cooccurrence matrix to glean statistical features from the imagery. This method subsequently utilized a probabilistic neural network (PNN) as a classifier to detect tumor. The evaluation results showed that the accuracy of this method in identifying normal brain tissues and brain tumors is close to 100 % (Varuna Shree and Kumar, 2018). In conclusion, machine learning techniques notably enhance the efficiency and precision of brain tumor detection, demonstrating robust performance. However, traditional machine learning algorithms face several limitations. Firstly, they often necessitate manual feature extraction. Secondly, their performance is highly contingent upon the quality and quantity of the data. Additionally, they are prone to issues of overfitting and underfitting. Lastly, when confronted with high-dimensional data or complex nonlinear relationships, their performance often falls short of expectations. Collectively, these factors constrain the overall effectiveness of traditional machine learning algorithms. Deep learning, as an emerging subset of machine learning, offers substantial advantages in overcoming these challenges. By employing data augmentation and synthetic data generation techniques, deep learning algorithms can significantly mitigate the dependency on large volumes of high-quality data. Through the implementation of regularization, early stopping, and ensemble learning methods, deep learning effectively curtails the risks of overfitting and underfitting. Moreover, the multi-layer NN architecture inherent in deep learning enables the automatic extraction of features across multiple levels of abstraction, demonstrating remarkable prowess in handling complex and high-dimensional datasets. As a result, deep learning is increasingly gaining favor among researchers.

An increasing number of deep learning algorithms have been developed and applied to the automated detection and identification of brain tumors in imaging. CNNs excel especially in images or two-dimensional data processing, utilizing convolutional layers to autonomously discern and learn the intrinsic features of images, eliminating the need for manual feature extraction. Within a CNN architecture, there are three primary types of layers: the convolutional layer, which filters the input data through convolution to extract features; the pooling layer, tasked with downscaling the feature maps; and the fully connected (dense) layer, which ultimately performs the classification task (Chen et al., 2023; Kuntz et al., 2021; Shah et al., 2023). Pereira et al. proposed an automatic segmentation method for the detection and segmentation of gliomas based on a CNN using 3×3 small kernels to design a

profound architecture and prevent overfitting (Pereira et al., 2016). When evaluated against the BRATS 2013 dataset, the algorithm achieved Dice similarity coefficients of 0.88 for the complete region, 0.83 for the core, and 0.77 for the enhancing areas of the tumor. In the assessment with the BRATS 2015 dataset, the corresponding coefficients for the complete, core, and enhancing tumor regions were 0.78, 0.65, and 0.75, respectively. Another fully automated CNN-based brain tumor segmentation method designed by Havaei has amplified the model's processing velocity by a factor of 30, attributable to the incorporation of a novel dual-path architecture that captures both intricate local details and expansive global context, in conjunction with the technique of stacking two CNNs to account for dependencies among local labels. The model's convolutional properties, coupled with the expedited computation capabilities of graphics processing units (GPUs), have condensed the segmentation time for the entire brain to a span of 25 seconds to 3 minutes, thereby significantly enhancing the velocity and efficiency of diagnosing brain glioma (Havaei et al., 2017). Mohammad et al. proposed a 3D-Znet model based on deep CNNs, which mainly consists of four modules as four encoders, four decoders, initial input and final output. The 3D-Znet structure, developed for processing 3D MRI data, was inspired and improved from the framework of previous 2D-Znet model, in which every encoder-decoder block includes a double-convolution 3D layer, 3D batch normalization, as well as an activation function (Chen et al., 2018; Ottom et al., 2023; Ottom et al., 2022). The model underwent training, validation and evaluating utilizing the multimodal stereotactic neuroimaging dataset from BRATS 2020, demonstrating robust performance with high Dice coefficient scores as the whole tumor= 0.91, tumor core= 0.85, and enhanced tumor= 0.86. Deep learning-based methods can autonomously distill the essential characteristics from data, diminishing the reliance on manual intervention. These methods are adept at capturing intricate and abstract data representations, exhibiting strong generalization capabilities. As a result, they demonstrate superior performance and remarkably high operational efficiency in the early identification and screening of brain tumors. Nonetheless, their deployment typically necessitates substantial datasets and the use of powerful GPUs or tensor processing units (TPUs), while also potentially encountering "black box" issues. The "black box" challenges refer to the phenomenon where the internal decision-making processes of some AI models, particularly complex deep learning models, are opaque and difficult to interpret (Gallée et al., 2023; Handelman et al., 2019). This is due to the fact that deep learning models typically contain an extremely large number of parameters that interact through multi-layered network structures, making the decision-making process hard to track and interpret. Additionally, the non-linear hierarchical nature of these models further complicates the relationship between inputs and outputs, exacerbating the issue of uninterpretability. During training, models form decision rules by learning implicit patterns from vast amounts of data, patterns that are often not easily interpretable through traditional methods. These factors collectively contribute to the emergence of the "black box" challenges. Consequently, in clinical practice, the choice suitable of AI-based models should be tailored to the specific context and the characteristics of the data in question.

Ensembling method is being applied gradually in order to improve the overall detection efficiency and reduce errors through the combination of multiple models. Li et al. designed a method for brain tumor detection called multi-CNNs that combines multi-modal information fusion with CNNs (Li et al., 2019). By combining MRI images, this method first extends 2D-CNN to multi-modal 3D-CNN to obtain the characteristics of brain lesions in three-dimensional space under different modes. Then, a weighted loss function was devised to diminish the impact of non-diseased regions and improve the accuracy of detection. The evaluation results showed that this multi-CNN method was significantly improved in terms of Dice coefficient, sensitivity and specificity compared with the original single-modal method. Preethi proposed another ensembling method for brain tumor detection and segmentation based on MRI and positron emission tomography (PET) images (Preethi and Aishwarya, 2021). Initially, the input images are fused through the application of discrete wavelet transform alongside a novel fusion strategy. Subsequently, gray-level co-occurrence matrix features are extracted. An optimal deep neural network (DNN) is then employed for the classification of brain tumor and normal brain tissue images. In this context, the selection of the network's weights of is performed optimally by employing the spider monkey optimization algorithm. Conclusively, a weighted k-means algorithm is implemented for the segmentation and identification of tumor areas. The proposed technique is further substantiated by validation against image repositories from diverse sources. The outcomes demonstrate a roughly 30 % improvement in performance over standard DNNs, with a sensitivity of 1.00, specificity of 0.89, and overall accuracy of 0.93.

AI-based models for detecting brain metastases are also being progressively developed. The deep learning method developed by Madhugiri et al. demonstrates a sensitivity of 79.2 % and a positive predictive value of 95.6 % in detecting brain metastases. Notably, for lesions smaller than 0.1 cc, the sensitivity of AI exceeds that of manual detection methods (Madhugiri and Prasad, 2025). The study conducted by Huang et al. has further enhanced the sensitivity and accuracy of brain metastasis detection to 97.5 % and 98.7 %, respectively, demonstrating exceptional performance (Huang et al., 2022).

It should be highlighted that molecular testing also plays a significant role in early screening, complementing conventional neuroimaging methods. Wang and colleagues utilized feature selection techniques based on SVM algorithms and mass spectrometry to pinpoint nine lipids as the most critical indicators for the early detection of early-stage lung cancer. They subsequently developed an AI-based detector for lung cancer that boasts a detection rate with a sensitivity exceeding 90.00 % and a specificity of 92.00 % (Wang et al., 2022). In glioma, Hollon has developed an AI-enabled rapid diagnostic screening system named DeepGlioma. This system is trained on multimodal datasets including stimulated Raman histology (SRH), large-scale genomic information, enabling it to swiftly screen for molecular alterations in glioma specimens (Hollon et al., 2023).

Hematology test outcomes could also be instrumental in the early detection of brain tumors. Tsvetkov et al. devised a cancer detection approach grounded in the plasma degradation profiles identified through differential scanning fluorimetry. With blood samples collected from 84 glioma patients and 63 healthy individuals, they discovered that this plasma degradation profiles could discern between cancer patients and healthy individuals with an automatic accuracy of 92 %, with the utilizing of machine learning algorithms (Tsvetkov et al., 2021). Likewise, Podnar et al. have demonstrated the viability of employing machine learning for screening brain tumors through routine blood tests, which achieved a detection accuracy that rivaled that of neuroimaging data, with respective sensitivities and specificities of 96 % and 74 % (Podnar et al., 2019). These studies confirm the practicality of conducting early screenings for brain tumors using standard blood tests, which has significant practical implications.

It is widely acknowledged that the higher the grade of a brain tumor upon diagnosis, the poorer the patient's survival prognosis tends to be. Consequently, early detection is crucial for enhancing the therapeutic outcomes and prognosis of patients with malignant brain tumors. In the realm of early brain tumor detection, AI-based technologies have demonstrated expansive potential for application. However, they face constraints due to the necessity for substantial and high-quality data, ethical and societal concerns, as well as the need for clinical validation and regulatory approval. These challenges are anticipated to be surmounted as technological progress is made and further research is conducted.

3.2. Tumor diagnosis and differential diagnosis

Brain tumors exhibit remarkable diversity, with over 150 distinct

varieties, and can develop in any region of the brain or skull (Gritsch et al., 2022; van den Bent et al., 2023). Accurate diagnosis and differentiation are essential elements for the treatment, follow-up, and management of brain tumor patients. Currently, a variety of well-established neuroimaging techniques, such as X-ray, CT, MRI, and PET, are extensively utilized for diagnosing and differentiating brain tumors. Nonetheless, due to the interference of human factors, characteristics of image data, and the intricate nature of disease, direct analysis from medical imaging still faces limitations in various respects. Traditional neuroimaging techniques face limitations in differentiating tumors from tumor-like lesions (Huisman, 2009), distinguishing benign from malignant growths (Schaff and Mellinghoff, 2023; Wang et al., 2020), identifying primary tumors versus brain metastases (Lah et al., 2020; Weller et al., 2015), and accurately monitoring post-treatment changes, such as pseudoprogression or radiation necrosis (Brandsma et al., 2008; Thust et al., 2018; Walker et al., 2014; Zikou et al., 2018). The integration of AI-based methods into brain tumor diagnosis has significantly mitigated these challenges.

Zahoor et al. proposed a novel two-stage hybrid framework for automated brain tumor detection and classification, leveraging a CNN-based boosted feature space to enhance the accuracy of both tumor identification and subsequent tumor type classification (Zahoor et al., 2022). The initial stage involved the creation of a CNN-based boosted feature space and an ensemble classifier scheme, designed to differentiate between tumorous and healthy brain images. The subsequent stage proposed a classification approach for brain tumor types, grounded in a deep hybrid feature space, capable of identifying various types of brain tumors, including meningioma, glioma, and pituitary tumors. Upon validation using standard benchmark datasets from reputable sources such as Kaggle (accessible online at: Kaggle Brain MRI Dataset) and FigShare (available online at: FigShare Brain Tumor Dataset), the tumor detection method achieved an accuracy of 99.56 % and a precision of 0.9991. Furthermore, when validated using Contrast-Enhanced-MRI datasets, the classification technique obtained an accuracy of 99.2 % and a precision of 0.9906. This innovative multi-stage framework streamlines the diagnostic process by sequentially performing tumor detection and classification. By breaking down the complex task into manageable steps, it significantly boosts the overall efficiency and accuracy. It offers new ideas and approaches for the automated diagnosis of brain tumors. Similarly, Sekhar et al. constructed a brain tumor classification model utilizing the principles of transfer learning. This model was trained and evaluated using the Contrast-Enhanced-MRI dataset from Figshare and demonstrated a robust ability to differentiate between meningiomas, gliomas, and pituitary tumors. The model achieved an impressive classification accuracy of 91.28 % (Sekhar et al., 2022). Moreover, with the Harvard medical repository datasets, the model achieved 95–100 % accuracy in classifying normal, glioblastoma, sarcoma, and metastatic bronchogenic carcinomas.

Kang and colleagues devised a method for classifying brain tumors that integrates deep features with machine learning classifiers. They employed nine distinct machine learning classifiers, including KNN, random forest, adaptive boosting, SVM, and others, to assess the deep features extracted from thirteen pre-trained CNNs. The top three deep features were selected to create a composite feature set (Kang et al., 2021). This amalgamation of deep features was then input into various machine learning classifiers to forecast the final outcome. This fully automated scheme for brain tumor classification has proven effective in categorizing brain tumors and has demonstrated commendable performance across three datasets (referred to as BT-Small-2c, BT-Large-2c, and BT-Large-4c) sourced from Kaggle.

Abdolmaleki and colleagues developed a three-tiered artificial neural network (ANN) aimed at differentiating malignant from benign brain tumors in individuals with astrocytic gliomas (Abdolmaleki et al., 1997). Utilizing thirteen distinctive parameters derived from the visual assessment of pre- and post-contrast MRI images from a cohort of 129 patients by three neuroradiologists, they constructed a relatively simple NN for tumor classification. This method demonstrated superior diagnostic capabilities, with an accuracy rate of 94 % for identifying tumors and 91 % for malignant ones, outperforming the 84 % accuracy achieved by neuroradiologists.

Furthermore, the deep learning model developed and verified by Tariciotti et al. was capable of reliably identifying fuzzy cases of regional glioblastoma, primary CNS lymphoma, and solitary brain metastases through MRI scans, which laid the groundwork for selecting appropriate subsequent therapeutic strategies (Tariciotti et al., 2022). Similarly, the approach grounded in machine learning, as put forward by Zacharaki et al., successfully differentiated primary brain tumors from brain metastases, achieving respective accuracy, sensitivity, and specificity rates of 85 %, 87 %, and 79 % (Zacharaki et al., 2009). This methodology has also demonstrated commendable performance in identifying various types of primary brain tumors, encompassing meningiomas, gliomas, and glioblastomas.

With the advent of novel therapeutic modalities, including drug therapy and cellular immunotherapy, the identification of pseudoprogression has become increasingly complex. For instance, immunotherapy works by stimulating the patient's immune system to target and destroy tumor cells. However, this process can also trigger immune cell infiltration and an inflammatory response, as well as tumor cell necrosis and the release of antigens. Additionally, the delayed effects of immunotherapy may cause the tumor to appear larger on imaging scans, creating a false impression of disease progression. Similarly, certain chemotherapy can also produce a similar illusion of pseudoprogression (Esparragosa Vazquez et al., 2023; Sharma et al., 2019). To effectively address these challenges, AI technology can integrate multiple imaging features with clinical data to offer a more comprehensive and accurate diagnostic support. For instance, the deep learning model developed by Moassefi et al. achieved an average accuracy of 76.4 %, an average area under the curve (AUC) of 0.7560, and an average sensitivity of 88.72 % in identifying true and false progression of glioblastoma (Moassefi et al., 2022). Lee et al. further proposed a CNN-LSTM model, which achieves a relatively high AUC of 0.81 under the optimal model configuration (Lee et al., 2020). Amino acid PET imaging using the tracer O-(2-[^{18}F]-fluoroethyl)-L-tyrosine (^{18}F-FET) has been demonstrated to provide valuable information for distinguishing true tumor progression from pseudoprogression. In a study by Kebir, a machine learning algorithm based on linear discriminant analysis achieved an AUC of 0.93 in identifying true and false progression in isocitrate dehydrogenase (IDH) wild-type glioblastoma (Kebir et al., 2020). This result is significantly higher than that of traditional manual interpretation methods for ^{18}F-FET PET imaging, suggesting that machine learning-enhanced ^{18}F-FET PET may offer greater accuracy in differentiating true from false progression.

Complementing the conventional use of imaging data for tumor diagnosis, Nadiya et al. discovered that microRNA profiling in cerebrospinal fluid (CSF) can serve as biomarker for identifying glioblastoma. Ulteriorly, by employing an SVM-based machine learning approach, it achieved a classification accuracy of 91–99 %, effectively distinguishing between glioblastoma and metastatic brain cancer (Teplyuk et al., 2012). In pediatric brain tumors, certain proteins in waste CSF have been identified as potential biomarkers for distinguishing brain tumors from non-neoplastic conditions. The integration of AI in this area may bring surprising results (Bruschi et al., 2021). Additionally, Capper and colleagues developed a machine learning-based tumor classifier designed to categorize CNS tumors using DNA methylation patterns (Capper et al., 2018). This innovative approach enhances diagnostic precision in neuropathology and holds the potential to revolutionize the field of tumor pathology. Mass spectrometry serves as a principal analytical instrument for omics-level studies, ranging from the molecular to the cellular scale. Cao and colleagues developed a Pd-Au synthetic alloy for the mapping and analysis of metabolic fingerprints using mass spectrometry. By employing machine learning techniques on these metabolic fingerprints, they were

able to distinguish medulloblastoma patients from healthy individuals with a sensitivity of 94.0 %, a specificity of 85.7 %, and an accuracy of 89.9 % (Cao et al., 2020).

3.3. Tumor grading and molecular features

Tumor grading is the process of evaluating the degree of malignancy based on the histological features and biological behavior of the tumor. Currently, gliomas are categorized using the grading system established by the World Health Organization (WHO), typically ranging from grade 1 to grade 4 (Louis et al., 2021). Grades 1 and 2 are identified as low-grade gliomas, which may be entirely excised through surgery. In contrast, grades 3 and 4, known as high-grade gliomas, exhibit pronounced malignant properties and are associated with a generally unfavorable prognosis. Precise grading is essential for formulating therapeutic strategies and forecasting patient outcomes.

Previously, Zacharaki introduced a machine learning-based model designed to extract features like tumor shape, intensity, and texture from MRI scans, employing SVM for feature subset selection (Zacharaki et al., 2009). This model achieved an accuracy, sensitivity, and specificity of 88 %, 85 %, and 96 %, respectively, in discerning between low-grade and high-grade gliomas. In recent years, Naser et al. developed a deep learning methodology, employing CNNs based on U-net integrated with transfer learning based on the VisualGeometry Group 16 pre-trained convolutional layers, and merged these with a fully connected classifier to facilitate tumor grading. The assessment demonstrated that the segmentation model achieved a tumor detection accuracy of 92 %. Furthermore, the classification model attained accuracy, sensitivity, and specificity rates of 95 %, 97 %, and 98 %, respectively, specifically for the identification of low-grade gliomas (Naser and Deen, 2020).

Beyond neuroimaging data, Chang et al. presented another study based on digital pathology data that integrated Fourier transform infrared microscopy with deep learning techniques for the grading of glioma tissue sections and identification of microvascular characteristics (Li et al., 2019). Microvascularity is a significant histological attribute of gliomas, closely associated with the tumor's grade and subtype. The result showed that this method offers a significantly expedited process, and promises enhanced accuracy, specificity, and sensitivity.

Molecular subtypes are categorized based on distinct genetic and molecular traits that mirror the tumor's biological actions. Molecular features offer supplementary insights for tumor grading, enabling the anticipation of a patient's therapeutic response and prognosis. Common molecular subtypes of gliomas encompass: IDH mutations, 1p/19q codeletion, TERT promoter mutations, epidermal growth factor receptor (EGFR) amplification, O^6-methylguanine-DNA methyltransferase (MGMT) methylation, H3K27M mutations, ATRX mutations, CDKN2A/

Table 3
Application of AI techniques in the prognostication of glioma molecular subtypes.

AI technique	Molecular features	Data type	Performance	Reference
A Machine learning model (support vector machine classifier)	IDH mutation	MRI (APTw)	AUC= 0.87; accuracy= 84 %	(Wu et al., 2024)
Cryosection Histopathology Assessment and Review Machine	IDH mutation	Histopathological data	AUC= 0.79–0.82	(Nasrallah et al., 2023)
3D-dense-Unets	MGMT methylation	MRI (T2WI)	AUC= 0.93; accuracy= 94.73 %; sensitivity= 96.31 %; specificity= 91.66 %	(Yogananda et al., 2021)
A machine learning model	MGMT methylation	18F-DOPA PET images	Accuracy= 80 % ± 10 %	(Qian et al., 2020)
Self-Supervised Transfer Learning	BRAF mutation	MRI	Training cohort: AUC of 0.82, 0.87, and 0.85 for BRAF wild type, BRAF fusion, and BRAF V600E, respectively; validation cohort: AUC of 0.72, 0.78, and 0.72 for BRAF wild type, BRAF fusion, and BRAF V600E, respectively	(Tak et al., 2024)
A deep learning model	TERT mutation	MRI	Training cohort: AUC= 0.990; validation cohort: AUC= 0.890	(Zhang et al., 2023)
Support vector machine	TERT mutation	MRI	Sensitivity= 85.7 %; specificity= 54.8 %; PPV= 75.9 %; NPV= 69.7 %; accuracy= 74.1 %	(Yamashita et al., 2019)
An automated machine learning	H3K27M mutation	MRI	Training cohort: accuracy= 0.788–0.867, AUC= 0.903, average precision= 0.911; validation cohort: accuracy= 0.60–0.84, AUC= 0.85, average precision= 0.855	(Su et al., 2020)
A machine learning model	EGFR amplification	Terahertz spectroscopic data	AUC= 85.8 %	(Wu et al., 2024)
A deep learning model	CDKN2A/B homozygous deletion	MRI	ResFN-Net: ACC= 0.813, AUC= 0.8804; FN-Net: ACC= 0.9236, AUC= 0.9704	(Zhang et al., 2024)
A single multi-task CNN	IDH mutation, 1p/19q codeletion	MRI	IDH-AUC= 0.90; 1p/19q-AUC= 0.85	(van der Voort et al., 2023)
A machine learning model	IDH mutation, 1p/19q codeletion	Genome-wide somatic copy number alteration data	IDH-AUC> 0.95; 1p/19q-AUC= 0.97	(Nuechterlein et al., 2021)
A spatial-temporal integration model	IDH mutation, 1p/19q codeletion, TERT mutation	MRI	Prospective cohort: accuracy-IDH1 = 0.85 ± 0.04, accuracy-TERTp = 0.84 ± 0.05, accuracy−1p/19q= 0.88 ± 0.04; AUC-IDH1 = 0.89 ± 0.02, AUC-TERTp= 0.80 ± 0.04, AUC−1p/19q= 0.85 ± 0.06	(Xie et al., 2023)
A weakly supervised deep learning	IDH mutation, ATRX mutation, 1p19q codeletion	Histopathological data	Training cohort: IDH-AUC= 0.95, ATRX-AUC= 0.90, 1p19q-AUC= 0.80; validation cohort: IDH-AUC= 0.90, ATRX-AUC= 0.79, 1p19q-AUC= 0.87	(Hewitt et al., 2023)
Optimal SVM predictive models	IDH mutation, ATRX loss	MRI	IDH1 mutation: accuracy= 94.74 %, AUC= 0.931, sensitivity= 100 %, specifity= 85.71 %, PPV= 92.31 %, NPV= 100 %; ATRX mutation: accuracy= 91.67 %, AUC= 0.926, sensitivity= 94.74 %, specifity= 88.24 %, PPV= 90.00 %, NPV= 93.75 %	(Ren et al., 2019)
A machine learning model	IDH mutation, MGMT methylation, 1p/19q codeletion	MRI	Training cohort: IDH-sensitivity= 0.88, IDH-specificity= 0.86, MGMT-sensitivity/specificity= 0.76–0.83, 1p/19q-sensitivity/specificity= 0.76–0.83; validation cohort: IDH-sensitivity and specificity= 0.83–0.85	(Jian et al., 2021)

B homozygous deletion (Horbinski et al., 2022; Smith et al., 2022). In Table 3, we list the applications of AI techniques in the prognostication of the predominant molecular subtypes of gliomas. To ascertain the molecular traits of gliomas, tissue samples are commonly procured through invasive surgery for subsequent immunohistochemical examination or gene sequencing. Nevertheless, with the ongoing advancements and deployments of AI models, there is an emerging prospect that the molecular classification of tumors may be achievable through non-invasive approaches.

IDH mutation is among the most prevalent molecular alterations in adult gliomas and serves as a significant prognostic indicator, typically correlated with a more favorable outcome. (Eckel-Passow et al., 2015). The 1p/19q codeletion subtype is predominantly identified in oligodendrogliomas and oligoastrocytomas, referring to a co-deletion of the chromosomal arms 1p and 19q. This molecular status is linked to heightened responsiveness to chemotherapy and radiotherapy and is generally associated with an extended survival (Familiari et al., 2023). Sebastian et al. have crafted a deep learning technique for glioma grading and molecular subtype prediction. They developed a multi-task CNN that harnesses MRI data to forecast the IDH mutation status, the 1p/19q co-deletion status, and the tumor grade for glioma patients. In the evaluation using a test set, the model secured an AUC of 0.90 for IDH prediction, an AUC of 0.85 for 1p/19q co-deletion, and an AUC of 0.81 for tumor grading, thereby facilitating the non-invasive prognostication of molecular features and tumor grading in gliomas (van der Voort et al., 2023).

TERT promoter mutations represent one of the most prevalent genetic modifications observed in adult-onset diffuse gliomas. Such mutations are implicated in the dysregulated upregulation of the TERT gene, a molecular aberration that correlates with increased tumor malignancy and a diminished patient prognosis (Hasanau et al., 2022). Fukuma designed a CNN to forecast tumor molecular subtypes directly from MRI data. By harnessing AlexNet on four types of MRI sequences to glean CNN textural features, followed by the application of a linear SVM for classification. The CNN texture features utilized in this deep learning mode provide superior capture of IDH and TERT genotype information in grade 2/3 gliomas compared to the traditional radiomic features (Fukuma et al., 2019). Fukuma designed a CNN to forecast tumor molecular subtypes directly from MRI data. By harnessing AlexNet on four types of MRI sequences to glean CNN textural features, followed by the application of a linear SVM for classification. The CNN texture features utilized in this deep learning mode provide superior capture of IDH and TERT genotype information in grade 2/3 gliomas compared to the traditional radiomic features (Fukuma et al., 2019).

The promoter region methylation of the MGMT gene is typically linked to increased sensitivity to alkylating agent-based chemotherapy and a more favorable prognosis. Maldjian and colleagues developed a deep learning network that utilized T2-weighted imaging solely to assess MGMT promoter methylation. The model achieved a mean accuracy, sensitivity, and specificity of 94.73 %, 96.31 %, and 91.66 %, respectively (Yogananda et al., 2021).

In summary, the application of AI for brain tumor grading and the forecasting of tumor molecular subtypes has demonstrated remarkable proficiency in both operational efficiency and precision. The utilization of novel datasets, including terahertz and multi-omics information, offers fresh perspectives for the precise identification of molecular features. And the neuroimaging-based AI techniques circumvent the need for any supplementary invasive procedures.

3.4. Diagnosis of pediatric brain tumors

Pediatric brain tumors exhibit significant differences in histology and molecular biology compared to adult brain tumors, making it inappropriate to extrapolate data from adults to children. Therefore, the development of specialized AI tools tailored for pediatric brain tumors is essential.

Most current research is primarily focused on developing tools for the diagnosis and differential diagnosis of pediatric brain tumors. Grist et al. employed a combination of multi-parametric MRI, univariate analysis, and machine learning techniques to differentiate between high-grade and low-grade pediatric brain tumors, achieving a high-precision classification accuracy of 85 % (Grist et al., 2020). Arle et al. developed a computer-based NN that integrates magnetic resonance spectroscopy data (ratios of N-acetyl-aspartate, choline, and creatine) with 10 characteristics of tumor tissue derived from MRI studies, as well as tumor size and patient age and sex, to diagnose posterior fossa tumors in children (Arle et al., 1997). When utilizing all available data, the NN achieved a 95 % accuracy rate in tumor identification, compared to a 73 % accuracy rate by neuroradiologists, thereby significantly enhancing the precision of tumor diagnosis. A recently reported study introduces an end-to-end, MRI-based federated learning platform for posterior fossa brain tumors, known as FL-PedBrain, which is built on a large pediatric dataset sourced from 19 international institutions (Lee et al., 2024). Compared to isolated learning from localized and limited data sources, the federated learning approach has demonstrated a 20–30 % improvement in tumor segmentation performance.

AI is also being developed to determine subtypes or grades within individual entities. Wang et al. combined machine learning with presurgical MRI to offer a noninvasive and cost-effective approach to predicting medulloblastoma molecular subsets (Wang et al., 2024). The AI diagnostic model exhibited highly accurate preoperative prediction of molecular subpopulations, achieving an AUC of $\geq$ 0.8 and an F1 score of $\geq$ 0.7 across internal, external, and continuous validation cohorts. This model holds promise in supporting surgical planning and optimizing the care of patients with medulloblastoma. Similarly, Lv et al. conducted a study that leveraged radiomic features derived from MRI and integrated them with machine learning techniques (Iv et al., 2019). Their approach also demonstrated outstanding performance in identifying the molecular subsets of medulloblastoma. Deep learning methods have also been developed to predict the molecular subtypes of pediatric low-grade gliomas in a non-invasive manner (Tak et al., 2024).

While the development of AI tools for pediatric brain tumors is still in its early stages, these tools hold great potential to transform the clinical diagnosis of pediatric tumors. Looking ahead, accelerating the development of these tools and fostering regional collaboration are expected to bring significant advancements.

4. Application of AI in brain tumor treatment

The application of AI in diagnosing brain tumors enhances diagnostic precision and aids in the subsequent establishing of therapeutic schemes. AI applications in brain tumor treatment encompass preoperative planning, intra-operative assistance, and post-operative care, facilitating personalized treatment plans, improving surgical outcomes, and aiding in prognostic evaluations.

4.1. Pre-operative planning

Exposing patients with advanced brain tumors to invasive procedures that minimally impact their survival or enhance their quality of life is not advisable. Thus, careful deliberation is essential when determining the suitability of surgical treatment for patients, particularly those with high-grade brain tumors. Predicting the survival of brain tumor patients and the operability of tumors is challenging, but an AI-based technique might provide some assistance. Ko and colleagues have shown that a machine learning-based approach can precisely forecast the progression and recurrence of meningiomas, utilizing solely preoperative radiological data (Ko et al., 2021). Oermann et al. utilized integrated clinical data, including patient age, systemic disease status, the type of primary tumor, and the count of metastatic tumors, and employed deep learning techniques to effectively forecast the one-year survival rate of patients with brain metastases who underwent

radiation surgery. And the predictive performance of their model outperformed that of conventional methods for survival prediction (Oermann et al., 2013).

Judging the resectability of brain tumors is also complicated due to the heterogeneity of their anatomical structure and the complexity of surgical resection. In cases of glioblastoma, for instance, complete resection is achieved in only approximately one-third of patients. Marcus and colleagues pinpointed the five most critical anatomical features indicative of glioblastoma excisability and leveraged these to devise a scoring system (Marcus et al., 2017). Utilizing a machine learning algorithm founded on ANN, their model is capable of precisely predicting the surgical resectability of glioblastoma, achieving an area under the curve and accuracy of 0.87 and 83 %, respectively (Marcus et al., 2020). The AI model developed by Marcus et al. accurately predicts the surgical resectability of glioblastoma, which can help guide surgical decision-making and potentially reduce unnecessary surgeries in patients with unresectable tumors, optimizing the allocation of medical resources. Looking ahead, AI-based technology may emerge as a vital tool to assist in the intricate decision-making processes for brain tumors.

4.2. Intra-operative assistance

The principal aim of brain tumor surgery is to accurately excise the tumor while sparing as much healthy brain tissue as feasible. Research indicates that the intraoperatively residual tumor tissue is the primary reason for tumor recurrence (Fabelo et al., 2019). Nonetheless, accurately discerning tumor from healthy tissue during an operation poses a significant challenge for neurosurgeons. At present, imaging technologies are utilized to assist with navigation during brain tumor surgeries, yet they encounter certain limitations. Employing preoperative imaging and an intraoperative navigation system enhances surgical guidance, yet the precision in defining tumor margins tends to diminish as the surgery advances (Gerard et al., 2017). The use of intraoperative MRI extends the duration of the procedure and necessitates sophisticated operating room setups (Gandhe and Bhave, 2018). Hyperspectral imaging, which captures and analyzes data across a broad spectrum of wavelengths, predominantly the visible and infrared ranges, offers a non-invasive, label-free, ionizing-free, and real-time imaging modality (Fabelo et al., 2018; Lu and Fei, 2014). Its potential in tumor imaging is anticipated to overcome the constraints of existing imaging techniques. Fabelo et al. employed hyperspectral imaging technology in brain tumor surgery and developed a deep learning model to process the hyperspectral data of brain tissues (Fabelo et al., 2019). This model produces thematic a map that outlines the brain's parenchymal regions and pinpoints the tumor's location, thereby facilitating surgeons in accurately and effectively excising the tumor. Additionally, the model includes an auxiliary visualization system that assists surgeons in adjusting the thematic map to identify the optimal classification threshold during surgery.

The extracellular acidosis that results from the metabolic reprogramming of cancer cells serves as a dependable marker of regions where tumors have infiltrated. Jin and colleagues developed a surface-enhanced Raman Scattering navigation system for the resection of brain tumor (Jin et al., 2022). This system analyzed the pH levels of metabolites through automated Raman spectroscopy, and by employing a deep learning algorithm to process the Raman spectra, the tumor resection margin is effectively demarcated. Compared with traditional surgery, Jin's surgery navigation system significantly improved overall survival in animal models. Furthermore, Song et al. designed a U-Net--based automatic segmentation model, processing computed tomography angiography images, for surgical navigation during pituitary adenoma surgery (Song et al., 2019). This model significantly minimized the risk of harming critical neurovascular structures throughout the surgical process.

AI technology has been implemented in the analysis of surgical workflows as well, yielding impressive outcomes. By employing computer vision to analyze surgical videos, AI is capable of recognizing surgical phases, operator movements, technical proficiency, anatomy structure, and pathological traits, while offering immediate feedback. The integration of AI for workflow analysis aids in refining surgical processes and pathways, standardizing surgical steps and protocols, detecting and cautioning about critical risk periods, producing surgical documentation, and supporting training and simulation endeavors. Through the collaborative agreement of an international expert panel, a workflow for endoscopic transsphenoidal resection of pituitary adenomas has been established (Marcus et al., 2021). On this basis, Khan et al. utilized CNN and RNN network models to analyze the corresponding surgical videos, with results indicating that the model could precisely discern surgical phases (with 91 % accuracy) and steps (with 76 % accuracy) (Khan et al., 2022). This research lays a foundation for future research into the analysis of surgical processes for pituitary adenomas and other brain tumors, and it is anticipated to be instrumental in the training of novice physicians and the advancement of automated surgical procedures, exerting a profound influence on the surgical practice for brain tumors.

Currently, the application and deployment of AI technology in brain tumor surgery predominantly centers on offering decision-making support and advancing surgical automation. This has demonstrated significant promise in enhancing the precision of surgical procedures, refining surgical techniques, and ameliorating patient outcomes. Over the past few decades, surgical robots have been increasingly utilized across a spectrum of surgical operations, encompassing neurosurgery (Miller et al., 2017; Rasouli et al., 2021). The combination of AI with surgical robotics represents an exceedingly promising research avenue, poised to facilitate a monumental stride in both automation and precision, and is anticipated to herald a new epoch in the surgical management of brain tumors. As AI research in neurosurgery continues to progress, it is bound to assume an increasingly pivotal role across all facets of surgical practice.

4.3. Postoperative care and management

AI-based techniques are also being developed and applied for the care and surveillance of brain tumor patients. The postoperative stage of brain tumor patients is fraught with risks. Post-surgery, they may encounter infections, venous thromboembolism, pressure ulcers, falls, and other complications or adverse events, with the potential for unintended hospital readmission (Alshehri et al., 2016; Salle et al., 2021). Consequently, the creation of a risk prediction and assessment system is deemed essential. Approximately 10 % of individuals who undergo transsphenoidal surgery for pituitary adenomas face the risk of unintended readmission, a risk that is challenging to forecast. By gathering patient data from various academic medical institutions, Cheng et al. designed a machine learning-based risk stratification system for the unpredictable readmission of patients subsequent to pituitary adenoma resection (Crabb et al., 2022). This system aids in the identification of high-risk patients and significantly enhances the quality of patient care. Furthermore, a multitude of AI-based programs have been devised to analyze patients' medical records in order to forecast the likelihood of infections or other potential postoperative complications (Hopkins et al., 2020; Howcroft et al., 2017; Hsiao et al., 2015). This facilitates the implementation of precautionary measures and diminishes the probability of postoperative problems.

4.4. Brain tumor radiotherapy

Malignant brain tumors often require adjuvant chemotherapy and/or radiotherapy. The deployment of AI in brain tumor radiotherapy primarily pertains to the delineation of gross target volume targets. As previously stated, the development of AI-based automated segmentation models for aids in the precise demarcation of the radiotherapy target area. During radiotherapy, it is crucial to minimize exposure of healthy brain tissue to radiation. Nevertheless, whole brain radiotherapy

continues to be a significant treatment option for patients presenting with multiple brain metastases. In the United States, over 200,000 individuals with brain tumors are treated with whole brain radiation therapy annually (Tsao et al., 2018). Exposure of healthy brain tissue to radiation can impair the hippocampus tissue, a region integral to learning and memory processes, potentially leading to post-radiation neurocognitive dysfunction (Gondi et al., 2012; Monje et al., 2002). Hence, it is crucial to avoid the hippocampus tissue during irradiation. Lin et al. developed a deep learning framework to create a fully automated process for hippocampal avoidance whole brain radiotherapy. Their model demonstrated the capability to rapidly and precisely produce a clinically viable radiation plan within approximately 10 minutes, thereby enhancing the therapeutic efficiency for patients with brain metastases (Lin et al., 2023).

4.5. Prediction of treatment response and patient prognosis

Accurate assessment of treatment response and prognostic outcomes is a crucial step for directing the therapy of brain tumors. The manual evaluation based on Response Assessment in Neuro-Oncology (RANO) or Response Evaluation Criteria in Solid Tumors (RECIST) criteria is cumbersome, labor-intensive and time-consuming, potentially missing vital tumor response details. Researches have manifested that AI-based methodologies offer enhanced reproducibility and standardization in assessing treatment responses on MRI images in neuro-oncology, surpassing the conventional manual two-dimensional measurements of tumor burden (Prezelski et al., 2024; Vollmuth et al., 2023). Papi et al. developed a U-Net architecture, utilizing the BRATS 2018 dataset, for the segmentation and classification of gliomas to assess the efficacy of treatment responses (Papi et al., 2023). Stember employed deep CNN, optimized through neuroevolution approach, to scrutinize MRI image data derived from metastatic brain tumors (Stember et al., 2023). This approach can precisely differentiate the progression from regression of brain metastases with an accuracy rate of 100 %. Likewise, a range of AI techniques have been devised to forecast prognostic indicators, including overall survival and progression-free survival, for primary or metastatic brain tumors, which facilitates an estimation of the disease progression (Kim et al., 2019; Li et al., 2023; Prasanna et al., 2017).

The application of amino acid PET for monitoring changes in the metabolic tumor volume has emerged as a significant tool in assessing the therapeutic response for brain tumor patients (Suchorska et al., 2015). Gutsche et al. developed an innovative no new U-Net ANN to process the ^{18}F-FET PET scan data (Gutsche et al., 2023). Deployed to a previously published ^{18}F-FET PET dataset, this model successfully identified 92 % of lesions with heightened uptake and 85 % of lesions with equal or diminished metabolism. The model ensures a dependable, robust, and comprehensive evaluation of metabolic tumor volume modifications in individuals with brain tumors.

Several gene expression biomarkers have also been suggested for the prediction of therapeutic response and patient prognosis. For instance, Chen et al. collected data of 173 meningioma patients to formulate a 34-gene expression risk score, which were then validated against data from 1856 additional patients (Chen et al., 2023). Their findings indicated that these biomarkers significantly enhanced the differentiation of outcomes for local recurrence and overall survival compared to all other systems evaluated within the clinical validation cohort, achieving a five-year area under the curve of 0.81 and 0.80, respectively. Moreover, this model identified that patients with meningiomas could potentially benefit from postoperative radiotherapy and suggested optimized postoperative management for 29.8 % of the patients. Similarly, Wang et al. constructed a 20-gene panel utilizing ANN that had the potential to act as biomarkers for foreseeing treatment outcomes and prognostic benefits post-immunotherapy in glioma patients (Wang et al., 2024). This model aided clinicians in precisely identifying patient likely to gain clinical benefits from such interventions.

Cell morphology serves as a significant biomarker as well. Liu developed and validated a machine learning framework based on cellular morphometric subtypes that extract specific cell morphometric information from tissue slice images. These subtypes were linked to distinct molecular signatures, immune microenvironments, therapeutic responses, and prognostic indicators, thereby enabling the prediction of treatment responses and outcomes for glioma patients (Liu et al., 2023).

4.6. Treatment of pediatric brain tumors

AI technology has also been increasingly utilized to guide the treatment of pediatric brain tumors. AI-guided drug screening is emerging as a powerful tool that could pave the way for promising and innovative treatments for pediatric brain tumors (Carvalho et al., 2022). In medulloblastoma, Bruschi et al. utilized a machine learning algorithm to analyze CSF proteins, successfully identifying the long-chain fatty acid transporter 4 (SLC27A4) and laminin B-type (LMNB1) as significant biomarkers indicative of tumor residuals and recurrences. The expression levels of SLC27A4 and LMNB1 could be used to inform treatment strategies and to forecast tumor relapse (Bruschi et al., 2022). The multimodal deep learning approach developed by Mahootiha et al., which leverages tumor characteristics from MRI, has enhanced postoperative risk stratification for pediatric low-grade gliomas and is anticipated to significantly inform and guide postoperative decision-making processes (Mahootiha et al., 2025). Similarly, the study by Grist et al. integrates multi-site MRI images with machine learning, employing survival characteristics for both unsupervised and supervised machine learning to identify new subgroups associated with survival outcomes. Their model achieves a high accuracy of 98 % in classifying high and low survival risks in pediatric brain tumors (Grist et al., 2021).

AI is also demonstrating robust performance in aiding surgical procedures. SRH has been employed for rapid intraoperative diagnosis of pediatric brain tumors. Utilizing image features derived from the SRH field of view, a decision-tree machine learning model was developed and validated. This model achieved 100 % accuracy in classifying 25 fresh pediatric surgical specimens into normal and diseased tissues, as well as low-grade and high-grade tumors (Hollon et al., 2018). This outstanding performance provides critical information to guide the surgical management of pediatric brain tumors. Robotic stereotactic assistants have also been developed for use in pediatric neurosurgery (De Benedictis et al., 2017). These image-guided devices provide precise spatial positioning and orientation guidance for a variety of neurosurgical instruments based on pre-planned trajectories. After offline planning, the surgeon can oversee the robot's autonomous execution of movements and can also directly control and maneuver surgical instruments during the procedure. This robotic stereotactic assistant is highly versatile, effectively enhancing the safety and feasibility of surgeries while reducing procedural risks and operative times. It can be utilized for a wide range of operations, as well as endoscopic guidance procedures and stereotactic biopsies.

5. Application of AI in brain tumor drug research

AI-based techniques are assuming a more pivotal role in the research of pharmaceuticals for brain tumors, with its utilization permeating various facets, including drug screening, research and development, and appropriate treatment options.

Machine learning and deep learning can be trained using high-throughput screening data to construct predictive models that forecast the responses of cancer cell lines and patients to novel drugs or drug combinations (Neves et al., 2020; Yang et al., 2018). Bui's research discovered octenidine as a new Bcl-xL inhibitor by employing deep learning algorithms of structural features and performing molecular docking on a library of approved pharmaceuticals (Bui et al., 2022). Octenidine has the capacity to directly target the anti-apoptotic protein Bcl-xL, inducing mitochondrial apoptosis in cancer cells and thus impeding the progression of tumors. Bui's study not only identifies

octenidine, an existing drug, as a novel Bcl-xL inhibitor, thereby offering new targets and strategies for cancer treatment, but also highlights the remarkable potential of AI-driven drug repurposing. Olsen's study employed an AI predictive engine of the PandaOmics TargetID to sort through hypothetic targets concerning cancer and aging (Olsen et al., 2023). This research suggested that CNGA3, GLUD1, and SIRT1 were prospective novel targets for therapeutic intervention for aging and glioblastomas. Furthermore, the Perturbation Theory Machine Learning models developed by Munteanu et al. can be employed for the virtual screening of nanoparticle-drug complexes in the context of glioblastoma (Munteanu et al., 2021). In pediatric patients with ACVR1-mutant diffuse intrinsic glioma, a potential therapeutic combination of vandetanib and everolimus was identified through an AI-based platform designed to search for effective compound treatments. Four patients who received this combination therapy experienced a significant extension in survival and a notable reduction in tumor burden (Carvalho et al., 2022). The finding suggest that AI-driven drug screening holds promise in informing and guiding clinical studies of brain tumors in children.

Houy et al. employed an AI model to explore an optimal personalized treatment plan for the administration of temozolomide (Houy and Le Grand, 2019). At the time of admission, patients' pharmacokinetic parameters were just partially observed. The model progressively refined its calculations through Bayesian inference as treatment progressed, adjusting the treatment regimen based on feedback from the patients' reactions to the medication. The personalized treatment plan derived from this model resulted in a notable decrease in tumor size, with an average reduction of 67.2 g compared to the standard maximum tolerated dose regimen after 12 cycles, and a decreased incidence of severe toxicity among patients.

A number of micro-robots endowed with self-propulsion and navigation capabilities are being progressively developed for non-invasive drug delivery, offering promising prospects for precision medicine. Nanorobots are minuscule robotic systems engineered for operations at the nanometer scale, and their use in drug delivery holds the potential to transform the treatment of brain cancer (Rai et al., 2023). Zhang and colleagues present a neutrophil-based microrobot capable of controllable and active cargo delivery to malignant gliomas in vivo (Zhang et al., 2021). In contrast to conventional drug injections, the targeted delivery mediated by these "neutrorobots" markedly suppressed the proliferation of tumor cells. These "neutrorobots" are propelled by a magnetic navigation system, with its movement behavior analyzed through computer vision software. AI algorithms can be employed to train intelligent controllers that dynamically adjust magnetic field parameters in response to real-time visual feedback, thereby enabling more precise path planning and motion control. Moreover, leveraging computer vision and deep learning algorithms allows for the real-time processing of imaging data to automatically identify and track the position of micro-robots within the body, thus providing more precise feedback signals for magnetic navigation systems. AI holds the potential to optimize the design and control of these microrobots, facilitating precise navigation, targeted drug delivery, and real-time feedback on their performance in complex brain environments.

6. AI reveals the brain tumor microenvironment

Brain is an intricate ecosystem where various cell types sustain its normal functioning through exact coordination and interaction. TME is a complex milieu consisting of not only tumor cells but also a variety of non-cancerous cells, including various immune cells, stromal cells, vascular endothelial cells, and other cells, all situated within the extracellular matrix (de Visser and Joyce, 2023). Within the TME of brain tumors, immune cells, encompassing T lymphocytes, B lymphocytes, neutrophils, macrophages, mast cells, innate lymphoid cell and so on, all play important roles. Research into the immune microenvironment of brain tumors offers vital insights into the dynamic changes and immune regulatory mechanisms of brain tumors and provides directions for the development of novel immunotherapeutic approaches.

In-silico multidimensional model refers to a computer-based model that integrates and analyzes data from various biological levels, such as gene expression, protein interactions, and metabolic pathways, to simulate the complex behaviors and characteristics of biological systems. In cancer research, in-silico multidimensional models are capable of simulating the evolving conditions within the TME, dissecting the intricate relationships between tumor and immune cells, and aiding researchers in gaining a deeper comprehension of the complex transformations that occur during tumor progression. These models offer innovative therapeutic approaches and fresh perspectives for the treatment of cancer. The research conducted by Ravi et al. employed an in-silico multidimensional model to scrutinize and integrate the spatial transcriptomics and single cell data of 45615 immune cells derived from 12 tumor specimens (Ravi et al., 2022). Their findings revealed that $HMOX1^{+}$ myeloid cell subsets, known to produce interleukin-10, were located within the mesenchymal-like tumor region and contribute to T cell exhaustion, thereby fostering an immunosuppressive microenvironment. This study underscores the significance of integrating single-cell with spatial transcriptomic data modeling in brain tumor research, which is instrumental in devising effective immunotherapeutic strategies. Employing large-scale machine learning techniques, Xiao et al. identified SOX10 as a significant immunomodulator of macrophages within gliomas (Xiao et al., 2022). SOX10 exhibited a positive correlation with the cytokine production of macrophages while exerting a negative regulatory effect on their chemotaxis and migration. The findings implied that SOX10 could represent a promising target for the immunotherapy of gliomas. Oliver et al. developed a 3D micrometer-scale blood-brain barrier niche platform to simulate the process by which tumor cells traverse the blood-brain barrier and infiltrate the cerebral microenvironment, leading to the establishment of brain metastases (Oliver et al., 2020). This model utilized fluorescence imaging and confocal tomography techniques to capture and reconstruct images that depict alterations within the TME and the progression of micro-metastases. By harnessing AI techniques, it becomes feasible to discern intrinsic phenotypic variations among cancer cells capable of brain metastasis, yielding quantifiable metrics of their metastatic propensity. Integrated with AI methods, the model can garner extensive data regarding the TME and brain metastases, which facilitates a deeper understanding of the mechanisms behind brain metastases formation, aids in the development of pertinent preventative strategies, and informs the creation of targeted therapeutic plans.

In recent years, the swift advancement in technologies such as single-cell transcriptome sequencing, spatial transcriptomic analysis, and multi-cycle immunofluorescence, alongside the broad application of AI technology, offers potent tools for researching the TME, the dynamics of cell-to-cell interactions, and the composition of tissue structures. Painting a detailed picture of TME within brain tumors aids not only in precise diagnoses, prediction of therapeutic responses and prognoses but also lays a theoretical foundation for strategies to more effectively inhibit tumor progression, prevent brain metastasis, and devise promising treatment approaches.

7. Challenges and future prospects

AI, with its robust capabilities in information recognition, analysis and combination, has brought about significant transformations across various domains, including the diagnosis, treatment, and research of brain tumors. It has demonstrated immense promise in enhancing the accuracy of diagnoses and the effectiveness of treatments, promoting patients' prognoses, as well as in advancing the research of diseases. Nonetheless, there are still challenge to overcome.

Acquisition of extensive and high-quality datasets is essential for the effective deployment of AI. In general, AI-based algorithms necessitate ample, dependable, and accessible data for both training and validation

processes (Balagurunathan et al., 2021; Luo et al., 2023). There is a growing need for multimodal datasets as well. While data from retrospective studies are typically easy to gather and compile, while the images or parameters derived from various studies may vary, impacting the model's training efficacy and the reproducibility of outcomes, and potentially causing algorithmic bias. If the data used to train the AI model is not representative of the general population, these variations can lead to biases, such as selection bias or performance bias (Nagendran et al., 2020). Consistently parameterized, high-quality data can be procured through randomized controlled trials, but it is costly in manpower, material resources and time. Consequently, this underscores the value of collaborative efforts among multiple agencies, as well as the coordination and sharing of data. Such collaboration and data sharing are instrumental in constructing larger datasets, thereby furnishing the ample and reliable data necessary for further AI research in the realm of brain tumor studies. Interdisciplinary cooperation is essential as well. The deployment of AI in brain tumor research necessitates the exchange and cooperation among professionals from various fields, encompassing neurology, radiology, pathology, bioinformatics and so on, but it can also encounter hurdles in communication and the alignment of efforts.

The model's interpretability and generalization capabilities are critical aspects that warrant attention (O'Sullivan et al., 2019; Reddy et al., 2020; Zwanenburg et al., 2020). Deep learning models, often considered "black boxes", obscure the mechanisms by which they convert input data into outputs, posing challenges related to transparency and the establishment of user trust. Therefore, it is essential for deep learning models to be interpretable, allowing users to comprehend the decision-making process, thereby instilling confidence in the model's application within clinical environments. Employing suitable interpretation methods and leveraging visualization techniques can enhance the model's transparency and credibility (Wen et al., 2024). Moreover, models must be capable of generalizing across diverse populations and types of tumors. Variances in image acquisition parameters can restrict a model's generalizability across different datasets. By incorporating a range of datasets to enrich the model's diversity and refining the model's architecture and training procedures, the AI models' generalization capabilities can be significantly improved (Midya et al., 2018; Zwanenburg, 2019). This ensures robust performance on unseen data, adapting effectively to a variety of clinical scenarios.

Ethical, legal, and social issues are topics of extensive debate (O'Sullivan et al., 2019). On one hand, during the data collection process, ensuring that patients provide informed consent, safeguarding their privacy, and preventing data breaches and misuse are deemed significant concerns. The onus of social responsibility and the demands of legal systems also emphasize the need for algorithmic fairness. Biases in research or imperfections in training data could result in discriminatory decisions, a scenario that must be circumvented (Ambe et al., 2020; Butterfield et al., 2022; Carrano et al., 2021). Furthermore, the deployment of AI systems risks perpetuating and exacerbating biases against gender, race, ethnicity, socioeconomic status, and other marginalized groups in society. To counter this, enhancing the diversity within AI development teams and incorporating a representative range of data encompassing different genders, races, ethnicities, socioeconomic backgrounds, and populations in the training datasets can aid in ensuring the algorithm's fairness and inclusivity.

The current application of AI technology in the brain tumor is predominantly concentrated on diagnosis and therapy, where it has demonstrated effective supportive capabilities. This includes areas such as early tumor screening, diagnosis, differential diagnosis, grading, molecular characteristic identification, preoperative planning, and surgical assistance. Looking ahead, the potential for AI to deliver remarkable outcomes in an expanded range of domains is promising. The integration of AI technology in the development and research of oncological drugs and the depiction of brain tumor microenvironment is a burgeoning field. Gaining insights into the mechanisms of tumor formation and progression is instrumental for crafting targeted treatment strategies. With the advent of multi-modal, large-sample databases that encompass radiology, pathology, and omics data, the prospect of utilizing AI to forecast the risk of brain tumors in the general population or to devise personalized prevention, diagnosis, treatment, and management protocols presents a highly valuable avenue for exploration. Furthermore, in the education of early-career physicians, the aggregation of extensive datasets and the evolution of AI-assisted tools are making significant contributions to the professional development of clinical practitioners.

Ultimately, the advancement of AI technology hinges on ongoing development and innovation to augment its efficacy in the diagnosis, treatment, management, and research of brain tumors and other malignancies. There is a pressing need for further exploration and the creation of novel algorithms and tools across various domains, including imaging techniques, computational models, and data fusion strategies. It is crucial to highlight that, while AI technology has achieved significant milestones in healthcare and even demonstrates the potential to outperform human capabilities in certain respects, it is not expected to entirely supplant the role of medical professionals. Instead, AI is more likely to serve as an auxiliary tool. The future of medical practice may increasingly integrate AI technology, yet the specialized expertise, clinical acumen, and compassionate care provided by physicians will remain irreplaceable.

8. Conclusions and discussion

Based on its robust capacity for information recognition and combination, extensive utilization of high-dimensional datasets, coupled with the evolution of sophisticated algorithmic models, AI is progressively transforming conventional diagnostic and therapeutic paradigms for brain tumors, holding out significant promise for the precision medicine of tomorrow. AI models, encompassing traditional algorithms to advanced deep learning techniques, have demonstrated significant potential in enhancing the accuracy and efficiency of brain tumor diagnosis, including screening, differential diagnosis, grading, and molecular characterization. Throughout the entire treatment process of brain tumors, AI technology also provides valuable support across various stages, including pre-operative planning, intra-operative assistance, postoperative care and management and prediction of treatment response and patient prognosis. In brain tumor scientific research, AI aids in drug screening, development, and the determination of optimal treatment plans, as well as in ensuring the precision of drug delivery. Moreover, it assists researchers in more accurately characterizing the brain tumor microenvironment and its dynamic evolution, laying a theoretical foundation for the development of innovative therapeutic strategies. This paper reviews the concepts of AI and its applications in the diagnosis, treatment, and scientific research of brain tumors (Fig. 3).

Nonetheless, the accessibility and reliability of the datasets, interpretability and generalization capabilities of the models, and the presence of ethical and legal concerns are also challenges that need to be addressed. Looking ahead, it is anticipated that with ongoing advancements and innovations in AI technology, along with the development of new algorithms and tools, these issues will be resolved. AI technology is poised to bring about even more remarkable transformations in the management of brain tumors and other diseases. While the future of medical practice may increasingly incorporate the application of AI technology, it will predominantly serve as an auxiliary tool. The specialized expertise, clinical experience, and human touch provided by physicians will always remain essential.

Ethics approval and consent to participate

Not applicable.

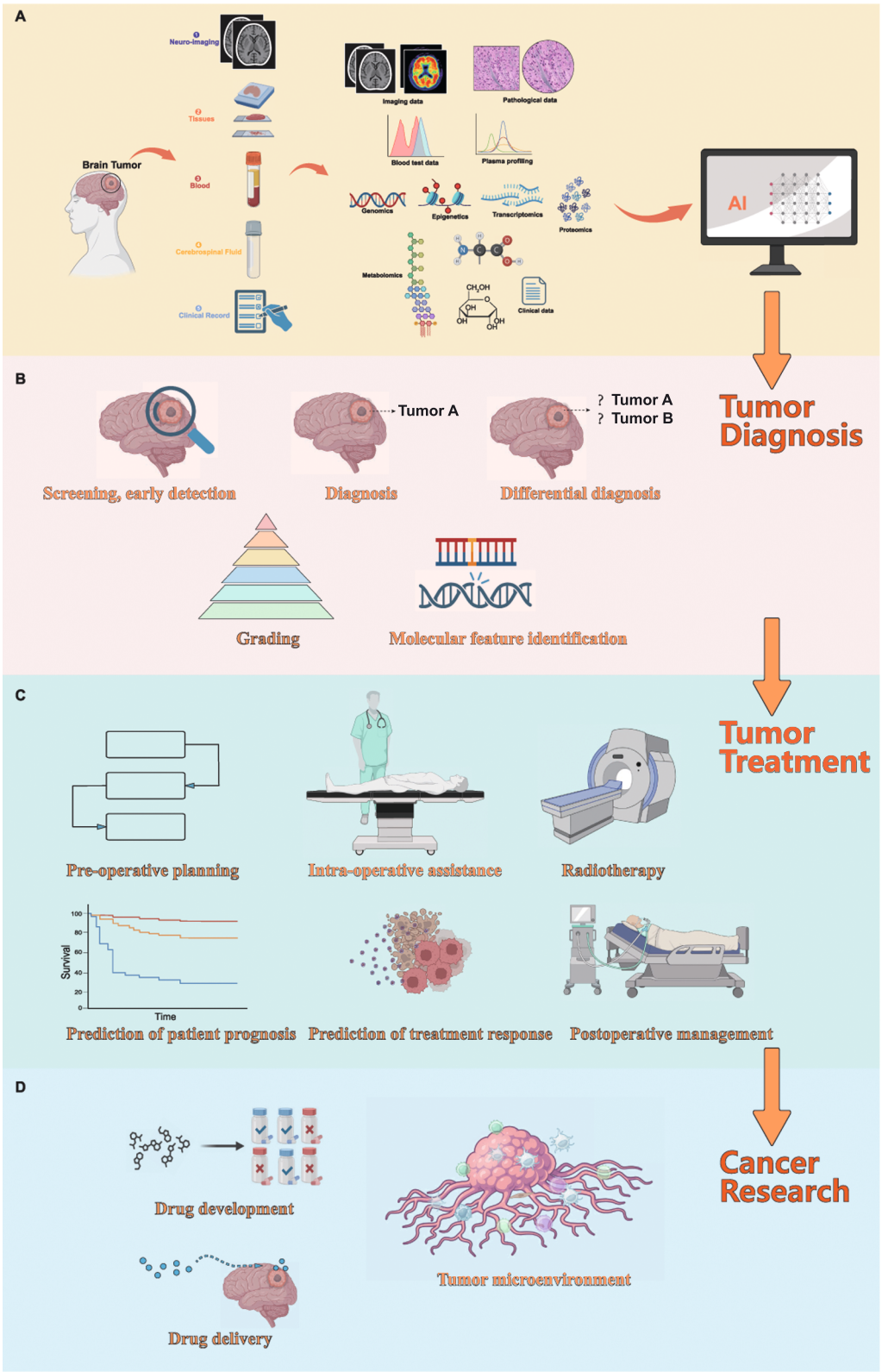

Fig. 3. Application of AI in clinical management and scientific research of brain tumors. (A) The integration of AI models and various types of patient data including neuroimaging, histopathology data, multi-omics data, clinical data and so on is widely used in clinical diagnosis, treatment and scientific research of brain tumors. (B)The application of AI in brain tumor diagnosis aids in tumor screening and early detection, diagnosis and differential diagnosis, grading and identification of molecular characteristics. (C)AI serves as a valuable auxiliary tool in the whole process of brain tumor treatment, including pre-surgical planning, intra-operative assistance, postoperative care and management, adjuvant radiotherapy, prediction of treatment response and patient prognosis. (D)The application of AI in brain tumor research facilitates drug developmen and precision delivery, and the study on tumor microenvironment, which offers a foundational mechanism for the innovation of novel therapeutic approaches.

Authors' contributions

YHZ and YYH contributed to the conception of the study and wrote the initial draft. XW and DCG reviewed the manuscript and provided suggestions for revision. All authors read and approved the final manuscript.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

Not applicable; all information in this review can be found in the reference list.

References

Abdolmaleki, P., Mihara, F., Masuda, K., Buadu, L.D., 1997. Neural networks analysis of astrocytic gliomas from MRI appearances. Cancer Lett. 118 (1), 69–78.
Abualhaj, B., Weng, G., Ong, M., Attarwala, A.A., Molina, F., Büsing, K., Glatting, G., 2017. Comparison of five cluster validity indices performance in brain [18 F]FET-PET image segmentation using k-means. Med. Phys. 44 (1), 209–220.
Acosta, J.N., Falcone, G.J., Rajpurkar, P., Topol, E.J., 2022. Multimodal biomedical AI. Nat. Med. 28 (9), 1773–1784.
Ahmed, F.E., Vos, P.W., Holbert, D., 2007. Modeling survival in colon cancer: a methodological review. Mol. Cancer 6, 15.
Alshehri, N., Cote, D.J., Hulou, M.M., Alghamdi, A., Alshahrani, A., Mekary, R.A., Smith, T.R., 2016. Venous thromboembolism prophylaxis in brain tumor patients undergoing craniotomy: a meta-analysis. J. Neuro Oncol. 130 (3), 561–570.
Ambe, S., Lyon, K.A., Oh, J., Rogers, M.K.N., Olanipekun, O., Basil, N.N., Fonkem, E., 2020. Racial disparities in malignant primary brain tumor survival in Texas From 1995 to 2013. Cureus 12 (11), e11710.
Anwar, S.M., Yousaf, S., Majid, M., 2018. Brain tumor segmentation on Multimodal MRI scans using EMAP Algorithm. Annu Int Conf. IEEE Eng. Med. Biol. Soc. 2018 550–553.
Arle, J.E., Morriss, C., Wang, Z.J., Zimmerman, R.A., Phillips, P.G., Sutton, L.N., 1997. Prediction of posterior fossa tumor type in children by means of magnetic resonance image properties, spectroscopy, and neural networks. J. Neurosurg. 86 (5), 755–761.
Babu, K.R., Nagajaneyulu, P.V., Prasad, K.S., 2021. Brain tumor segmentation of T1w MRI images based on clustering using dimensionality reduction random projection technique. Curr. Med. Imaging 17 (3), 331–341.
Bai, X., Zhang, Y., Liu, H., Wang, Y., 2019. Intuitionistic center-free FCM clustering for MR brain image segmentation. IEEE J. Biomed. Health Inf. 23 (5), 2039–2051.
Balagurunathan, Y., Mitchell, R., El Naqa, I., 2021. Requirements and reliability of AI in the medical context. Phys. Med. 83, 72–78.
Battalapalli, D., Rao, B.V., Yogeeswari, P., Kesavadas, C., Rajagopalan, V., 2022. An optimal brain tumor segmentation algorithm for clinical MRI dataset with low resolution and non-contiguous slices. BMC Med. Imaging 22 (1), 89.
Bhinder, B., Gilvary, C., Madhukar, N.S., Elemento, O., 2021. Artificial intelligence in cancer research and precision medicine. Cancer Discov. 11 (4), 900–915.
Bini, S.A., 2018. Artificial intelligence, machine learning, deep learning, and cognitive computing: what do these terms mean and how will they impact health care? J. Arthroplast. 33 (8), 2358–2361.
Biratu, E.S., Schwenker, F., Debelee, T.G., Kebede, S.R., Negera, W.G., Molla, H.T., 2021. Enhanced region growing for brain tumor MR image segmentation. J. Imaging 7 (2).
Brandsma, D., Stalpers, L., Taal, W., Sminia, P., van den Bent, M.J., 2008. Clinical features, mechanisms, and management of pseudoprogression in malignant gliomas. Lancet Oncol. 9 (5), 453–461.
Bruschi, M., Kajana, X., Petretto, A., Bartolucci, M., Pavanello, M., Ghiggeri, G.M., Panfoli, I., Candiano, G., 2022. Weighted gene co-expression network analysis and support vector machine learning in the proteomic profiling of cerebrospinal fluid from extraventricular drainage in child medulloblastoma. Metabolites 12 (8).
Bruschi, M., Petretto, A., Cama, A., Pavanello, M., Bartolucci, M., Morana, G., Ramenghi, L.A., Garré, M.L., Ghiggeri, G.M., Panfoli, I., Candiano, G., 2021. Potential biomarkers of childhood brain tumor identified by proteomics of cerebrospinal fluid from extraventricular drainage (EVD). Sci. Rep. 11 (1), 1818.
Bui, A.T.N., Son, H., Park, S., Oh, S., Kim, J.-S., Cho, J.H., Hwang, H.-J., Kim, J.-H., Yi, G.-S., Chi, S.-W., 2022. Artificial intelligence-based identification of octenidine as a Bcl-xL inhibitor. Biochem Biophys. Res. Commun. 588.
Butterfield, J.T., Golzarian, S., Johnson, R., Fellows, E., Dhawan, S., Chen, C.C., Marcotte, E.L., Venteicher, A.S., 2022. Racial disparities in recommendations for surgical resection of primary brain tumours: a registry-based cohort analysis. Lancet 400 (10368), 2063–2073.
Cao, J., Shi, X., Gurav, D.D., Huang, L., Su, H., Li, K., Niu, J., Zhang, M., Wang, Q., Jiang, M., Qian, K., 2020. Metabolic fingerprinting on synthetic alloys for medulloblastoma diagnosis and radiotherapy evaluation. Adv. Mater. 32 (23), e2000906.
Capper, D., Jones, D.T.W., Sill, M., Hovestadt, V., Schrimpf, D., Sturm, D., Koelsche, C., Sahm, F., Chavez, L., Reuss, D.E., Kratz, A., Wefers, A.K., Huang, K., Pajtler, K.W., Schweizer, L., Stichel, D., Olar, A., Engel, N.W., Lindenberg, K., Harter, P.N., Braczynski, A.K., Plate, K.H., Dohmen, H., Garvalov, B.K., Coras, R., Hölsken, A., Hewer, E., Bewerunge-Hudler, M., Schick, M., Fischer, R., Beschorner, R., Schittenhelm, J., Staszewski, O., Wani, K., Varlet, P., Pages, M., Temming, P., Lohmann, D., Selt, F., Witt, H., Milde, T., Witt, O., Aronica, E., Giangaspero, F., Rushing, E., Scheurlen, W., Geisenberger, C., Rodriguez, F.J., Becker, A., Preusser, M., Haberler, C., Bjerkvig, R., Cryan, J., Farrell, M., Deckert, M., Hench, J., Frank, S., Serrano, J., Kannan, K., Tsirigos, A., Brück, W., Hofer, S., Brehmer, S., Seiz-Rosenhagen, M., Hänggi, D., Hans, V., Rozsnoki, S., Hansford, J.R., Kohlhof, P., Kristensen, B.W., Lechner, M., Lopes, B., Mawrin, C., Ketter, R., Kulozik, A., Khatib, Z., Heppner, F., Koch, A., Jouvet, A., Keohane, C., Mühleisen, H., Mueller, W., Pohl, U., Prinz, M., Benner, A., Zapatka, M., Gottardo, N.G., Driever, P. H., Kramm, C.M., Müller, H.L., Rutkowski, S., von Hoff, K., Frühwald, M.C., Gnekow, A., Fleischhack, G., Tippelt, S., Calaminus, G., Monoranu, C.-M., Perry, A., Jones, C., Jacques, T.S., Radlwimmer, B., Gessi, M., Pietsch, T., Schramm, J., Schackert, G., Westphal, M., Reifenberger, G., Wesseling, P., Weller, M., Collins, V. P., Blümcke, I., Bendszus, M., Debus, J., Huang, A., Jabado, N., Northcott, P.A., Paulus, W., Gajjar, A., Robinson, G.W., Taylor, M.D., Jaunmuktane, Z., Ryzhova, M., Platten, M., Unterberg, A., Wick, W., Karajannis, M.A., Mittelbronn, M., Acker, T., Hartmann, C., Aldape, K., Schüller, U., Buslei, R., Lichter, P., Kool, M., Herold-Mende, C., Ellison, D.W., Hasselblatt, M., Snuderl, M., Brandner, S., Korshunov, A., von Deimling, A., Pfister, S.M., 2018. DNA methylation-based classification of central nervous system tumours. Nature 555 (7697), 469–474.
Carrano, A., Juarez, J.J., Incontri, D., Ibarra, A., Guerrero Cazares, H., 2021. Sex-specific differences in glioblastoma. Cells 10 (7).
Carvalho, D.M., Richardson, P.J., Olaciregui, N., Stankunaite, R., Lavarino, C., Molinari, V., Corley, E.A., Smith, D.P., Ruddle, R., Donovan, A., Pal, A., Raynaud, F. I., Temelso, S., Mackay, A., Overington, J.P., Phelan, A., Sheppard, D., Mackinnon, A., Zebian, B., Al-Sarraj, S., Merve, A., Pryce, J., Grill, J., Hubank, M., Cruz, O., Morales La Madrid, A., Mueller, S., Carcaboso, A.M., Carceller, F., Jones, C., 2022. Repurposing vandetanib plus everolimus for the treatment of ACVR1-mutant diffuse intrinsic pontine glioma. Cancer Discov. 12 (2), 416–431.
Castiglioni, I., Rundo, L., Codari, M., Di Leo, G., Salvatore, C., Interlenghi, M., Gallivanone, F., Cozzi, A., D'Amico, N.C., Sardanelli, F., 2021. AI applications to medical images: from machine learning to deep learning. Phys. Med 83.
Chaddad, A., 2015. Automated feature extraction in brain tumor by magnetic resonance imaging using gaussian mixture models. Int. J. Biomed. Imaging 2015, 868031.
Chahid, I., Elmiad, A.K., Badaoui, M., 2023. Data Preprocessing For Machine Learning Applications in Healthcare: A Review, 2023 14th International Conference on Intelligent Systems: Theories and Applications (SITA). pp. 1-6..
Chen, L., Bentley, P., Mori, K., Misawa, K., Fujiwara, M., Rueckert, D., 2018. DRINet for medical image segmentation. IEEE Trans. Med. Imaging 37 (11), 2453–2462.
Chen, W.C., Choudhury, A., Youngblood, M.W., Polley, M.-Y.C., Lucas, C.-H.G., Mirchia, K., Maas, S.L.N., Suwala, A.K., Won, M., Bayley, J.C., Harmanci, A.S., Harmanci, A.O., Klisch, T.J., Nguyen, M.P., Vasudevan, H.N., McCortney, K., Yu, T. J., Bhave, V., Lam, T.-C., Pu, J.K.-S., Li, L.-F., Leung, G.K.-K., Chan, J.W., Perlow, H. K., Palmer, J.D., Haberler, C., Berghoff, A.S., Preusser, M., Nicolaides, T.P., Mawrin, C., Agnihotri, S., Resnick, A., Rood, B.R., Chew, J., Young, J.S., Boreta, L., Braunstein, S.E., Schulte, J., Butowski, N., Santagata, S., Spetzler, D., Bush, N.A.O., Villanueva-Meyer, J.E., Chandler, J.P., Solomon, D.A., Rogers, C.L., Pugh, S.L., Mehta, M.P., Sneed, P.K., Berger, M.S., Horbinski, C.M., McDermott, M.W., Perry, A., Bi, W.L., Patel, A.J., Sahm, F., Magill, S.T., Raleigh, D.R., 2023. Targeted gene expression profiling predicts meningioma outcomes and radiotherapy responses. Nat. Med. 29 (12), 3067–3076.
Chen, D., Liu, Z., Wang, J., Yang, C., Pan, C., Tang, Y., Zhang, P., Liu, N., Li, G., Li, Y., Wu, Z., Xia, F., Zhang, C., Nie, H., Tang, Z., 2022. Integrative genomic analysis facilitates precision strategies for glioblastoma treatment. iScience 25 (11), 105276.
Chen, J., Xu, L., Li, X., Park, S., 2023. Deep learning models for cancer stem cell detection: a brief review. Front. Immunol. 14, 1214425.
Chen, B., Zhang, L., Chen, H., Liang, K., Chen, X., 2021. A novel extended Kalman filter with support vector machine based method for the automatic diagnosis and segmentation of brain tumors. Comput. Methods Prog. Biomed. 200, 105797.
Ching, T., Zhu, X., Garmire, L.X., 2018. Cox-nnet: an artificial neural network method for prognosis prediction of high-throughput omics data. PLoS Comput. Biol. 14 (4), e1006076.
Clarke, J.L., Chang, S., 2009. Pseudoprogression and pseudoresponse: challenges in brain tumor imaging. Curr. Neurol. Neurosci. Rep. 9 (3), 241–246.

Comelli, A., Stefano, A., Bignardi, S., Russo, G., Sabini, M.G., Ippolito, M., Barone, S., Yezzi, A., 2019. Active contour algorithm with discriminant analysis for delineating tumors in positron emission tomography. Artif. Intell. Med. 94, 67–78.
Crabb, B.T., Hamrick, F., Campbell, J.M., Vignolles-Jeong, J., Magill, S.T., Prevedello, D. M., Carrau, R.L., Otto, B.A., Hardesty, D.A., Couldwell, W.T., Karsy, M., 2022. Machine learning-based analysis and prediction of unplanned 30-day readmissions after pituitary adenoma resection: a multi-institutional retrospective study with external validation. Neurosurgery 91 (2), 263–271.
De Benedictis, A., Trezza, A., Carai, A., Genovese, E., Procaccini, E., Messina, R., Randi, F., Cossu, S., Esposito, G., Palma, P., Amante, P., Rizzi, M., Marras, C.E., 2017. Robot-assisted procedures in pediatric neurosurgery. Neurosurg. Focus 42 (5), E7.
van den Bent, M.J., Geurts, M., French, P.J., Smits, M., Capper, D., Bromberg, J.E.C., Chang, S.M., 2023. Primary brain tumours in adults. Lancet 402 (10412), 1564–1579.
Deo, R.C., 2015. Machine learning in medicine. Circulation 132 (20), 1920–1930.
van der Voort, S.R., Incekara, F., Wijnenga, M.M.J., Kapsas, G., Gahrmann, R., Schouten, J.W., Nandoe Tewarie, R., Lycklama, G.J., De Witt Hamer, P.C., Eijgelaar, R.S., French, P.J., Dubbink, H.J., Vincent, A.J.P.E., Niessen, W.J., van den Bent, M.J., Smits, M., Klein, S., 2023. Combined molecular subtyping, grading, and segmentation of glioma using multi-task deep learning. Neuro-Oncol. 25 (2), 279–289.
Din, N.M.U., Dar, R.A., Rasool, M., Assad, A., 2022. Breast cancer detection using deep learning: Datasets, methods, and challenges ahead. Comput. Biol. Med. 149, 106073.
Eckel-Passow, J.E., Lachance, D.H., Molinaro, A.M., Walsh, K.M., Decker, P.A., Sicotte, H., Pekmezci, M., Rice, T., Kosel, M.L., Smirnov, I.V., Sarkar, G., Caron, A.A., Kollmeyer, T.M., Praska, C.E., Chada, A.R., Halder, C., Hansen, H.M., McCoy, L.S., Bracci, P.M., Marshall, R., Zheng, S., Reis, G.F., Pico, A.R., O'Neill, B.P., Buckner, J. C., Giannini, C., Huse, J.T., Perry, A., Tihan, T., Berger, M.S., Chang, S.M., Prados, M. D., Wiemels, J., Wiencke, J.K., Wrensch, M.R., Jenkins, R.B., 2015. Glioma Groups Based on 1p/19q, IDH, and TERT promoter mutations in tumors. N. Engl. J. Med. 372 (26), 2499–2508.
El Kader, I.A., Xu, G., Shuai, Z., Saminu, S., 2021. Brain tumor detection and classification by hybrid CNN-DWA model using MR images. Curr. Med. Imaging 17 (10), 1248–1255.
El-Hag, N.A., Sedik, A., El-Banby, G.M., El-Shafai, W., Khalaf, A.A.M., Al-Nuaimy, W., Abd El-Samie, F.E., El-Hoseny, H.M., 2021. Utilization of image interpolation and fusion in brain tumor segmentation. Int J. Numer. Method Biomed. Eng. 37 (8), e3449.
Esparragosa Vazquez, I., Ndiaye, M., Di Stefano, A.L., Younan, N., Larrieu-Ciron, D., Seyve, A., Picart, T., Meyronet, D., Boutet, C., Vassal, F., Carpentier, C., Figarella-Branger, D., Dehais, C., Forest, F., Rivoirard, R., Ducray, F., 2023. T2-Fluid-attenuated inversion recovery (FLAIR) pseudoprogression in patients with anaplastic oligodendrogliomas treated with procarbazine, lomustine and vincristine (PCV) chemotherapy alone. Eur. J. Neurol. 30 (9), 2879–2883.
Essadike, A., Ouabida, E., Bouzid, A., 2018. Brain tumor segmentation with Vander Lugt correlator based active contour. Comput. Methods Prog. Biomed. 160, 103–117.
Eyraud, R., Ayache, S., Tsvetkov, P.O., Kalidindi, S.S., Baksheeva, V.E., Boissonneau, S., Jiguet-Jiglaire, C., Appay, R., Nanni-Metellus, I., Chinot, O., Devred, F., Tabouret, E., 2023. Plasma nanoDSF denaturation profile at baseline is predictive of glioblastoma EGFR status. Cancers 15 (3).
Fabelo, H., Halicek, M., Ortega, S., Shahedi, M., Szolna, A., Piñeiro, J.F., Sosa, C., O'Shanahan, A.J., Bisshopp, S., Espino, C., Márquez, M., Hernández, M., Carrera, D., Morera, J., Callico, G.M., Sarmiento, R., Fei, B., 2019. Deep learning-based framework for in vivo identification of glioblastoma tumor using hyperspectral images of human brain. Sensors 19 (4).
Fabelo, H., Ortega, S., Lazcano, R., Madroñal, D., M Callicó, G., Juárez, E., Salvador, R., Bulters, D., Bulstrode, H., Szolna, A., Piñeiro, J.F., Sosa, C., J O'Shanahan, A., Bisshopp, S., Hernández, M., Morera, J., Ravi, D., Kiran, B.R., Vega, A., Báez-Quevedo, A., Yang, G.-Z., Stanciulescu, B., Sarmiento, R., 2018. An intraoperative visualization system using hyperspectral imaging to aid in brain tumor delineation. Sensors 18 (2).
Familiari, P., Lapolla, P., Picotti, V., Palmieri, M., Pesce, A., Carosi, G., Relucenti, M., Nottola, S., Gianno, F., Minasi, S., Antonelli, M., Frati, A., Santoro, A., D'Andrea, G., Bruzzaniti, P., La Pira, B., 2023. Role of 1p/19q codeletion in diffuse low-grade glioma tumour prognosis. Anticancer Res. 43 (6), 2659–2670.
Fathi, S., Ahmadi, M., Dehnad, A., 2022. Early diagnosis of Alzheimer's disease based on deep learning: a systematic review. Comput. Biol. Med. 146, 105634.
Fukuma, R., Yanagisawa, T., Kinoshita, M., Shinozaki, T., Arita, H., Kawaguchi, A., Takahashi, M., Narita, Y., Terakawa, Y., Tsuyuguchi, N., Okita, Y., Nonaka, M., Moriuchi, S., Takagaki, M., Fujimoto, Y., Fukai, J., Izumoto, S., Ishibashi, K., Nakajima, Y., Shofuda, T., Kanematsu, D., Yoshioka, E., Kodama, Y., Mano, M., Mori, K., Ichimura, K., Kanemura, Y., Kishima, H., 2019. Prediction of IDH and TERT promoter mutations in low-grade glioma from magnetic resonance images using a convolutional neural network. Sci. Rep. 9 (1), 20311.
Fukuya, Y., Ikuta, S., Maruyama, T., Nitta, M., Saito, T., Tsuzuki, S., Chernov, M., Kawamata, T., Muragaki, Y., 2019. Tumor recurrence patterns after surgical resection of intracranial low-grade gliomas. J. Neuro-Oncol. 144 (3), 519–528.
Gallée, L., Kniesel, H., Ropinski, T., Götz, M., 2023. Artificial intelligence in radiology - beyond the black box. Rofo 195 (9), 797–803.
Gandhe, R.U., Bhave, C.P., 2018. Intraoperative magnetic resonance imaging for neurosurgery - an anaesthesiologist's challenge. Indian J. Anaesth. 62 (6), 411–417.
Gavdush, A.A., Chernomyrdin, N.V., Malakhov, K.M., Beshplav, S.-I.T., Dolganova, I.N., Kosyrkova, A.V., Nikitin, P.V., Musina, G.R., Katyba, G.M., Reshetov, I.V., Cherkasova, O.P., Komandin, G.A., Karasik, V.E., Potapov, A.A., Tuchin, V.V., Zaytsev, K.I., 2019. Terahertz spectroscopy of gelatin-embedded human brain gliomas of different grades: a road toward intraoperative THz diagnosis. J. Biomed. Opt. 24 (2), 1–5.
Gerard, I.J., Kersten-Oertel, M., Petrecca, K., Sirhan, D., Hall, J.A., Collins, D.L., 2017. Brain shift in neuronavigation of brain tumors: a review. Med. Image Anal. 35, 403–420.
Gondi, V., Hermann, B.P., Mehta, M.P., Tomé, W.A., 2012. Hippocampal dosimetry predicts neurocognitive function impairment after fractionated stereotactic radiotherapy for benign or low-grade adult brain tumors. Int. J. Radiat. Oncol. Biol. Phys. 83 (4), e487–e493.
Greener, J.G., Kandathil, S.M., Moffat, L., Jones, D.T., 2022. A guide to machine learning for biologists. Nat. Rev. Mol. Cell Biol. 23 (1), 40–55.
Grist, J.T., Withey, S., Bennett, C., Rose, H.E.L., MacPherson, L., Oates, A., Powell, S., Novak, J., Abernethy, L., Pizer, B., Bailey, S., Clifford, S.C., Mitra, D., Arvanitis, T.N., Auer, D.P., Avula, S., Grundy, R., Peet, A.C., 2021. Combining multi-site magnetic resonance imaging with machine learning predicts survival in pediatric brain tumors. Sci. Rep. 11 (1), 18897.
Grist, J.T., Withey, S., MacPherson, L., Oates, A., Powell, S., Novak, J., Abernethy, L., Pizer, B., Grundy, R., Bailey, S., Mitra, D., Arvanitis, T.N., Auer, D.P., Avula, S., Peet, A.C., 2020. Distinguishing between paediatric brain tumour types using multi-parametric magnetic resonance imaging and machine learning: a multi-site study. Neuroimage Clin. 25, 102172.
Gritsch, S., Batchelor, T.T., Gonzalez Castro, L.N., 2022. Diagnostic, therapeutic, and prognostic implications of the 2021 World Health Organization classification of tumors of the central nervous system. Cancer 128 (1), 47–58.
Guo, S., Chen, Q., Wang, L., Wang, L., Zhu, Y., 2023. nnUnetFormer: an automatic method based on nnUnet and transformer for brain tumor segmentation with multimodal MR images. Phys. Med. Biol. 68 (24).
Gutsche, R., Lowis, C., Ziemons, K., Kocher, M., Ceccon, G., Régio Brambilla, C., Shah, N. J., Langen, K.-J., Galldiks, N., Isensee, F., Lohmann, P., 2023. Automated brain tumor detection and segmentation for treatment response assessment using amino acid PET. J. Nucl. Med. 64 (10), 1594–1602.
Hamet, P., Tremblay, J., 2017. Artificial intelligence in medicine. Metabolism 69S, S36–S40.
Handelman, G.S., Kok, H.K., Chandra, R.V., Razavi, A.H., Huang, S., Brooks, M., Lee, M. J., Asadi, H., 2019. Peering into the black box of artificial intelligence: evaluation metrics of machine learning methods. AJR Am. J. Roentgenol. 212 (1), 38–43.
Hasanau, T., Pisarev, E., Kisil, O., Nonoguchi, N., Le Calvez-Kelm, F., Zvereva, M., 2022. Detection of TERT promoter mutations as a prognostic biomarker in gliomas: methodology, prospects, and advances. Biomedicines 10 (3).
Hashimoto, D.A., Witkowski, E., Gao, L., Meireles, O., Rosman, G., 2020. Artificial intelligence in anesthesiology: current techniques, clinical applications, and limitations. Anesthesiology 132 (2), 379–394.
Haug, C.J., Drazen, J.M., 2023. Artificial intelligence and machine learning in clinical medicine. N. Engl. J. Med. 388 (13), 1201–1208.
Havaei, M., Davy, A., Warde-Farley, D., Biard, A., Courville, A., Bengio, Y., Pal, C., Jodoin, P.-M., Larochelle, H., 2017. Brain tumor segmentation with Deep Neural Networks. Med. Image Anal. 35, 18–31.
He, Q., Duan, Y., Miles, J., Takahashi, N., 2007. A context-sensitive active contour for 2D corpus callosum segmentation. Int. J. Biomed. Imaging 2007, 24826.
He, X., Liu, X., Zuo, F., Shi, H., Jing, J., 2023. Artificial intelligence-based multi-omics analysis fuels cancer precision medicine. Semin. Cancer Biol. 88, 187–200.
Herrgott, G.A., Snyder, J.M., She, R., Malta, T.M., Sabedot, T.S., Lee, I.Y., Pawloski, J., Podolsky-Gondim, G.G., Asmaro, K.P., Zhang, J., Cannella, C.E., Nelson, K., Thomas, B., deCarvalho, A.C., Hasselbach, L.A., Tundo, K.M., Newaz, R., Transou, A., Morosini, N., Francisco, V., Poisson, L.M., Chitale, D., Mukherjee, A., Mosella, M.S., Robin, A.M., Walbert, T., Rosenblum, M., Mikkelsen, T., Kalkanis, S., Tirapelli, D.P.C., Weisenberger, D.J., Carlotti, C.G., Rock, J., Castro, A.V., Noushmehr, H., 2023. Detection of diagnostic and prognostic methylation-based signatures in liquid biopsy specimens from patients with meningiomas. Nat. Commun. 14 (1), 5669.
Hewitt, K.J., Löffler, C.M.L., Muti, H.S., Berghoff, A.S., Eisenlöffel, C., van Treeck, M., Carrero, Z.I., El Nahhas, O.S.M., Veldhuizen, G.P., Weil, S., Saldanha, O.L., Bejan, L., Millner, T.O., Brandner, S., Brückmann, S., Kather, J.N., 2023. Direct image to subtype prediction for brain tumors using deep learning. Neurooncol Adv. 5 (1), vdad139.
Hollon, T., Jiang, C., Chowdury, A., Nasir-Moin, M., Kondepudi, A., Aabedi, A., Adapa, A., Al-Holou, W., Heth, J., Sagher, O., Lowenstein, P., Castro, M., Wadiura, L. I., Widhalm, G., Neuschmelting, V., Reinecke, D., von Spreckelsen, N., Berger, M.S., Hervey-Jumper, S.L., Golfinos, J.G., Snuderl, M., Camelo-Piragua, S., Freudiger, C., Lee, H., Orringer, D.A., 2023. Artificial-intelligence-based molecular classification of diffuse gliomas using rapid, label-free optical imaging. Nat. Med. 29 (4), 828–832.
Hollon, T.C., Lewis, S., Pandian, B., Niknafs, Y.S., Garrard, M.R., Garton, H., Maher, C.O., McFadden, K., Snuderl, M., Lieberman, A.P., Muraszko, K., Camelo-Piragua, S., Orringer, D.A., 2018. Rapid intraoperative diagnosis of pediatric brain tumors using stimulated raman histology. Cancer Res. 78 (1), 278–289.
Hollon, T., Orringer, D.A., 2021. Label-free brain tumor imaging using Raman-based methods. J. Neuro-Oncol. 151 (3), 393–402.
Hopkins, B.S., Mazmudar, A., Driscoll, C., Svet, M., Goergen, J., Kelsten, M., Shlobin, N. A., Kesavabhotla, K., Smith, Z.A., Dahdaleh, N.S., 2020. Using artificial intelligence (AI) to predict postoperative surgical site infection: a retrospective cohort of 4046 posterior spinal fusions. Clin. Neurol. Neurosurg. 192, 105718.
Horbinski, C., Berger, T., Packer, R.J., Wen, P.Y., 2022. Clinical implications of the 2021 edition of the WHO classification of central nervous system tumours. Nat. Rev. Neurol. 18 (9), 515–529.
Houy, N., Le Grand, F., 2019. Personalized oncology with artificial intelligence: the case of temozolomide. Artif. Intell. Med. 99, 101693.

Howcroft, J., Kofman, J., Lemaire, E.D., 2017. Prospective fall-risk prediction models for older adults based on wearable sensors. IEEE Trans. Neural Syst. Rehabil. Eng. 25 (10), 1812–1820.
Hsiao, R.-S., Mi, Z., Yang, B.-R., Kau, L.-J., Bitew, M.A., Li, T.-Y., 2015. Body posture recognition and turning recording system for the care of bed bound patients. Technol. Health Care 24 (1), S307–S312.
Huang, Y., Bert, C., Sommer, P., Frey, B., Gaipl, U., Distel, L.V., Weissmann, T., Uder, M., Schmidt, M.A., Dörfler, A., Maier, A., Fietkau, R., Putz, F., 2022. Deep learning for brain metastasis detection and segmentation in longitudinal MRI data. Med. Phys. 49 (9), 5773–5786.
Huisman, T.A., 2009. Tumor-like lesions of the brain. Cancer Imaging 9 (Spec A(Special A)), S10–S13.
Huynh, T., Nibali, A., He, Z., 2022. Semi-supervised learning for medical image classification using imbalanced training data. Comput. Methods Prog. Biomed. 216, 106628.
Islam, A., Reza, S.M.S., Iftekharuddin, K.M., 2013. Multifractal texture estimation for detection and segmentation of brain tumors. IEEE Trans. Biomed. Eng. 60 (11), 3204–3215.
Iv, M., Zhou, M., Shpanskaya, K., Perreault, S., Wang, Z., Tranvinh, E., Lanzman, B., Vajapeyam, S., Vitanza, N.A., Fisher, P.G., Cho, Y.J., Laughlin, S., Ramaswamy, V., Taylor, M.D., Cheshier, S.H., Grant, G.A., Young Poussaint, T., Gevaert, O., Yeom, K. W., 2019. MR imaging-based radiomic signatures of distinct molecular subgroups of medulloblastoma. AJNR Am. J. Neuroradiol. 40 (1), 154–161.
Jian, A., Jang, K., Manuguerra, M., Liu, S., Magnussen, J., Di Ieva, A., 2021. Machine learning for the prediction of molecular markers in glioma on magnetic resonance imaging: a systematic review and meta-analysis. Neurosurgery 89 (1), 31–44.
Jiang, T., Gradus, J.L., Rosellini, A.J., 2020. Supervised machine learning: a brief primer. Behav. Ther. 51 (5), 675–687.
Jin, Z., Yue, Q., Duan, W., Sui, A., Zhao, B., Deng, Y., Zhai, Y., Zhang, Y., Sun, T., Zhang, G.-P., Han, L., Mao, Y., Yu, J., Zhang, X.-Y., Li, C., 2022. Intelligent SERS navigation system guiding brain tumor surgery by intraoperatively delineating the metabolic acidosis. Adv. Sci. 9 (7), e2104935.
Julesz, B., 1981. Textons, the elements of texture perception, and their interactions. Nature 290 (5802), 91–97.
Jumiawi, W.A.H., El-Zaart, A., 2022. A boosted minimum cross entropy thresholding for medical images segmentation based on heterogeneous mean filters approaches. J. Imaging 8 (2).
Juvekar, P., Dorent, R., Kögl, F., Torio, E., Barr, C., Rigolo, L., Galvin, C., Jowkar, N., Kazi, A., Haouchine, N., Cheema, H., Navab, N., Pieper, S., Wells, W.M., Bi, W.L., Golby, A., Frisken, S., Kapur, T., 2024. ReMIND: the brain resection multimodal imaging database. Sci. Data 11 (1), 494.
Kamireddy, R.R., Kandala, R.N., Dhuli, R., Polinati, S., Sonti, K., Tadeusiewicz, R., Pławiak, P., 2024. Brain MRI detection and classification: harnessing convolutional neural networks and multi-level thresholding. PLoS One 19 (8), e0306492.
Kang, J., Ullah, Z., Gwak, J., 2021. MRI-based brain tumor classification using ensemble of deep features and machine learning classifiers. Sensors 21 (6).
Kanmani, P., Marikkannu, P., 2018. MRI brain images classification: a multi-level threshold based region optimization technique. J. Med. Syst. 42 (4), 62.
Katzman, J.L., Shaham, U., Cloninger, A., Bates, J., Jiang, T., Kluger, Y., 2018. DeepSurv: personalized treatment recommender system using a Cox proportional hazards deep neural network. BMC Med. Res. Methodol. 18 (1), 24.
Kebir, S., Schmidt, T., Weber, M., Lazaridis, L., Galldiks, N., Langen, K.-J., Kleinschnitz, C., Hattingen, E., Herrlinger, U., Lohmann, P., Glas, M., 2020. A preliminary study on machine learning-based evaluation of static and dynamic FET-PET for the detection of pseudoprogression in patients with IDH-wildtype glioblastoma. Cancers 12 (11).
Khan, D.Z., Luengo, I., Barbarisi, S., Addis, C., Culshaw, L., Dorward, N.L., Haikka, P., Jain, A., Kerr, K., Koh, C.H., Layard Horsfall, H., Muirhead, W., Palmisciano, P., Vasey, B., Stoyanov, D., Marcus, H.J., 2022. Automated operative workflow analysis of endoscopic pituitary surgery using machine learning: development and preclinical evaluation (IDEAL stage 0). J. Neurosurg. 137 (1), 51–58.
Khosravanian, A., Rahmanimanesh, M., Keshavarzi, P., Mozaffari, S., 2021. A level set method based on domain transformation and bias correction for MRI brain tumor segmentation. J. Neurosci. Methods 352, 109091.
Kifle, N., Teti, S., Ning, B., Donoho, D.A., Katz, I., Keating, R., Cha, R.J., 2023. Pediatric brain tissue segmentation using a snapshot hyperspectral imaging (sHSI) camera and machine learning classifier. Bioengineering 10 (10).
Kim, J.Y., Yoon, M.J., Park, J.E., Choi, E.J., Lee, J., Kim, H.S., 2019. Radiomics in peritumoral non-enhancing regions: fractional anisotropy and cerebral blood volume improve prediction of local progression and overall survival in patients with glioblastoma. Neuroradiology 61 (11), 1261–1272.
Ko, C.-C., Zhang, Y., Chen, J.-H., Chang, K.-T., Chen, T.-Y., Lim, S.-W., Wu, T.-C., Su, M.-Y., 2021. Pre-operative MRI radiomics for the prediction of progression and recurrence in meningiomas. Front. Neurol. 12, 636235.
Kuntz, S., Krieghoff-Henning, E., Kather, J.N., Jutzi, T., Höhn, J., Kiehl, L., Hekler, A., Alwers, E., von Kalle, C., Fröhling, S., Utikal, J.S., Brenner, H., Hoffmeister, M., Brinker, T.J., 2021. Gastrointestinal cancer classification and prognostication from histology using deep learning: Systematic review. Eur. J. Cancer 155, 200–215.
Lah, T.T., Novak, M., Breznik, B., 2020. Brain malignancies: glioblastoma and brain metastases. Semin Cancer Biol. 60, 262–273.
Lamba, N., Wen, P.Y., Aizer, A.A., 2021. Epidemiology of brain metastases and leptomeningeal disease. Neuro-Oncol. 23 (9), 1447–1456.
Lee, E.H., Han, M., Wright, J., Kuwabara, M., Mevorach, J., Fu, G., Choudhury, O., Ratan, U., Zhang, M., Wagner, M.W., Goetti, R., Toescu, S., Perreault, S., Dogan, H., Altinmakas, E., Mohammadzadeh, M., Szymanski, K.A., Campen, C.J., Lai, H., Eghbal, A., Radmanesh, A., Mankad, K., Aquilina, K., Said, M., Vossough, A., Oztekin, O., Ertl-Wagner, B., Poussaint, T., Thompson, E.M., Ho, C.Y., Jaju, A., Curran, J., Ramaswamy, V., Cheshier, S.H., Grant, G.A., Wong, S.S., Moseley, M.E., Lober, R.M., Wilms, M., Forkert, N.D., Vitanza, N.A., Miller, J.H., Prolo, L.M., Yeom, K.W., 2024. An international study presenting a federated learning AI platform for pediatric brain tumors. Nat. Commun. 15 (1), 7615.
Lee, J., Wang, N., Turk, S., Mohammed, S., Lobo, R., Kim, J., Liao, E., Camelo-Piragua, S., Kim, M., Junck, L., Bapuraj, J., Srinivasan, A., Rao, A., 2020. Discriminating pseudoprogression and true progression in diffuse infiltrating glioma using multi-parametric MRI data through deep learning. Sci. Rep. 10 (1), 20331.
Letteboer, M.M.J., Olsen, O.F., Dam, E.B., Willems, P.W.A., Viergever, M.A., Niessen, W. J., 2004. Segmentation of tumors in magnetic resonance brain images using an interactive multiscale watershed algorithm. Acad. Radio. 11 (10), 1125–1138.
Li, M., Kuang, L., Xu, S., Sha, Z., 2019. Brain tumor detection based on multimodal information fusion and convolutional neural network. IEEE Access 7, 180134–180146.
Li, C., Liu, M., Zhang, Y., Wang, Y., Li, J., Sun, S., Liu, X., Wu, H., Feng, C., Yao, P., Jia, Y., Zhang, Y., Wei, X., Wu, F., Du, C., Zhao, X., Zhang, S., Qu, J., 2023. Novel models by machine learning to predict prognosis of breast cancer brain metastases. J. Transl. Med. 21 (1), 404.
Li, X., Tang, Q., Yu, J., Wang, Y., Shi, Z., 2019. Microvascularity detection and quantification in glioma: a novel deep-learning-based framework. Lab Invest 99 (10), 1515–1526.
Lin, C.-Y., Chou, L.-S., Wu, Y.-H., Kuo, J.S., Mehta, M.P., Shiau, A.-C., Liang, J.-A., Hsu, S.-M., Wang, T.-H., 2023. Developing an AI-assisted planning pipeline for hippocampal avoidance whole brain radiotherapy. Radio. Oncol. 181, 109528.
Liu, X.-P., Jin, X., Seyed Ahmadian, S., Yang, X., Tian, S.-F., Cai, Y.-X., Chawla, K., Snijders, A.M., Xia, Y., van Diest, P.J., Weiss, W.A., Mao, J.-H., Li, Z.-Q., Vogel, H., Chang, H., 2023. Clinical significance and molecular annotation of cellular morphometric subtypes in lower-grade gliomas discovered by machine learning. Neuro-Oncol. 25 (1), 68–81.
Lo Vercio, L., Amador, K., Bannister, J.J., Crites, S., Gutierrez, A., MacDonald, M.E., Moore, J., Mouches, P., Rajashekar, D., Schimert, S., Subbanna, N., Tuladhar, A., Wang, N., Wilms, M., Winder, A., Forkert, N.D., 2020. Supervised machine learning tools: a tutorial for clinicians. J. Neural Eng. 17 (6).
Louis, D.N., Perry, A., Wesseling, P., Brat, D.J., Cree, I.A., Figarella-Branger, D., Hawkins, C., Ng, H.K., Pfister, S.M., Reifenberger, G., Soffietti, R., von Deimling, A., Ellison, D.W., 2021. The 2021 WHO classification of tumors of the central nervous system: a summary. Neuro-Oncol. 23 (8), 1231–1251.
Lu, G., Fei, B., 2014. Medical hyperspectral imaging: a review. J. Biomed. Opt. 19 (1), 10901.
Luo, J., Pan, M., Mo, K., Mao, Y., Zou, D., 2023. Emerging role of artificial intelligence in diagnosis, classification and clinical management of glioma. Semin. Cancer Biol. 91, 110–123.
Madhugiri, V.S., Prasad, D., 2025. Early experience with an artificial intelligence-based module for brain metastasis detection and segmentation. J. Neuro-Oncol. 171 (2), 365–372.
Mahootiha, M., Tak, D., Ye, Z., Zapaishchykova, A., Likitlersuang, J., Climent Pardo, J.C., Boyd, A., Vajapeyam, S., Chopra, R., Prabhu, S.P., Liu, K.X., Elhalawani, H., Nabavizadeh, A., Familiar, A., Mueller, S., Aerts, H.J.W.L., Bandopadhayay, P., Ligon, K.L., Haas-Kogan, D., Poussaint, T.Y., Qadir, H.A., Balasingham, I., Kann, B. H., 2025. Multimodal deep learning improves recurrence risk prediction in pediatric low-grade gliomas. Neuro-Oncol. 27 (1), 277–290.
Marcus, H.J., Khan, D.Z., Borg, A., Buchfelder, M., Cetas, J.S., Collins, J.W., Dorward, N. L., Fleseriu, M., Gurnell, M., Javadpour, M., Jones, P.S., Koh, C.H., Layard Horsfall, H., Mamelak, A.N., Mortini, P., Muirhead, W., Oyesiku, N.M., Schwartz, T. H., Sinha, S., Stoyanov, D., Syro, L.V., Tsermoulas, G., Williams, A., Winder, M.J., Zada, G., Laws, E.R., 2021. Pituitary society expert Delphi consensus: operative workflow in endoscopic transsphenoidal pituitary adenoma resection. Pituitary 24 (6), 839–853.
Marcus, A.P., Marcus, H.J., Camp, S.J., Nandi, D., Kitchen, N., Thorne, L., 2020. Improved prediction of surgical resectability in patients with glioblastoma using an artificial neural network. Sci. Rep. 10 (1), 5143.
Marcus, H.J., Williams, S., Hughes-Hallett, A., Camp, S.J., Nandi, D., Thorne, L., 2017. Predicting surgical outcome in patients with glioblastoma multiforme using pre-operative magnetic resonance imaging: development and preliminary validation of a grading system. Neurosurg. Rev. 40 (4), 621–631.
Md Ashafuddula, N.I., Islam, R., 2024. ContourTL-Net: contour-based transfer learning algorithm for early-stage brain tumor detection. Int. J. Biomed. Imaging 2024, 6347920.
Meng, K., Chen, T.-n, Chen, T., Zhu, L.-g, Liu, Q., Li, Z., Li, F., Zhong, S.-c, Li, Z.-r, Feng, H., Zhao, J.-h, 2014. Terahertz pulsed spectroscopy of paraffin-embedded brain glioma. J. Biomed. Opt. 19 (7), 077001.
Midya, A., Chakraborty, J., Gönen, M., Do, R.K.G., Simpson, A.L., 2018. Influence of CT acquisition and reconstruction parameters on radiomic feature reproducibility. J. Med. Imaging (Bellingham 5 (1), 011020.
Miller, B.A., Salehi, A., Limbrick, D.D., Smyth, M.D., 2017. Applications of a robotic stereotactic arm for pediatric epilepsy and neurooncology surgery. J. Neurosurg. Pedia 20 (4), 364–370.
Mittal, N., Tayal, S., 2021. Advance computer analysis of magnetic resonance imaging (MRI) for early brain tumor detection. Int J. Neurosci. 131 (6), 555–570.
Moassefi, M., Faghani, S., Conte, G.M., Kowalchuk, R.O., Vahdati, S., Crompton, D.J., Perez-Vega, C., Cabreja, R.A.D., Vora, S.A., Quiñones-Hinojosa, A., Parney, I.F., Trifiletti, D.M., Erickson, B.J., 2022. A deep learning model for discriminating true progression from pseudoprogression in glioblastoma patients. J. Neuro-Oncol. 159 (2), 447–455.

Monje, M.L., Mizumatsu, S., Fike, J.R., Palmer, T.D., 2002. Irradiation induces neural precursor-cell dysfunction. Nat. Med. 8 (9), 955–962.
Munteanu, C.R., Gutiérrez-Asorey, P., Blanes-Rodríguez, M., Hidalgo-Delgado, I., Blanco Liverio, Md.J., Castiñeiras Galdo, B., Porto-Pazos, A.B., Gestal, M., Arrasate, S., González-Díaz, H., 2021. Prediction of anti-glioblastoma drug-decorated nanoparticle delivery systems using molecular descriptors and machine learning. Int. J. Mol. Sci. 22 (21).
Na, A., Haghigi, N., Drummond, K.J., 2014. Cerebral radiation necrosis. Asia Pac. J. Clin. Oncol. 10 (1), 11–21.
Nagendran, M., Chen, Y., Lovejoy, C.A., Gordon, A.C., Komorowski, M., Harvey, H., Topol, E.J., Ioannidis, J.P.A., Collins, G.S., Maruthappu, M., 2020. Artificial intelligence versus clinicians: systematic review of design, reporting standards, and claims of deep learning studies. BMJ 368, m689.
Naser, M.A., Deen, M.J., 2020. Brain tumor segmentation and grading of lower-grade glioma using deep learning in MRI images. Comput. Biol. Med. 121, 103758.
Nasrallah, M.P., Zhao, J., Tsai, C.C., Meredith, D., Marostica, E., Ligon, K.L., Golden, J.A., Yu, K.-H., 2023. Machine learning for cryosection pathology predicts the 2021 WHO classification of glioma. Medicine 4 (8).
Neves, B.J., Agnes, J.P., Gomes, Md.N., Henriques Donza, M.R., Gonçalves, R.M., Delgobo, M., Ribeiro de Souza Neto, L., Senger, M.R., Silva-Junior, F.P., Ferreira, S. B., Zanotto-Filho, A., Andrade, C.H., 2020. Efficient identification of novel anti-glioma lead compounds by machine learning models. Eur. J. Med Chem. 189, 111981.
Nowosielski, M., DiFranco, M.D., Putzer, D., Seiz, M., Recheis, W., Jacobs, A.H., Stockhammer, G., Hutterer, M., 2014. An intra-individual comparison of MRI, [18F]-FET and [18F]-FLT PET in patients with high-grade gliomas. PLoS One 9 (4), e95830.
Nuechterlein, N., Shapiro, L.G., Holland, E.C., Cimino, P.J., 2021. Machine learning modeling of genome-wide copy number alteration signatures reliably predicts IDH mutational status in adult diffuse glioma. Acta Neuropathol. Commun. 9 (1), 191.
Oermann, E.K., Kress, M.-A.S., Collins, B.T., Collins, S.P., Morris, D., Ahalt, S.C., Ewend, M.G., 2013. Predicting survival in patients with brain metastases treated with radiosurgery using artificial neural networks. Neurosurgery 72 (6).
Oliver, C.R., Westerhof, T.M., Castro, M.G., Merajver, S.D., 2020. Quantifying the brain metastatic tumor micro-environment using an organ-On-A Chip 3D model, machine learning, and confocal tomography. J. Vis. Exp. (162).
Olsen, A., Harpaz, Z., Ren, C., Shneyderman, A., Veviorskiy, A., Dralkina, M., Konnov, S., Shcheglova, O., Pun, F.W., Leung, G.H.D., Leung, H.W., Ozerov, I.V., Aliper, A., Korzinkin, M., Zhavoronkov, A., 2023. Identification of dual-purpose therapeutic targets implicated in aging and glioblastoma multiforme using PandaOmics - an AI-enabled biological target discovery platform. Aging 15 (8), 2863–2876.
O'Sullivan, S., Nevejans, N., Allen, C., Blyth, A., Leonard, S., Pagallo, U., Holzinger, K., Holzinger, A., Sajid, M.I., Ashrafian, H., 2019. Legal, regulatory, and ethical frameworks for development of standards in artificial intelligence (AI) and autonomous robotic surgery. Int J. Med. Robot 15 (1), e1968.
Ottom, M.A., Abdul Rahman, H., Alazzam, I.M., Dinov, I.D., 2023. Multimodal stereotactic brain tumor segmentation using 3D-Znet. Bioengineering 10 (5).
Ottom, M.A., Rahman, H.A., Dinov, I.D., 2022. Znet: deep learning approach for 2D MRI brain tumor segmentation. IEEE J. Transl. Eng. Health Med. 10, 1800508.
Papi, Z., Fathi, S., Dalvand, F., Vali, M., Yousefi, A., Tabatabaei, M.H., Amouheidari, A., Abedi, I., 2023. Auto-segmentation and classification of glioma tumors with the goals of treatment response assessment using deep learning based on magnetic resonance imaging. Neuroinformatics 21 (4), 641–650.
Pei, L., Bakas, S., Vossough, A., Reza, S.M.S., Davatzikos, C., Iftekharuddin, K.M., 2020. Longitudinal brain tumor segmentation prediction in MRI using feature and label fusion. Biomed. Signal Process Control 55.
Pereira, S., Meier, R., McKinley, R., Wiest, R., Alves, V., Silva, C.A., Reyes, M., 2018. Enhancing interpretability of automatically extracted machine learning features: application to a RBM-Random Forest system on brain lesion segmentation. Med. Image Anal. 44, 228–244.
Pereira, S., Pinto, A., Alves, V., Silva, C.A., 2016. Brain tumor segmentation using convolutional neural networks in MRI images. IEEE Trans. Med. Imaging 35 (5), 1240–1251.
Podnar, S., Kukar, M., Gunčar, G., Notar, M., Gošnjak, N., Notar, M., 2019. Diagnosing brain tumours by routine blood tests using machine learning. Sci. Rep. 9 (1), 14481.
Prasanna, P., Patel, J., Partovi, S., Madabhushi, A., Tiwari, P., 2017. Radiomic features from the peritumoral brain parenchyma on treatment-naïve multi-parametric MR imaging predict long versus short-term survival in glioblastoma multiforme: preliminary findings. Eur. Radio. 27 (10), 4188–4197.
Preethi, S., Aishwarya, P., 2021. An efficient wavelet-based image fusion for brain tumor detection and segmentation over PET and MRI image. Multimed. Tools Appl. 80 (10), 14789–14806.
Prentice, R.L., Zhao, S., 2021. Regression models and multivariate life tables. J. Am. Stat. Assoc. 116 (535), 1330–1345.
Prezelski, K., Hsu, D.G., Del Balzo, L., Heller, E., Ma, J., Pike, L.R.G., Ballangrud, Å., Aristophanous, M., 2024. Artificial-intelligence-driven measurements of brain metastases' response to SRS compare favorably with current manual standards of assessment. Neurooncol Adv. 6 (1), vdae015.
Qian, J., Herman, M.G., Brinkmann, D.H., Laack, N.N., Kemp, B.J., Hunt, C.H., Lowe, V., Pafundi, D.H., 2020. Prediction of MGMT status for glioblastoma patients using radiomics feature extraction from 18F-DOPA-PET imaging. Int. J. Radiat. Oncol. Biol. Phys. 108 (5), 1339–1346.
Rai, A., Shah, K., Dewangan, H.K., 2023. Review on the artificial intelligence-based nanorobotics targeted drug delivery system for brain-specific targeting. Curr. Pharm. Des. 29 (44), 3519–3531.
Rajan, P.G., Sundar, C., 2019. Brain tumor detection and segmentation by intensity adjustment. J. Med. Syst. 43 (8), 282.
Rasouli, J.J., Shao, J., Neifert, S., Gibbs, W.N., Habboub, G., Steinmetz, M.P., Benzel, E., Mroz, T.E., 2021. Artificial intelligence and robotics in spine surgery. Glob. Spine J. 11 (4), 556–564.
Ravi, V.M., Neidert, N., Will, P., Joseph, K., Maier, J.P., Kückelhaus, J., Vollmer, L., Goeldner, J.M., Behringer, S.P., Scherer, F., Boerries, M., Follo, M., Weiss, T., Delev, D., Kernbach, J., Franco, P., Schallner, N., Dierks, C., Carro, M.S., Hofmann, U.G., Fung, C., Sankowski, R., Prinz, M., Beck, J., Salié, H., Bengsch, B., Schnell, O., Heiland, D.H., 2022. T-cell dysfunction in the glioblastoma microenvironment is mediated by myeloid cells releasing interleukin-10. Nat. Commun. 13 (1), 925.
Reddy, S., Allan, S., Coghlan, S., Cooper, P., 2020. A governance model for the application of AI in health care. J. Am. Med. Inf. Assoc. 27 (3), 491–497.
Ren, Y., Zhang, X., Rui, W., Pang, H., Qiu, T., Wang, J., Xie, Q., Jin, T., Zhang, H., Chen, H., Zhang, Y., Lu, H., Yao, Z., Zhang, J., Feng, X., 2019. Noninvasive prediction of IDH1 mutation and ATRX expression loss in low-grade gliomas using multiparametric MR radiomic features. J. Magn. Reson Imaging 49 (3), 808–817.
Resmini, R., Silva, L., Araujo, A.S., Medeiros, P., Muchaluat-Saade, D., Conci, A., 2021. Combining genetic algorithms and svm for breast cancer diagnosis using infrared thermography. Sensors 21 (14).
Salle, H., Deluche, E., Couvé-Deacon, E., Beaujeux, A.-C., Pallud, J., Roux, A., Dagain, A., de Barros, A., Voirin, J., Seizeur, R., Belmabrouk, H., Lemnos, L., Emery, E., Fotso, M.-J., Engelhardt, J., Jecko, V., Zemmoura, I., Le Van, T., Berhouma, M., Cebula, H., Peyre, M., Preux, P.-M., Caire, F., 2021. Surgical Site Infections after glioblastoma surgery: results of a multicentric retrospective study. Infection 49 (2), 267–275.
Salvi, M., Acharya, U.R., Molinari, F., Meiburger, K.M., 2021. The impact of pre- and post-image processing techniques on deep learning frameworks: a comprehensive review for digital pathology image analysis. Comput. Biol. Med. 128, 104129.
Schaff, L.R., Mellinghoff, I.K., 2023. Glioblastoma and other primary brain malignancies in adults: a review. JAMA 329 (7), 574–587.
Sekhar, A., Biswas, S., Hazra, R., Sunaniya, A.K., Mukherjee, A., Yang, L., 2022. Brain tumor classification using fine-tuned GoogLeNet features and machine learning algorithms: IoMT Enabled CAD System. IEEE J. Biomed. Health Inf. 26 (3), 983–991.
Shah, A.A., Malik, H.A.M., Muhammad, A., Alourani, A., Butt, Z.A., 2023. Deep learning ensemble 2D CNN approach towards the detection of lung cancer. Sci. Rep. 13 (1), 2987.
Sharma, A.M., Willcock, M., Bucher, O., Amaratunga, T., Khan, M.N., Loewen, S.K., Quon, H., Essig, M., Pitz, M., 2019. Institutional review of glial tumors treated with chemotherapy: the first description of PCV-related pseudoprogression. Neurooncol Pr. 6 (1), 22–29.
Siegel, R.L., Miller, K.D., Fuchs, H.E., Jemal, A., 2022. Cancer statistics, 2022. CA Cancer J. Clin. 72 (1), 7–33.
Sivakumar, V., Janakiraman, N., 2020. A novel method for segmenting brain tumor using modified watershed algorithm in MRI image with FPGA. Biosystems 198, 104226.
Smith, H.L., Wadhwani, N., Horbinski, C., 2022. Major Features of the 2021 WHO classification of CNS tumors. Neurotherapeutics 19 (6), 1691–1704.
Song, H.-S., Yoon, H.-S., Lee, S., Hong, C.-K., Yi, B.-J., 2019. Surgical navigation system for transsphenoidal pituitary surgery applying U-net-based automatic segmentation and bendable devices. Appl. Sci.
Soomro, T.A., Zheng, L., Afifi, A.J., Ali, A., Soomro, S., Yin, M., Gao, J., 2023. Image segmentation for MR brain tumor detection using machine learning: a review. IEEE Rev. Biomed. Eng. 16, 70–90.
Stember, J.N., Young, R.J., Shalu, H., 2023. Direct evaluation of treatment response in brain metastatic disease with deep neuroevolution. J. Digit Imaging 36 (2), 536–546.
Su, X., Chen, N., Sun, H., Liu, Y., Yang, X., Wang, W., Zhang, S., Tan, Q., Su, J., Gong, Q., Yue, Q., 2020. Automated machine learning based on radiomics features predicts H3 K27M mutation in midline gliomas of the brain. Neuro-Oncol. 22 (3), 393–401.
Subrahmanya, S.V.G., Shetty, D.K., Patil, V., Hameed, B.M.Z., Paul, R., Smriti, K., Naik, N., Somani, B.K., 2022. The role of data science in healthcare advancements: applications, benefits, and future prospects. Ir. J. Med. Sci. 191 (4), 1473–1483.
Suchorska, B., Jansen, N.L., Linn, J., Kretzschmar, H., Janssen, H., Eigenbrod, S., Simon, M., Pöpperl, G., Kreth, F.W., la Fougere, C., Weller, M., Tonn, J.C., 2015. Biological tumor volume in 18FET-PET before radiochemotherapy correlates with survival in GBM. Neurology 84 (7), 710–719.
Sung, H., Ferlay, J., Siegel, R.L., Laversanne, M., Soerjomataram, I., Jemal, A., Bray, F., 2021. Global Cancer Statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA Cancer J. Clin. 71 (3), 209–249.
Tak, D., Ye, Z., Zapaischykova, A., Zha, Y., Boyd, A., Vajapeyam, S., Chopra, R., Hayat, H., Prabhu, S.P., Liu, K.X., Elhalawani, H., Nabavizadeh, A., Familiar, A., Resnick, A.C., Mueller, S., Aerts, H.J.W.L., Bandopadhayay, P., Ligon, K.L., Haas-Kogan, D.A., Poussaint, T.Y., Kann, B.H., 2024. Noninvasive molecular subtyping of pediatric low-grade glioma with self-supervised transfer learning. Radio. Artif. Intell. 6 (3), e230333.
Tan, A.C., Ashley, D.M., Lopez, G.Y., Malinzak, M., Friedman, H.S., Khasraw, M., 2020. Management of glioblastoma: state of the art and future directions. CA Cancer J. Clin. 70 (4), 299–312.
Tariciotti, L., Caccavella, V.M., Fiore, G., Schisano, L., Carrabba, G., Borsa, S., Giordano, M., Palmisciano, P., Remoli, G., Remore, L.G., Pluderi, M., Caroli, M., Conte, G., Triulzi, F., Locatelli, M., Bertani, G., 2022. A deep learning model for preoperative differentiation of glioblastoma, brain metastasis and primary central nervous system lymphoma: a pilot study. Front. Oncol. 12, 816638.
Teplyuk, N.M., Mollenhauer, B., Gabriely, G., Giese, A., Kim, E., Smolsky, M., Kim, R.Y., Saria, M.G., Pastorino, S., Kesari, S., Krichevsky, A.M., 2012. MicroRNAs in

cerebrospinal fluid identify glioblastoma and metastatic brain cancers and reflect disease activity. Neuro-Oncol. 14 (6), 689–700.
Thust, S.C., van den Bent, M.J., Smits, M., 2018. Pseudoprogression of brain tumors. J. Magn. Reson Imaging 48 (3), 571–589.
Tsao, M.N., Xu, W., Wong, R.K., Lloyd, N., Laperriere, N., Sahgal, A., Rakovitch, E., Chow, E., 2018. Whole brain radiotherapy for the treatment of newly diagnosed multiple brain metastases. Cochrane Database Syst. Rev. 1 (1), CD003869.
Tsvetkov, P.O., Eyraud, R., Ayache, S., Bougaev, A.A., Malesinski, S., Benazha, H., Gorokhova, S., Buffat, C., Dehais, C., Sanson, M., Bielle, F., Figarella Branger, D., Chinot, O., Tabouret, E., Devred, F., 2021. An AI-powered blood test to detect cancer using NanoDSF. Cancers 13 (6).
Varuna Shree, N., Kumar, T.N.R., 2018. Identification and classification of brain tumor MRI images with feature extraction using DWT and probabilistic neural network. Brain Inf. 5 (1), 23–30.
de Visser, K.E., Joyce, J.A., 2023. The evolving tumor microenvironment: from cancer initiation to metastatic outgrowth. Cancer Cell 41 (3), 374–403.
Vollmuth, P., Foltyn, M., Huang, R.Y., Galldiks, N., Petersen, J., Isensee, F., van den Bent, M.J., Barkhof, F., Park, J.E., Park, Y.W., Ahn, S.S., Brugnara, G., Meredig, H., Jain, R., Smits, M., Pope, W.B., Maier-Hein, K., Weller, M., Wen, P.Y., Wick, W., Bendszus, M., 2023. Artificial intelligence (AI)-based decision support improves reproducibility of tumor response assessment in neuro-oncology: An international multi-reader study. Neuro-Oncol. 25 (3), 533–543.
Walker, A.J., Ruzevick, J., Malayeri, A.A., Rigamonti, D., Lim, M., Redmond, K.J., Kleinberg, L., 2014. Postradiation imaging changes in the CNS: how can we differentiate between treatment effect and disease progression? Future Oncol. 10 (7), 1277–1297.
Wang, H., Fu, T., Du, Y., Gao, W., Huang, K., Liu, Z., Chandak, P., Liu, S., Van Katwyk, P., Deac, A., Anandkumar, A., Bergen, K., Gomes, C.P., Ho, S., Kohli, P., Lasenby, J., Leskovec, J., Liu, T.-Y., Manrai, A., Marks, D., Ramsundar, B., Song, L., Sun, J., Tang, J., Veličković, P., Welling, M., Zhang, L., Coley, C.W., Bengio, Y., Zitnik, M., 2023. Scientific discovery in the age of artificial intelligence. Nature 620 (7972), 47–60.
Wang, F., He, Y., Li, C., Wang, Y., Zhong, L., 2020. Malignant craniopharyngioma: a report of seven cases and review of the literature. World Neurosurg. 135, e194–e201.
Wang, G., Qiu, M., Xing, X., Zhou, J., Yao, H., Li, M., Yin, R., Hou, Y., Li, Y., Pan, S., Huang, Y., Yang, F., Bai, F., Nie, H., Di, S., Guo, L., Meng, Z., Wang, J., Yin, Y., 2022. Lung cancer scRNA-seq and lipidomics reveal aberrant lipid metabolism for early-stage diagnosis. Sci. Transl. Med. 14 (630), eabk2756.
Wang, Y., Wang, Z., Guo, X., Cao, Y., Xing, H., Wang, Y., Xing, B., Wang, Y., Yao, Y., Ma, W., 2024. Artificial neural network identified a 20-gene panel in predicting immunotherapy response and survival benefits after anti-PD1/PD-L1 treatment in glioblastoma patients. Cancer Med. 13 (9), e7218.
Wang, Y.-R.J., Wang, P., Yan, Z., Zhou, Q., Gunturkun, F., Li, P., Hu, Y., Wu, W.E., Zhao, K., Zhang, M., Lv, H., Fu, L., Jin, J., Du, Q., Wang, H., Chen, K., Qu, L., Lin, K., Iv, M., Wang, H., Sun, X., Vogel, H., Han, S., Tian, L., Wu, F., Gong, J., 2024. Advancing presurgical non-invasive molecular subgroup prediction in medulloblastoma using artificial intelligence and MRI signatures. Cancer Cell 42 (7).
Weller, M., Wick, W., Aldape, K., Brada, M., Berger, M., Pfister, S.M., Nishikawa, R., Rosenthal, M., Wen, P.Y., Stupp, R., Reifenberger, G., 2015. Glioma. Nat. Rev. Dis. Prim. 1, 15017.
Wen, D., Soltan, A., Trucco, E., Matin, R.N., 2024. From data to diagnosis: skin cancer image datasets for artificial intelligence. Clin. Exp. Dermatol. 49 (7), 675–685.
Wu, M., Jiang, T., Guo, M., Duan, Y., Zhuo, Z., Weng, J., Xie, C., Sun, J., Li, J., Cheng, D., Liu, X., Du, J., Zhang, X., Zhang, Y., Liu, Y., 2024. Amide proton transfer-weighted imaging and derived radiomics in the classification of adult-type diffuse gliomas. Eur. Radio. 34 (5), 2986–2996.
Wu, X., Tao, R., Sun, Z., Zhang, T., Li, X., Yuan, Y., Zheng, S., Cao, C., Zhang, Z., Zhao, X., Yang, P., 2024. Ensemble learning prediction framework for EGFR amplification status of glioma based on terahertz spectral features. Spectrochim. Acta A Mol. Biomol. Spectrosc. 316, 124351.
Xiao, G., Wang, K., Wang, Z., Dai, Z., Liang, X., Ye, W., Luo, P., Zhang, J., Liu, Z., Cheng, Q., Peng, R., 2022. Machine learning-based identification of SOX10 as an immune regulator of macrophage in gliomas. Front. Immunol. 13, 1007461.
Xie, X., Shen, C., Zhang, X., Wu, G., Yang, B., Qi, Z., Tang, Q., Wang, Y., Ding, H., Shi, Z., Yu, J., 2023. Rapid intraoperative multi-molecular diagnosis of glioma with ultrasound radio frequency signals and deep learning. EBioMedicine 98, 104899.
Xu, Q., Xu, H., Liu, J., Zhou, M., Li, M., Xu, J., Zhu, H., 2022. MR image classification for brain tumor texture based on pseudo-label learning and optimized feature extraction. Comput. Math. Methods Med. 2022, 7746991.
Yamashita, K., Hatae, R., Hiwatashi, A., Togao, O., Kikuchi, K., Momosaka, D., Yamashita, Y., Kuga, D., Hata, N., Yoshimoto, K., Suzuki, S.O., Iwaki, T., Iihara, K., Honda, H., 2019. Predicting TERT promoter mutation using MR images in patients with wild-type IDH1 glioblastoma. Diagn. Inter. Imaging 100 (7-8), 411–419.
Yang, G., Lee, W., Seo, Y., Lee, C., Seok, W., Park, J., Sim, D., Park, C., 2023. Unsupervised Spiking neural network with dynamic learning of inhibitory neurons. Sensors 23 (16).
Yang, M., Simm, J., Lam, C.C., Zakeri, P., van Westen, G.J.P., Moreau, Y., Saez-Rodriguez, J., 2018. Linking drug target and pathway activation for effective therapy using multi-task learning. Sci. Rep. 8 (1), 8322.
Yogananda, C.G.B., Shah, B.R., Nalawade, S.S., Murugesan, G.K., Yu, F.F., Pinho, M.C., Wagner, B.C., Mickey, B., Patel, T.R., Fei, B., Madhuranthakam, A.J., Maldjian, J.A., 2021. MRI-based deep-learning method for determining glioma MGMT promoter methylation status. AJNR Am. J. Neuroradiol. 42 (5), 845–852.
Yu, K., Tian, Q., Feng, S., Zhang, Y., Cheng, Z., Li, M., Zhu, H., He, J., Li, M., Xiong, X., 2024. Integration analysis of cell division cycle-associated family genes revealed potential mechanisms of gliomagenesis and constructed an artificial intelligence-driven prognostic signature. Cell Signal 119, 111168.
Yurt, M., Dalmaz, O., Dar, S., Ozbey, M., Tinaz, B., Oguz, K., Cukur, T., 2022. Semi-supervised learning of MRI synthesis without fully-sampled ground truths. IEEE Trans. Med. Imaging 41 (12), 3895–3906.
Zacharaki, E.I., Wang, S., Chawla, S., Soo Yoo, D., Wolf, R., Melhem, E.R., Davatzikos, C., 2009. Classification of brain tumor type and grade using MRI texture and shape in a machine learning scheme. Magn. Reson Med. 62 (6), 1609–1618.
Zahoor, M.M., Qureshi, S.A., Bibi, S., Khan, S.H., Khan, A., Ghafoor, U., Bhutta, M.R., 2022. A New deep hybrid boosted and ensemble learning-based brain tumor analysis using MRI. Sensors 22 (7).
Zhang, W., Dang, R., Liu, H., Dai, L., Liu, H., Adegboro, A.A., Zhang, Y., Li, W., Peng, K., Hong, J., Li, X., 2024. Machine learning-based investigation of regulated cell death for predicting prognosis and immunotherapy response in glioma patients. Sci. Rep. 14 (1), 4173.
Zhang, H., Li, Z., Gao, C., Fan, X., Pang, Y., Li, T., Wu, Z., Xie, H., He, Q., 2021. Dual-responsive biohybrid neutrobots for active target delivery. Sci. Robot 6 (52).
Zhang, H., Liu, J., Zhu, Z., Li, H., 2011. An automated and simple method for brain MR image extraction. Biomed. Eng. Online 10, 81.
Zhang, L., Wang, R., Gao, J., Tang, Y., Xu, X., Kan, Y., Cao, X., Wen, Z., Liu, Z., Cui, S., Li, Y., 2024. A novel MRI-based deep learning networks combined with attention mechanism for predicting CDKN2A/B homozygous deletion status in IDH-mutant astrocytoma. Eur. Radio. 34 (1), 391–399.
Zhang, W., Wu, Y., Yang, B., Hu, S., Wu, L., Dhelimd, S., 2021. Overview of multi-modal brain tumor MR image segmentation. Healthcare 9 (8).
Zhang, H., Zhang, H., Zhang, Y., Zhou, B., Wu, L., Lei, Y., Huang, B., 2023. Deep learning radiomics for the assessment of telomerase reverse transcriptase promoter mutation status in patients with glioblastoma using multiparametric MRI. J. Magn. Reson Imaging 58 (5), 1441–1451.
Zhou, J., Chan, K.L., Chong, V.F., Krishnan, S.M., 2005. Extraction of brain tumor from MR images using one-class support vector machine. Conf. Proc. IEEE Eng. Med. Biol. Soc. 2005, 6411–6414.
Zhou, L., Ji, Q., Peng, H., Chen, F., Zheng, Y., Jiao, Z., Gong, J., Li, W., 2024. Automatic image segmentation and online survival prediction model of medulloblastoma based on machine learning. Eur. Radio. 34 (6), 3644–3655.
Zikou, A., Sioka, C., Alexiou, G.A., Fotopoulos, A., Voulgaris, S., Argyropoulou, M.I., 2018. Radiation necrosis, pseudoprogression, pseudoresponse, and tumor recurrence: imaging challenges for the evaluation of treated gliomas. Contrast Media Mol. Imaging 2018, 6828396.
Zwanenburg, A., 2019. Radiomics in nuclear medicine: robustness, reproducibility, standardization, and how to avoid data analysis traps and replication crisis. Eur. J. Nucl. Med. Mol. Imaging 46 (13), 2638–2655.
Zwanenburg, A., Vallières, M., Abdalah, M.A., Aerts, H.J.W.L., Andrearczyk, V., Apte, A., Ashrafinia, S., Bakas, S., Beukinga, R.J., Boellaard, R., Bogowicz, M., Boldrini, L., Buvat, I., Cook, G.J.R., Davatzikos, C., Depeursinge, A., Desseroit, M.-C., Dinapoli, N., Dinh, C.V., Echegaray, S., El Naqa, I., Fedorov, A.Y., Gatta, R., Gillies, R.J., Goh, V., Götz, M., Guckenberger, M., Ha, S.M., Hatt, M., Isensee, F., Lambin, P., Leger, S., Leijenaar, R.T.H., Lenkowicz, J., Lippert, F., Losnegård, A., Maier-Hein, K.H., Morin, O., Müller, H., Napel, S., Nioche, C., Orlhac, F., Pati, S., Pfaehler, E.A.G., Rahmim, A., Rao, A.U.K., Scherer, J., Siddique, M.M., Sijtsema, N. M., Socarras Fernandez, J., Spezi, E., Steenbakkers, R.J.H.M., Tanadini-Lang, S., Thorwarth, D., Troost, E.G.C., Upadhaya, T., Valentini, V., van Dijk, L.V., van Griethuysen, J., van Velden, F.H.P., Whybra, P., Richter, C., Löck, S., 2020. The image biomarker standardization initiative: standardized quantitative radiomics for high-throughput image-based phenotyping. Radiology 295 (2), 328–338.

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