



A Review of Computational Intelligence Models for Brain Tumour Classification and Prediction

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ABSTRACT

This review aims to systematically analyze ML models from four aspects: type of ML technique, estimation accuracy, model comparison, and estimation context. A systematic literature review of empirical studies was conducted on the ML models published in the last decades. Fifty-one primary studies relevant to the objective of this research were revealed. After investigating these studies, five ML techniques have been employed in brain tumor classification and prediction. Ultimately, the estimation accuracy of these ML models could be regarded and accepted and outperformed non-ML models. ML models have been revealed to be useful in brain tumor classification and prediction. Genetic algorithm among the ML models achieved an accuracy of 100%. Nevertheless, ML models are still restricted in the industry, so initiative and encouragement are needed to make ML models easier. Further work is required on these ML models to verify the accuracy and consider other performance metrics other than the accuracy.

KEYWORDS

Brain Tumour, Classification, Genetic Algorithm, Prediction, Segmentation

INTRODUCTION

Machine learning (ML) as a field in computer science gives computers the ability to learn without being explicitly programmed. Algorithms that can learn from a large body of data and make predictions on the data result from machine learning, which evolved from pattern recognition and computational learning theory in artificial intelligence (Copeland, 2016). Machine learning is applied to a wide range of computing tasks, such as email filtering, detection of network intruders or malicious insiders working towards a data breach, optical character recognition, learning to rank, and computer vision.

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Researchers are discovering innovative ways to apply machine learning to improve healthcare systems (Liu et al., 2017). In these systems, biomedical engineering as a discipline which advances knowledge in engineering, biology, and medicine to improve human health through cross-disciplinary activities becomes useful (Frosini et al., 2015). This includes applying traditional engineering expertise to analyze and solve biology and medicine problems, providing an overall enhancement of health care. Recently, there have been rapid developments in advanced computing and imaging systems in biomedical engineering, giving rise to a new research dimension. Iqbal, Khan, Saba, & Rehman (2018) highlights a few of the practical applications of medical image analysis. Among which we have: locating abnormal region and other pathologies, measuring tissue sizes, computer-guided surgery, computer-aided diagnosis, radiotherapy, treatment planning, the study of anatomical structure and identification of malignant parts within tumor area in order to minimize the risk of sampling errors in the biopsy. Recently, the number of deaths caused by brain tumors have significantly increased by over 300%. Therefore, researchers have focused on computerized brain tumor diagnosis to obtain important clinical information regarding tumor presence, location, and type.

The human body is made up of different types of cells with each playing a peculiar function. Hence, the human body has to be kept in good condition. To achieve that, the cells in the body multiply and differentiate in a structured way. Although only a few cells fail to regulate their growth, they grow improperly and shape a mass of the tissue known as a tumor that results in extra cells' formation. Brain tumors are a solid neoplasm within the skull that typically occurs in the brain or elsewhere, like in lymphatic tissue, in blood vessels, in cranial nerves, and in brain envelopes. Brain tumors can be categorized by tumor location, tissue type, malignant or benign. The tumors may be either malignant or benign. Malignant tumors lead to cancer, while benign tumors are not cancerous, as shown in Figure 1. In most cases, tumors in the kidney, luminous tissue, breast, or skin melanoma spread to the brain to cause secondary brain damage.

One of the most common medical problems in this field of study is tumor detection as illustrated in Figure 2. One approach to its detection is segmentation.

Segmentation is the process of dividing an image into regions of interest (ROIs) to facilitate the characterization, delineation, and visualization of the data. The goal of this process is to increase the significance and accessibility of the interpretation of CT or MRI images in terms of the tumour's

Figure 1. An Image Describing Benign and Malignant Tumour (Doru & Fayed, 2019)

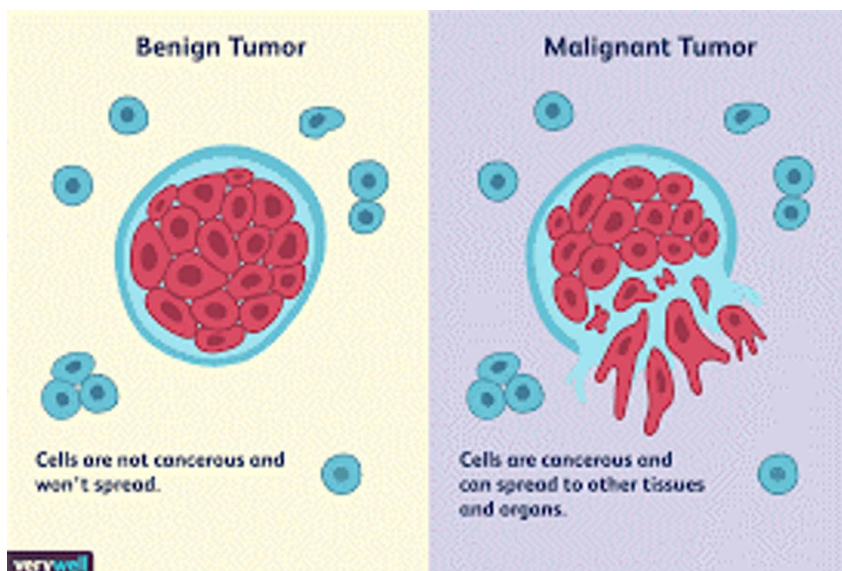
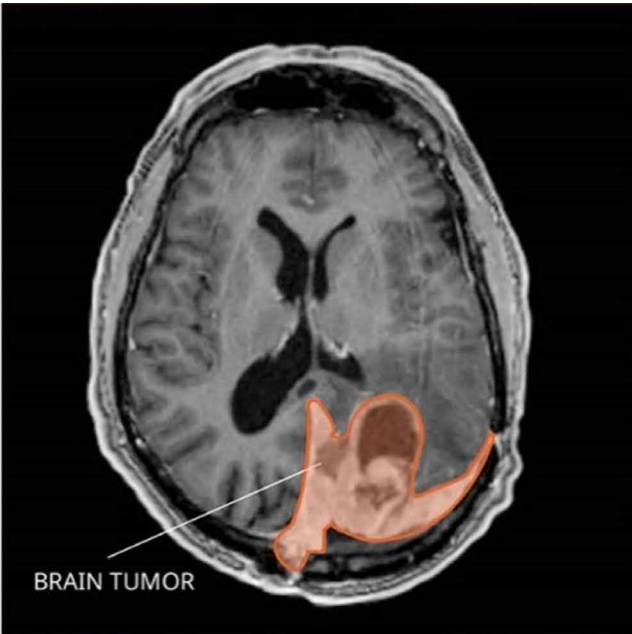


Figure 2. An MRI Image of the Brain with a Tumour (National Cancer Institute, 2018)



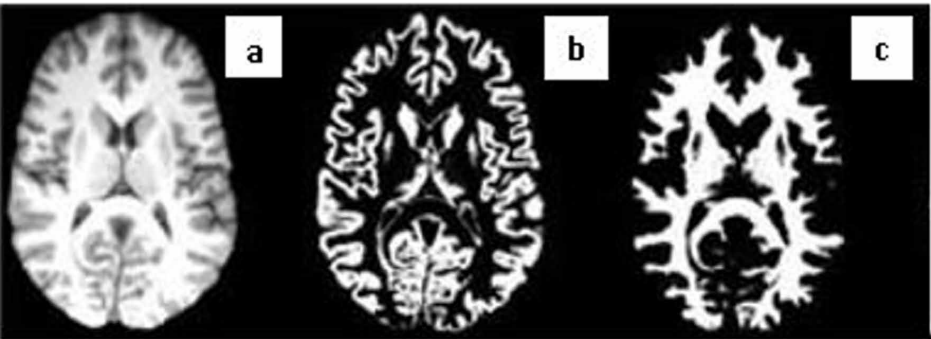
location and constraints. Segmentation separates the tumor tissues, such as necrotic and edema, from normal tissues, such as white matter (WM) and gray matter (GM), as seen in Figure 3. Once segmentation is achieved, classification can be carried out.

Classification involves assigning the input features to various classes or divisions. Feature extraction and selection are vital for classification, particularly brain tumor classification, requiring many CT or MRI scans from different training cases. The brain tumor classification’s primary goal is to classify tumors as benign or malignant or classify the tumor grade using CT or MRI images.

RESEARCH NEEDS ASSESSMENT

Brain tumor segmentation has remain a challenging task due to its varying structural and functional behavior (Z. Li, Wang, Yu, Guo, & Cao, 2017). Beside, one person’s tumor severity differs significantly

Figure 3. (a) General brain MR image, (b) Gray Matter, (c) White Matter (Tiwari, Srivastava, & Pant, 2019)



from another. Presently, the most preferred image modalities for diagnostics are Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) due to their non-invasive nature and superior image contrast in soft tissues. In their operations, they create various types of tissue contrast images, allowing useful structural information to be collected so that tumors can be diagnosed and treated along with their sub-regions. These concepts only facilitates the annotation of different regions of the brain tumor by the radiologist. However, the annotation process is laborious and time-consuming as they work on the various slice of brain tumors from MRI scans. Due to this, accurate segmentation and characterization of these abnormalities may not be genuine though this radiologist are specialized in detecting the occurrence of abnormal tissues.. Resolving this intermittent challenge, requires the adoption of automatic segmentation with computer vision algorithms. This creates the need to develop suitable machine learning algorithms that will improve segmentation accuracy and detect abnormalities in brain tumors.

Studies has shown that the area of computer vision has the ultimate goal to mimic perception and human vision through machines. It also can form inferences based on visual inputs and taking the appropriate action. For standard computerized process, these actions may be low, medium or high level in the interpretation of images in computer vision. Low-level procedures include basic operations such as noise reduction by preprocessing images, sharpening images, and enhancing contrast (Mohan & Subashini, 2018; Alweshah et al., 2020). Mid-level processing includes segmentation and classification while High-level treatment involves performing vision-associated cognitive functions. In the area of medical image analysis we have the following categories, thus enhancement, registration, segmentation, visualization, quantization, and modelling (Mohan & Subashini, 2018). Among these the key and most demanding are registration, segmentation, and modeling. The manual qualitative analysis is still bounded by the human vision system, despite the expert's experience and expertise. The explanation is that the human eye is not able to distinguish between tens of gray levels. There is much more to a human vision than the amount of information found in an image of CT or MR because the present CT or MRI devices will create pictures equivalent to 65.535 gray levels (Mohan & Subashini, 2018). Consequently, it leads to the machine being used as the second eye to recognize CT or MRI images with high bit depth and high-resolution.

LITERATURE REVIEW

Researchers in a few decades have focused on the application of digital image processing techniques to extract, analyze, and categorize data from minimally invasive imaging procedures such as: computed tomography, ultrasonography, endoscopy, confocal microscopy, computed radiography, or magnetic resonance imaging (Iqbal et al., 2018). Park et al. (2018) in their study concluded that computer-based medical image interpretation systems comprise a significant application area providing significant medical diagnosis assistance. The design of these systems is regarded in most cases to emulate the doctor's knowledge in identifying malignant areas. The aim is to improve the expert's capacity to recognize malignant areas while reducing the need for intervention and retaining a precise diagnosis capability. Furthermore, it may be possible to examine a larger area, studying living tissue in vivo, possibly at a distance and, thus, minimize the shortcomings of biopsies such as discomfort for the patient, delay in diagnosis, and a limited number of tissue samples. There is, therefore, the need for more effective methods of early detection, such as those that computer-assisted medical diagnosis systems aim to provide (Park et al., 2018). Iqbal et al. (2018) in their recent report on brain tumor multiclass classification using MRI identified a set of standard parameters. These parameters were compared to other related studies. The article emphasized that brain tumor classification schemes published by World Health Organization are considered comprehensive and standard amidst different brain tumor classification schemes that have been presented by the research community. However, few works reported on the multiclass classification of brain images where each part of the image containing the tumor is tagged with major and minor categories. The precise classification is difficult

to achieve due to ambiguities in images and overlapping characteristics of different tumors. It was revealed that, although advanced MRI sequences and techniques may produce better results to some extent, however, they are time-consuming and costly. Therefore, there is a requirement to find better computational models to be used with anatomical MRI scans for efficient and cost-effective solutions.

Lina & Latifi (2017) proposed a method to automatically predict patients' survival rate with a glioma brain tumor by classifying the patient's MRI image using machine learning (ML) methods. In improving the prediction results, various types of features of the dataset were extracted and trained by various ML methods. Features considered included volumetric, statistical and intensity texture, histograms, and deep features while ML techniques employed included support vector machine (SVM), k-nearest neighbors (KNN), linear discriminant, tree, ensemble, and logistic regression. The first step of the implementation is the extraction of meaningful features to describe each specific class from the labeled MRI-image modalities. The second step involved the development of the prediction model given the extracted features. The dataset used in the study is BraTS 2017, which has 163 samples; each sample having four sequences of MRI brain images, the overall survival time in days, and the patient's age. The dataset is labeled into three classes of survivors: short-term, mid-term, and long-term. Finally, each classifier's performance was evaluated by calculating each class's accuracy separately and the overall model. The best prediction accuracy based on classification was achieved using deep learning features extracted from a pre-trained convolutional neural network (CNN) and trained by a linear discriminant. According to Hebli & Gupta (2017), accurate segmentation and characterization of abnormalities can be achieved if morphological operators are leveraged on for the segmentation stage while the discrete wavelet transform (DWT) are used for tumor feature extraction. In the classification stage, the Support Vector Machine (SVM) was used. The total tumor features extracted were fourteen including structural, statistical, and textural features. In the study, three datasets were used. The first was a clinical database containing 24 images, 16 for training, and 8 for testing. The second dataset was developed from the Whole Brain Atlas and some from Google images. In all, a total of 40 images were curated, 30 for training, and 10 for testing. The last dataset was the combination of the above two: Internet images and images collected from the radiologist totaling 70 images, where 50 were used for training, and 20 for testing. Three SVM kernels thus: Linear, Polynomial, and RBF were used on the datasets, and accuracies were compared. The study demonstrated that RBF and polynomial kernels give 100% accuracy for training and testing on the combined database, and in clinical and non-clinical databases, RBF gives 100% results for training and testing. Hence it is clear from the study that RBF provides better results for all the three databases adopted.

Ge, Qu, Gu, & Jakola (2018) addresses some limitations of grading brain tumor and glioma in Magnetic Resonance Images (MRIs) using deep learning methods. The existing deep learning methods often use convolutional neural networks (CNNs) to extract single-scale features without considering that the scales of brain tumor features vary depending on structure/shape, size, tissue smoothness, and locations. The method consisted of three modules: Block-1 is designed for extracting features by using multiscale convolutional layers, whose input is 3D brain MR images. Block-2 is designed for fusing and refining multiscale features by using multiscale fusion layers. Block-3 is designed for glioma grading/classification by using fully connected (FC) layers, whose output is the predicted class labels. Experiments were conducted on an open dataset containing 3D brain volume images, including low-grade glioma (LGG) and high-grade glioma (HGG), downloaded from the MICCAI BraTS 2017 competition. The dataset consists of 3D brain volume images from 4 different sensors, where only enhanced-T1-MRIs were used in our experiments. The main contributions of the paper are: (a) propose a novel 3D multiscale convolutional network architecture for the dedicated task of glioma grading; (b) propose a novel feature fusion scheme that further refines multiscale features generated from multiscale convolutional layers; (c) propose a saliency-aware strategy to enhance tumor regions of MRIs. According to Pashaei, Sajedi, & Jazayeri (2018), the classification of different types of brain tumors is not a trivial task, and the accuracy depends on the experience of radiologists only. Human identification has two main errors; first, they cannot be used in situations where the number

of data is high. Second, the reproduction of information is not possible in this method. In order to the classification of brain tumors, two methods are presented in this work. In the first method, a CNN model is used for this classification, and in the second method, we use features extracted by CNN as the input of the KELM method. The brain T1-weighted CE-MRI dataset was acquired from Nanfang Hospital, Guangzhou, China, General Hospital, Tianjing Medical University, China, from 2005 to 2010. The dataset contained 3064 slices from 233 patients, containing 708 meningiomas, 1426 gliomas, and 930 pituitary tumors. The proposed method was compared with other classifiers such as SVM, stacking, XGBoost, RBF, and MLP in terms of accuracy. The proposed method (KELM) with 93.68% accuracy in the classification of features extracted by CNN is the best classification algorithm among other algorithms.

Yang, Tang, Tjio, Yeo, & Su (2019) also proposed multi-task learning architecture that solves point and angle detection tasks simultaneously by exploiting the commonalities and differences across these tasks. This results improved learning efficiency and prediction accuracy for the task-specific models compared to training individual models separately. After deriving the AC-PC line and symmetry line on the sagittal image and axial image, respectively, the corresponding scan coverage is then determined by using an image processing approach. In the study, an online database of MRI images containing brain tumor is taken while a machine learning model is developed using the Particle Swarm Optimization (PSO) algorithm for feature selection. The Support Vector Machine (SVM) classifier is used to classify the type of tumor present in brain MRI images. In Polly, Shil, Hossain, Ayman, & Jang (2018), a computerized system is proposed to differentiate between a normal brain and an abnormal brain with a tumor in the MRI images and further classify the abnormal brain tumors into HGG or LGG tumors. The proposed computerized system uses k-means as the segmentation technique for clustering. The Discrete Wavelet Transform (DWT) known for feature extraction and Principal Component Analysis (PCA) noted for feature reduction were used in the study. In all the total number of images used was 440, thus 100 normal images and 340 abnormal images. In the initial experiment, 100 normal images and 180 abnormal tumor images are used while in the second stage, 80 HGG and 80 LGG images were used. Computational results suggest that, the system successfully classified HGG and LGG with accuracy, sensitivity, specificity of 99%, 100%, and 98.03%, respectively. Ge, Gu, Store Jakola, & Yang (2019) also tackled two issues that may impact brain tumor characterization performance observed in deep learning: insufficiently large training dataset and incomplete collection of MRIs from different modalities. The proposed method's motivation is thus twofold: one is to generate synthetic brain images where image scans in these modalities are missing; the other is to enlarge the training dataset by generating many synthetic images nearly similar to the real data. A training dataset consisting the originally scanned images and pairwise-GAN generated images was used in the proposed method. A deep learning framework is used to learn the brain tumor characteristics, followed by a classifier to output labels. Experiments were conducted on an open TCGA dataset, containing 167 subjects for classifying IDH genotypes (mutation or wild-type). The dataset used in the experiments contains 3D brain volume images from projects TCGA-GBM and TCGA-LGG. It consists of 3D brain volume images from 4 different modalities (T1-MRI, Enhanced-T1-MRI, T2-MRI, FLAIR) and tumor segmentation results. In this set of experiments, the training dataset is formed by combining two parts of MR images: (a) a complete set of training MR images from all modalities; (b) a set of GAN-generated synthetic images for all modalities, which is equivalent to generating synthetic MRIs for non-existing (or fake) patients, where 198 fake subjects with 792 MRIs were added. Test results from two experimental settings have supported the proposed method, where glioma classification performance has consistently improved by using mixed real and augmented data (test accuracy 81.03%, with 2.57% improvement).

According to Mittal, Mohan, Kaur, Kaur, & Verma (2019), several methodologies have been developed to enhance the automated system's segmentation efficiency. However, there is always scope for improvement in the segmentation process of medical image analysis. In this work, a deep learning-based approach is proposed for brain tumor image segmentation. The proposed method includes the

concept of Stationary Wavelet Transform (SWT) and the new Growing Convolution Neural Network (GCNN). 11% for FLAIR-weighted MRI dataset were obtained. A multiclass neoplasm classification segmentation has an extraction performed employing a dataset of 428 MRI images. A combination of SWT and GCNN is used in the study to carry out the segmentation process automatically. The proposed combination has proven to be more effective than the individual automation process. An approximately 2% improvement in PSNR and SSIM has been achieved with the proposed method over the conventional CNN approach. The Mean Square Error also reduced significantly in the proposed GCNN approach compared to the conventional CNN approach. Finally, Lahmiri, Dawson, & Shmuel (2018) evaluated the performance of machine learning-based techniques for Parkinson's disease (PD) diagnosis based on dysphonia symptoms. Early appearing symptoms of PD include tremor, rigidity, and vocal impairment (dysphonia). In this regard, computer-aided-diagnosis systems based on machine learning can be useful in assisting clinicians in identifying PD patients. The study evaluated and discussed the performance of machine learning-based techniques for PD diagnosis based on dysphonia symptoms. Furthermore, it compared the performances of linear discriminant analysis (LDA), k nearest-neighbors (k-NN), naïve Bayes (NB), regression trees (RT), radial basis function neural networks (RBFNN), support vector machine (SVM), and Mahalanobis distance classifier (MDC). The support vector machine classifier displayed superior performance compared to the other classifiers. It was concluded that future work could further consider feature selection to improve SVM performance and other machine learning classifiers. This implies the need for advanced computer-aided-diagnosis systems.

In general, it has been identified that the common recommendation of the recent researches discussed is to develop deep learning-based approaches to solve problems precisely and accurately. However, there are several ways in which these changes in datasets will create new problems for modeling. Furthermore, datasets are rapidly growing and becoming complex as they become multimodal and multifaceted. The incorporation of machine learning has profound implications for neuroscience and biomedical science (Khurram Afridi, 2017).

REVIEW PROTOCOL AND IMPLEMENTATION

This section of the study gives a detailed explanation of how the review was carried out. It starts with research questions the study seeks to address, and the protocols in selection appropriate research articles for the review.

Research Questions

The questions this study seeks to address is as listed below:

- *RQ1: Which machine learning techniques have been used for brain tumor classification and prediction?*

RQ1 aims at identifying the ML techniques that have been used to classify and predict brain tumors. Clinicians can use the ML strategies described as part of the approaches. Scientists and researchers should explore the possibility of using ML approaches that have not yet been investigated in brain tumor classification and prediction.

- *RQ2: What is the overall estimation accuracy of the ML models?*

RQ2 addresses concerns with the estimation accuracy of ML models. Accuracy estimation is the key performance metric for ML models. This question focuses on the following four aspects of

determining accuracy: accuracy metric, accuracy value, data set for model construction and model validation method.

- *RQ3: Are there any ML models that distinctly outperform other ML models?*

There could be evidence that comparisons are made between different ML models to determine which ML models consistently outperform other ML models. RQ3 therefore aims to classify relatively consistent and high performing ML models.

- *RQ4: Do ML models perform well compared to standard guidelines (traditional methods) for tumor classification and prediction?*

The proposed ML models are compared to traditional or standard (non ML) models while estimating their accuracies and time efficiencies in most research. Consequently, RQ5 aims to test whether ML patterns have advantages over non-ML patterns.

Search Strategy

To answer these research questions, exiting studies relevant to the field of study are required. In distinguishing what is relevant to this study, a search strategy is needed. The search strategy for the study includes: search terms, literature resources, and search process as detailed below.

Search Terms

The following guidelines were adopted in constructing the appropriate search terms (reference):

1. derive significant terms from the research questions.
2. identify alternative keywords and synonyms for significant terms.
3. check the keywords in relevant papers or books.
4. use the boolean OR to incorporate alternative spellings and synonyms.
5. use the boolean AND to link the significant terms.

Subject to the above guideline, the following string was generated for this study: brain tumors AND (classification OR segmentation OR segregation) AND (determin* OR predict*) AND (machine learning OR “data mining” OR “artificial intelligence” OR “deep learning” OR “nearest neighbor*” OR “decision tree*” OR “regression tree*” OR “classification tree*” OR “neural net*” OR “support vector machine*” OR “support vector regression”).

Literature Sources

The literature resources used to search for primary studies include the following electronic databases: IEEE Xplore, ACM Digital Library, Nature, ScienceDirect, Semantic Scholar, and Google Scholar. Out of this list only three was of primary focus: thus IEEE Xplore, ACM Digital Library and ScienceDirect. The previously designed search terms were used in all this online databases to scan for articles and conference papers. However, the search terms was slightly modified for each databases as they have their own syntax acceptable by their search engines. The search was conducted on all databases covering title, abstract, and keywords. Furthermore, the search was restricted to the period from January 1, 2013 to December 15, 2019, in order to assess the reserch relevance to the scientific community.

Search Process

After the identification and acceptance of the literature sources, the review process requires a comprehensive search of all relevant sources. For this reason, the search process was defined and divided into the following two phases.

- *Search phase 1:* Search the electronic databases separately and gather the returned papers together to form the set of prospective papers.
- *Search phase 2:* Scan the relevant papers' reference lists to find extra relevant papers, if any, add them to the set.

Mendeley Desktop Software package (<https://www.mendeley.com>) was used to store and manage the search results. The following enumerated list gives the specifics of each database.

1. ACM Digital Library

Within ACM Digital library, a search query was run from 2013 to 2019, using “brain tumor classification and prediction using machine learning”. This resulted in a total of 17,822 papers. However, in using the advanced search option “Where Title matches any of the following words or phrases: brain tumor classification and prediction using machine learning AND Where Publication Year matches are in the range 2013-2019”, 17,82 articles were obtained. Additionally, another search query was run using the advanced search option “Where Title matches any of the following words or phrases: brain tumor classification and prediction using machine learning AND Where Abstract matches any of the following words or phrases: brain tumor”. This approach resulted in 68 articles. Moving further, another search query was run using the advanced search option “Where Title matches any of the following words or phrases: brain tumor classification and prediction using machine learning AND Where Abstract matches all of the following words or phrases: brain tumor AND Where Publication Year matches is in the range 2013-2019”. This final query resulted in 16 articles which were found to be relevant to the study.

2. IEEE Xplore

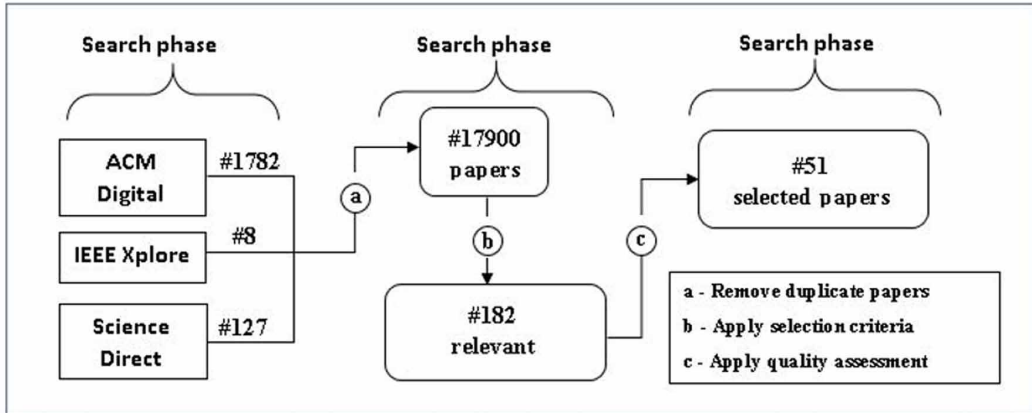
Within the IEEE Xplore, a search query was run from 2013 to 2019, using “brain tumor classification and prediction using machine learning” which resulted in 15 papers. Out of the 15 papers, 11 were found to be conference papers and the remaining 4 were journals. With the advanced search option using “brain tumor” AND “classification” AND “machine learning”, 85 articles were obtained. 70 of the 85 articles were conference papers, and the remaining 15 were journals.

3. ScienceDirect

Within the ScienceDirect, a search query was run, using “brain tumor classification and prediction using machine learning” to find articles containing these terms and initially obtained 1,271 papers. The advanced search option was also used to run a more specific search (between 2013 - 2019), limiting the article types to research articles, book chapters, book reviews, data articles, discussions, examinations, software publications, resulting in 718 articles. Furthermore, the advanced search title was limited to “brain tumor,” and a final 81 articles were obtained for the study.

The outcome of the selection process is as illustrated in Figure 4.

Figure 4. The Search and Selection Process



STUDY SELECTION

From the first phase of the search process, a total of 182 articles were found to be relevant. However, a quick scan reveals that not all the papers provided knowledge relevant to the study issues raised by this review. This problem further suggests the need for more filters necessary to identify papers that are more connected as outlined below:

- *Selection phase 1:* Apply the inclusion and exclusion criteria to the potential papers to identify the relevant papers, which have potential data for providing solutions to the research questions.
- *Selection phase 2:* Apply the quality assessment criteria to the relevant papers to select the papers with acceptable quality, which are eventually used for data extraction.

The inclusion and exclusion criteria used for the study is as defined below. These criterion were applied while reading the titles, abstracts, or/and the full text of the papers.

Inclusion Criteria

- use of ML techniques to preprocess data
- use of ML technique to estimate classification and prediction accuracy
- use of hybrid models that employs at least two ML techniques or combines ML technique with non-ML technique to estimate classification and detection accuracy
- only research papers including conference paper published in journals are to be considered
- only most complete and newest papers are to be considered in instances where there are knowledge duplications.

Exclusion Criteria

- papers that only describe how ML techniques work without estimating them.
- papers that describe the process of classification and detection only, without ML or non-ML techniques.
- review papers are excluded.

After the selection phase, the quality assessment criteria is applied resulting in 51 articles. The details of the assessmet follows in the section below.

STUDY QUALITY ASSESSMENT

The initial phases of the review protocol collectively made use of what is known as consistency assessment. The assessment was mainly focused on meta analysis and data synthesis on a quantitative basis resulting in fewer data. Next is the quality assessment to reveal the understanding of the review outcome and also to show the inferences' accuracy. This only serves as an additional criterion for the study's selection. The quality assessment (QA) questions needed for this study to assess the rigorousness, credibility, and relevance of the selected papers is as shown in Table 1. Each question is graded on a 3-like scale where 1 denotes a "Yes", 0.5 for "Partly" and 0 for "No". The "Yes" also tagged as "Sufficient" implies there are two or more datasets used. The "Partly" tagged as "Partly Sufficient" implies only on dataset was used and "No" tagged as "Insufficient" implies no dataset used in their study. For a given study, its quality score is computed by summing up the answers' scores to the QA questions. To ensure the reliability of this review's findings, the relevant studies are considered of acceptable quality if the score equal or greater than 2.5 (thus: 50%). These selected papers are subsequently used for the data extraction and synthesis. The quality scores is shown in Table 2, where the first column is a numeric value assigned to the selected paper after the "Study Selection". The papers and their IDs can be found as supplementary material.

DATA EXTRACTION

The selected studies were further exploited to curate data that addressed the research questions posed in this review. It was noticed that the term "experiment" is used with varying meanings in the brain tumor community, and most of the selected studies used this term without clearly defining it. To avoid this inherent ambiguity, the word experiment is explicitly defined as a method in which the procedure or algorithm with sufficient performance metrics is analyzed based on a given set of data. For the chosen studies, data extraction cards is used to collect data which are later verified and documented in the of data synthesis phase. However, not all data can be extracted explicitly from a chosen study nonetheless, implicit interpretation can be made with the data available. Another issue expected in the data extraction stage is the use different terminologies to refer to the same ML technique.

DATA SYNTHESIS

The purpose of the data synthesis is to extract information to answer research questions for the chosen study. Each piece of evidence may probably have a tiny amount of proof, but many of it might add up to make valid points. In this analysis, the details retrieved include quantitative (such as: an estimate of accuracy values) and qualitative (such as: ML techniques strengths and weaknesses) data. Various strategies are used to synthesize the retrieved data against the research questions. In this study, the narrative synthesis approach was used to answer RQ1 and RQ2. The narrative synthesis are aided with visualization tools like bar chart, box plot, pie chart and among others. The vote counting

Table 1. Quality Assessment questions

Question Tags	Questions
QA1	Are the aims of the research clearly defined?
QA2	Is the estimation context adequately described?
QA3	Are the estimation methods well defined and deliberate?
QA4	Is the estimation accuracy measured and reported?
QA5	Is the experiment applied to sufficient project data sets?

Table 2. Quality Scores of Selected Studies

Paper ID	QA1	QA2	QA3	QA4	QA5	Total
1	1	1	1	1	1	5
2	0.5	0.5	1	1	0.5	3.5
3	1	1	1	1	0.5	4.5
4	1	0.5	1	1	0	3.5
5	1	1	1	1	0	4
6	1	0.5	1	1	0	3.5
7	1	1	0.5	0	0.5	3
8	0.5	1	1	1	0	3.5
9	1	0.5	1	1	0	3.5
10	1	1	1	1	1	5
11	1	1	1	1	1	5
12	1	0.5	1	1	1	4.5
13	0.5	1	1	1	1	4.5
14	1	1	1	1	0	4
15	1	1	1	1	0	4
16	1	0.5	1	1	0	3.5
17	1	1	1	1	0	4
18	0.5	1	1	1	1	4.5
19	1	0.5	1	1	0	3.5
20	1	1	1	1	1	5
21	1	1	0.5	0	0	2.5
22	1	1	1	1	0.5	4.5
23	1	0.5	1	1	1	4.5
24	0.5	1	1	1	0	3.5
25	1	1	1	1	0.5	4.5
26	1	1	1	1	0.5	4.5
27	1	0.5	1	1	0.5	4
28	1	1	1	1	0.5	4.5
29	1	1	1	1	0	4
30	0.5	0.5	1	1	0.5	3.5
31	0.5	1	1	1	0.5	4
32	1	1	1	1	0	4
33	1	1	0.5	0	0	2.5
34	1	1	1	1	0	4
35	0.5	1	1	1	0	3.5

continued on following page

Table 2. Continued

Paper ID	QA1	QA2	QA3	QA4	QA5	Total
36	1	0.5	1	1	1	4.5
37	1	1	1	1	0	4
38	0.5	1	0.5	0	1	3
39	1	0.5	1	1	0	3.5
40	1	1	1	1	1	5
41	0.5	1	1	1	0.5	4
42	1	0.5	1	1	0.5	4
43	1	1	1	1	0.5	4.5
44	1	1	1	1	0.5	4.5
45	0.5	0.5	1	1	0	3
46	1	1	1	1	0	4
47	1	0.5	1	1	0	3.5
48	1	1	1	1	1	5
49	1	1	0.5	0	0.5	3
50	1	1	1	1	0	4
51	0.5	0.5	1	1	0	3

methods was however applied to answer RQ3 and RQ4 while focusing on accuracy comparison between different models. That is, assuming a comparison between model A and model B are to be synthesized, the number of experiments reporting Model A to have outperformed Model B, and the number of experiments reporting that Model B to have outperformed Model A is counted. The two values are then used to evaluate the comparison between model A and model B. This allows us to get a general idea of whether an estimation technique is said to have higher accuracy than a different technique. The results of implementing the review protocol is as follows in the next section.

RESULTS AND DISCUSSION

The outcomes of this review are presented in this section. For each research question, we have the findings reported and discussed. Some of the related works to justify the outcomes have also been presented (Amin, Sharif, Yasmin, & Fernandes, 2017; Deepak & Ameer, 2019; Delen & Zolbanin, 2018; Ito, Nakae, Hata, Okano, & Ishii, 2019; Kebir & Mekaoui, 2019; J. Li, Yu, Gu, Liu, & Li, 2019; Mittal et al., 2019; Parveen & Singh, 2015; Ren et al., 2019; Talo, Baloglu, Yıldırım, & Rajendra Acharya, 2019; Tarkhaneh & Shen, 2019; Thaha et al., 2019).

Types of ML Techniques (RQ1)

This section presents the different ML techniques that were used in the 51 selected papers. The ML techniques extracted from the resultant papers is as shown in Table 3.

Independent Versus Hybrid Techniques

From the study it was observed that many articles adopted the practice of fusing multiple methods to build a hybrid technique. By simple distribution of the data as shown in Figure 5, 13 articles representing 25% used only one ML or non-ML technique while the remaining 38 signifying 75% used

Table 3. ML techniques used in the various papers

Paper ID	Techniques
1	Support Vector Machine + Gaussian Radial Based Function (RBF)+Linear and Cubic
2	GoogleNet + Support Vector Machine (SVM)+KNearest Neighbor
3	Deep Neural Network (DNN)
4	K-mean + Convolutional Neural Network (CNN)
5	Kernel-based Fuzzy C-mean (KFCOM) + Weighted fuzzy kernel clustering (WKFCOM)
6	Adaptive Fuzzy K-mean (AFKM)
7	Convolutional Neural Network (CNN)
8	Adaptive Differential Evolution with Lévy Distribution (ALDE)
9	Hybrid Fuzzy C-Mean + Support Vector Machine (SVM)
10	Convolutional Neural Network (CNN)
11	Multi-Cascade Convolutional Neural Network (MCCNN) + Conditional Random Fields (CRFs)
12	Convolutional Neural Network (CNN)
13	Deep Convolutional Neural Network (DCNN) + Conditional Random Fields (CRFs)
14	Cuckoo Search Algorithm Tsallis entropy + Regularized level set
15	Neural Networks (NN)
16	Fuzzy C-Mean (FCM) + Support Vector Machine (SVM)
17	Fast Fourier Transform (FFT) + Minimum Redundancy Maximum Relevance (MRMR) + Support Vector Machine (SVM)
18	KIFCM (hybrid K-mean + Fuzzy C-Mean) +Active Contour (Level Set Contouring)
19	Wiener filter + Principal Component Analysis (PCA) + Radial Basis Function - kernel based Support Vector Machine (SVM)
20	Convolutional Neural Network (CNN) + Recurrent Neural Network (RNN)
21	Deep Convolutional Neural Network (DCNN)
22	Deep Convolutional Neural Network (DCNN)
23	Barkeley Wavelet Transform (BWT) + Support Vector Machine (SVM)
24	K- nearest neighbor (K-NN) + Support Vector Machine (SVM) + Chan- vese Segmentation
25	Deep Convolutional Neural Network (DCNN)
26	Enhanced Darwinian Particle Swarm Optimization (EDPSO)+ Adaptive Neuro Fuzzy Inference System
27	Hybrid Genetic Algorithm (GA) + Particle Swarm Optimization (PSO)
28	Kernelized fuzzy entropy clustering + Particle Swarm Optimization (PSO)
29	Particle Swarm Optimization (PSO) + Support Vector Machine (SVM) + Cuckoo Search
30	Particle Swarm Optimization (PSO) + Support Vector Machine (SVM)
31	Particle Swarm Optimization (PSO) + Fuzzy C-Mean (FCM)
32	Particle Swarm Optimization (PSO) + Otsu
33	Particle Swarm Optimization (PSO)

continued on following page

Table 3. Continued

Paper ID	Techniques
34	Particle Swarm Optimization (PSO) + Chicken Based Swarm Optimization + Support Vector Machine (SVM)
35	Learning Vector Quantization (LVQ) + Particle Swarm Optimization (PSO)
36	Teaching learning based Optimization (TLBO), Shannon' s entropy, level set method
37	Particle Swarm Optimization (PSO) + Discrete Wavelet Transform (DWT) +Kernel based Support Vector Machine (SVM)
38	Teaching learning based Optimization (TLBO), Fuzzy Tsallis entropy, level set method
39	Particle Swarm Optimization (PSO)
40	Particle Swarm Optimization (PSO) + Bacteria Foraging Optimization (BFO) + Modified Fuzzy C- Mean (MFCM)
41	Bacteria Foraging Optimization (BFO) + Modified Fuzzy K – Means algorithm (MFKM)
42	Particle Swarm Optimization (PSO) + Fuzzy C-Mean (FCM)
43	Modified Fuzzy C- Mean (MFCM) + Optimized Ant Colony
44	Convolutional Neural Network (CNN) + Genetic Algorithm (GA)
45	Genetic Algorithm (GA)
46	Genetic Algorithm (GA) + Fuzzy C-Mean (FCM)
47	Deep Convolutional Neural Network (DCNN) + Genetic Algorithm (GA)
48	Artificial Neural Network (ANN) + Genetic Algorithm (GA)
49	Artificial Bee Colony (ABC) + Fuzzy C-Mean (FCM)
50	Bat Algorithm + Fuzzy C-Mean (FCM)
51	Bat Algorithm + K- nearest neighbor (K-NN)

a hybrid technique in their research. Figure 6 also gives a distribution of techniques used independently. Justification of the distribution is detailed in the discussion section.

Estimation Accuracy of ML Models (RQ2)

Since ML models are data-driven, their construction and validation are also data dependant. Table 4 shows the accuracy value reported by each paper. Papers that did not report any performance measure in their study has “N/A” defined in the table as their accuracy value.

ML Models That Outperform Other ML Models (RQ3)

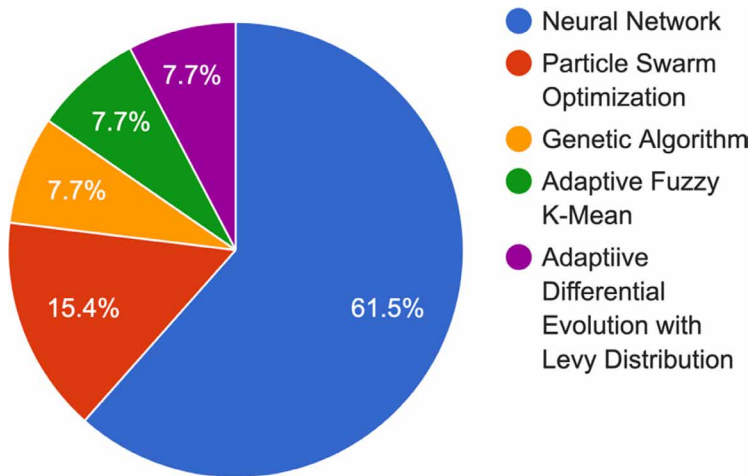
In Table 5 we present models that performs quite well when implemented independently without creating hybrid models with them. Models are considered to perform quite well if their performance are above a threshold value of 90%. These are models could be used in other research work or further investigated.

Table 6 on the other hand shows hybrid model with performance greater than the threshold value of 90%. These hybrid models by recommendation of this study can be used in other research works or further investigated under some defined constrains.

Figure 5. Distribution of Single Technique Over Hybrid Techniques



Figure 6. Distribution of Single Techniques



DISCUSSION

Types of ML Techniques (RQ1)

From the data collected it is obvious that all the different ML techniques used can be grouped into either independent or hybrid techniques. The independent techniques can further be grouped into four main types, thus: Neural Networks (DNN, CNN), Support Vector Machine (SVM) (Kernel, Regularization, Margin), Fuzzy C-Mean (FCM), Swarm Intelligence (Particle Swarm Optimization (PSO) and Genetic Algorithm). Among the above-listed ML techniques, Neural Network (DNN, CNN) and Particle Swarm Optimization (PSO) are the two most widely used accounting for approximately 76% of the selected studies. The detailed information about which ML techniques were used in each

Table 4. Model Performance

Paper ID	Model Performance	Paper ID	Model Performance
1	97.10%	27	62%
2	92.3% (Deep Transfer Learning) 97.8% (SVM+DCNN) 98.0 (KNN+DCNN)	28	90.19% (Jaccard Index)
3	94% (Mean Dice Coefficient)	29	99.59%
4	95%	30	95.23%
5	93.33%	31	93.11%
6	N/A	32	N/A
7	86.40% gray matter, 89.70%, white matter and 84.86% and cerebrospinal fluid, (Dice Coefficient)	33	N/A
8	N/A	34	99.90%
9	91.66% (Linear)	35	Maximum 93.4%, Average 88.5%
10	92%	36	94.13%
11	88.24% Whole Tumor BRATS 2018 (Dice Coefficient)	37	85%
12	89.2% (Dice Coefficient))	38	N/A
13	90.1% (Dice Coefficient)	39	77.14% (Jaccard Index)
14	More than 99%	40	97.22% (Similarity Index)
15	83%	41	95.77% (Similarity Index)
16	99%	42	96..39% White Matter, 96.61% Gray Matter (Jaccard Index)
17	98.90%	43	97.53%
18	100%	44	94.20%
19	94%	45	97%
20	84% BRATS 2016 (Dice Coefficient)	46	99%
21	N/A	47	67.25%
22	88% BRATS 2013 (Dice Coefficient)	48	90%
23	96.51%	49	N/A
24	90%	50	88.09% (Jaccard Index)
25	89% (Dice Coefficient)	51	93.72%
26	95%		

Table 5. Single Technique Models with Performance Above 90%

Paper ID	Single Technique Models	Performance (Accuracy)	% Increase
3	Deep Neural Network (DNN)	94% (Mean Dice Coefficient)	4%
10	Convolutional Neural Network (CNN)	92%	2%
45	Genetic Algorithm (GA)	97%	7%

Table 6. Hybrid Models with Perfirnance Above 90%

Paper ID	Hybrid Models	Performance (Accuracy)	% Increase
1	Support Vector Machine + Gaussian Radial Based Function (RBF)+Linear and Cubic	97.10%	7.10%
2	GoogleNet + Support Vector Machine (SVM)+KNearest Neighbor	98%	8%
3	K-mean + Convolutional Neural Network (CNN)	95%	5%
4	Kernel-based Fuzzy C-mean (KFCOM) + Weighted fuzzy kernel clustering (WKFCOM)	93.33%	3.33%
5	Hybrid Fuzzy C-Mean + Support Vector Machine (SVM)	91.66%	1.66%
7	Deep Convolutional Neural Network (DCNN) + Conditional Random Fields (CRFs)	90.10%	0.10%
8	Cuckoo Search Algorithm Tsallis entropy + Regularized level set	99%	9%
9	Fuzzy C-Mean (FCM) + Support Vector Machine (SVM)	99%	9%
10	Fast Fourier Transform (FFT) + Minimum Redundancy Maximum Relevance (MRMR) + Support Vector Machine (SVM)	98.90%	8.9%
11	KIFCM (hybrid K-mean + Fuzzy C-Mean) +Active Contour (Level Set Contouring)	100%	10%
12	Wiener filter + Principal Component Analysis (PCA) + Radial Basis Function - kernel based Support Vector Machine (SVM)	94%	4%
14	Barkeley Wavelet Transform (BWT) + Support Vector Machine (SVM)	96.51%	6.51%
15	K- nearest neighbor (K-NN) + Support Vector Machine (SVM) + Chan- vese Segmentation	90%	0%
16	Enhanced Darwinian Particle Swarm Optimization (EDPSO)+ Adaptive Neuro Fuzzy Inference System	95%	5%
18	Kernelized fuzzy entropy clustering + Particle Swarm Optimization (PSO)	90.19%	0.19%
19	Particle Swarm Optimization (PSO) + Support Vector Machine (SVM) + Cuckoo Search	99.59%	9.59%
20	Particle Swarm Optimization (PSO) + Support Vector Machine (SVM)	95.23%	5.23%
21	Particle Swarm Optimization (PSO) + Fuzzy C-Mean (FCM)	93.11%	3.11%
23	Particle Swarm Optimization (PSO) + Chicken Based Swarm Optimization + Support Vector Machine (SVM)	99.90%	9.90%
24	Learning Vector Quantization (LVQ) + Particle Swarm Optimization (PSO)	93.40%	3.40%
25	Teaching learning based Optimization (TLBO), Shannon' s entropy, level set method	94.13%	4.13%
28	Particle Swarm Optimization (PSO) + Bacteria Foraging Optimization (BFO) + Modified Fuzzy C- Mean (MFCM)	97.22%	7.22%
29	Bacteria Foraging Optimization (BFO) + Modified Fuzzy K – Means algorithm (MFKM)	95.77%	5.77%
30	Particle Swarm Optimization (PSO) + Fuzzy C-Mean (FCM)	96.61%	6.61%
31	Modified Fuzzy C- Mean (MFCM) + Optimized Ant Colony	97.53%	7.53%
32	Convolutional Neural Network (CNN) + Genetic Algorithm (GA)	94.20%	4.20%
33	Genetic Algorithm (GA) + Fuzzy C-Mean (FCM)	99%	9%
35	Artificial Neural Network (ANN) + Genetic Algorithm (GA)	90%	0%
38	Bat Algorithm + K- nearest neighbor (K-NN)	93.72%	3.72%

selected study can be found in Table 3. The independent techniques used are presented as follows: 1 (approx. 8%) of Genetic Algorithm, 1 (approx. 8%), 1 (approx. 8%) Adaptive Fuzzy K-mean (AFKM), 1 (approx. 8%) Adaptive Differential Evolution with Lévy Distribution (ALDE), 2 (approx. 15%) Particle Swarm Optimization and 8 (approx. 61%) Neural Network. Relative to the hybrid models, it was observed that the distribution is unique as no permutation of models got repeated in the selected articles studied.

Estimation Accuracy of ML Models (RQ2)

Regarding the evaluation of ML models, the accuracy metric should also be regarded. Different methods can be used to compute the accuracy and different aspects can measure the accuracy from different metrics. It is therefore necessary to follow appropriate/standardized accuracy metrics to evaluate the performance of a given model to address RQ2 correctly. The accuracy of the different single techniques ranges from 0 to 97%, and the accuracy of the hybrid technique also ranges from 0% to 100%. Considering the single technique, the Genetic Algorithm had the highest performance accuracy, which was 97%. Some neural networks performed poorly (0%) and other neural networks attained as high as 94% accuracy as shown in Table 4. Amongst the hybrid techniques like, Particle Swarm Optimization (PSO) + Otsu, Teaching Learning Based Optimization (TLBO), Fuzzy Tsallis Entropy, Level Set Method, and Artificial Bee Colony (ABC) + Fuzzy C-Mean (FCM) performed the least (0%). Cuckoo Search Algorithm Tsallis entropy + Regularized level set, Fuzzy C-Mean (FCM) + Support Vector Machine (SVM), KIFCM (hybrid K-mean + Fuzzy C-Mean) + Active Contour (Level Set Contouring), Particle Swarm Optimization (PSO) + Support Vector Machine (SVM) + Cuckoo Search and Particle Swarm Optimization (PSO) + Chicken Based Swarm Optimization + Support Vector Machine (SVM) also performed between 99% to 100%. This could be attributed to the fact that, these hybrid models resolved their deficiencies and improves upon their advantages leading to a best global solution.

ML Models That Outperform Other ML Models (RQ3)

From these study it can be concluded that the hybrid technique performs relatively higher with an accuracy of 100% compared to 97% of the independent techniques. Observing the independent techniques in the light of performance, 23% (3 out of 13) papers had performance accuracy of 90% and above, while 76% of the hybrid techniques (29 out 38) papers had performance accuracy of 90% and above. Therefore, it is suggested that a suitable hybrid technique that meet a defined constraint will perform better than an independent technique.

CONCLUSION AND FUTURE WORK

This review examined the classification and prediction models for brain tumors from four perspectives: type of ML technique, ML model estimation accuracy (including ML model versus non-ML model), and context estimation from the ML model. A thorough literature search for relevant studies has been conducted between 2013-2019, and 51 primary empirical studies have finally been identified in the review on the five research questions (RQs). In estimating the ML model's efficiency or the contrast of the ML with other models, only accuracy metrics were regarded as they are the most dominant metric used. However, other performance metrics such as widespread capacity and interpretability ignored in this review may be looked into as further study. Furthermore, the synthesized approximation accuracy tests under what circumstances and to what degree they remain can be difficult to explain. This poses as a threat to validity which can be further investigated as well. Generally speaking, the experimental design requires the compilation of evidence for model creation and a testing process for model validation. Additionally, experimental design may include preprocessing data steps to delete outliers, weight characteristics, or select subsets of features.

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