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Application of Radiomics in Central Nervous System Diseases: a Systematic literature review

Yanghua Fan, Ming Feng*, Renzhi Wang*

Department of Neurosurgery, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China

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ABSTRACT

Central nervous system (CNS) diseases are associated with complexity and diversity; as a result, it is urgent to search for a simple approach for effectively improving the clinical decision-making ability and precise treatment currently. Radiomics can collect plenty of quantitative features based on the massive medical image data; meanwhile, related diagnosis and prediction can be performed through quantitative analysis. The main steps of radiomics analysis include image collection as well as reconstruction, segmentation of the region of interest (ROI), feature extraction as well as quantification, and establishment of the predictive as well as prognostic models. Compared with traditional imaging features, radiomics allows to transform the visual image data to the in-depth features, so as to carry out quantitative research. Our findings suggest that radiomics has broad application prospects in the early screening, accurate diagnosis, grading and staging, treatment and prognosis, and molecular characteristics of CNS diseases, which can improve the capacities to diagnose and predict CNS diseases prognosis through complementing and combining with traditional imaging.

1. Introduction

Central nervous system (CNS) diseases are remarkable with their complexity and diversity, along with dismal prognosis [1]. Therefore, it is of crucial importance for the early diagnosis of CNS diseases, especially for CNS tumors, the aberrant cell growth within the brain that may be either benign or malignant; for instance, gliomas are still poorly typed and have poor prognosis. Besides, it remains difficult to diagnose diseases such as Parkinson's disease (PD) and schizophrenia. Consequently, it is urgent to search for a simple and effective way to improve the clinical decision-making capacity and precise treatment currently.

In addition to the clinical value of image interpretation, imaging has rapidly transformed from a qualitative diagnostic tool to an enormous source of information over the past few decades, which has supported the notion that images are not just pictures, instead, they represent a rich source of patient data and health information [2]. According to findings from recent research, images have contained data complementary to the demographical as well as genomic data, which would contribute to radiomics [3,4]. Moreover, neuroimaging is beneficial for addressing the vital scientific questions in new drug discovery, clinical research, clinical trials, and outcome measures of CNS diseases [5].

However, the diagnosis based on traditional medical images remains on the anatomic changes, and a majority of radiological information has been reported in a qualitative as well as subjective way; thus, there is still a great deal of effective information to be extracted and utilized. Along with the advanced quality of imaging technology, the potential of imaging has been further expanded thanks to the software advances and novel computational methods. Radiomics has marked the emerging area, which can transform the available medical imaging information to the extractable data [6]. Compared with conventional mining of radiological information, the collective radiomics data mining is associated with two unique advantages. Firstly, the radiomics method allows to semi-automatically or automatically extract the radiological features, which will also offer abundant data compared to the subjective reading by readers or qualitative analyses. Secondly, the high-dimensional radiomics information would shed light on the heterogeneity within region through identifying the sub-regions as well as by presenting the disease spatial complexity [7]. On this account, radiomics can serve as a particularly promising approach in individualized medication in terms of oncology, and it requires to clearly understand tumor heterogeneity for each case.

Thus, this study aims to introduce and review the advances in

Abbreviations: CNS, Central nervous system; ROI, Region of interest; AUC, Under the curve; IDH, Isocitrate dehydrogenase; NFPAs, Non-functioning pituitary adenomas; NCAs, Null cell adenomas; ADHD, Attention deficit hyperactivity disorder; GBM, Glioblastoma; LGG, Low grade glioma; HGG, High grade glioma

* Corresponding authors at: Department of Neurosurgery, Pituitary Center, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences, No. 1 Shuaifuyuan, Dongcheng District, Beijing 100730, China.

E-mail addresses: pumchfengming@163.com (M. Feng), wangrz@126.com (R. Wang).

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radiomics and explore the progress and challenges of imaging studies for investigating CNS diseases, so as to improve the diagnostic accuracy and differentiation of CNS diseases, and to provide the evidence-based support for accurate medical treatment.

2. Radiomics overview

Radiomics has marked the new area of study, which will extract, process and analyze the quantitative and high-throughput data, so as to explore the relationship with the valuable information [8]. Typically, the relevant valuable information has been directed to the pathologic and genomic data; alternatively, it may be specific to different clinical endpoints. Originally, the suffix -omics has depicted the collective characterization as well as quantification of biological data; for instance, genomics, proteomics and metabolomics [7]. Moreover, the concept of -omics in radiomics has been applied as radiomics, which has used millions of voxels based on the tomographic or volumetric imaging information for multiple sections from one individual patient, thus potentially representing the biological information for one disease in a comprehensive way.

Such information may subsequently be “mined” with the machine-learning tools, followed by validation as the quantitative imaging biomarkers to characterize the intratumoral dynamics during the whole treatment course [9]. Recently, the analytical methods for cancer imaging have shed new lights on the early markers for treatment response, risk factors, as well as the subsequent tailoring of the best therapeutic schemes [5,10–12]. Therefore, the calculation models based on images have become the critical technology to identify, analyze and validate the quantitative features extracted. In this review, the available radiomics methodologies have been discussed, which may serve as the markers to predict the diagnosis, prognosis, as well as therapeutic planning for CNS diseases.

Radiomics consists of the coming generation of imaging. As a high-throughput non-invasive approach, radiomics has provided a new choice for cancer research. Specifically, both macro- and micro-analysis can be carried out from genome to the clinically relevant factors based on the same extracted data. Besides, radiomics has offered a non-invasive and dynamic monitoring way based on tumor heterogeneity at various levels (such as genome, cells, tissues, and individuals), which is convenient and low-cost [13,14].

3. The flow of radiomics

Radiomics has a distinct superiority, which is that, the clinical workflow will not be markedly disrupted under ideal condition. Afterwards, images for the diagnosis by a physician would be reconstructed to the 2D or 3D images by the radiologic technicians. To be specific, the radiomics process will first convert the radiographic images into the mineable data, which has involved 4 steps, namely, (a) image acquisition as well as reconstruction, (b) segmentation or labeling of the region of interest (ROI), (c) feature extraction as well as quantification, and (d) statistical analysis, establishment of the predictive and prognostic models.

3.1. Image acquisition of CNS diseases

Image acquisition has laid the foundation for radiomics. Generally speaking, tremendous image data may be obtained by CT, MRI, and PET-CT examinations; however, these images are usually not standardized in the medical imaging centers, which has rendered great differences in the acquired image parameters. Previous studies have shown that different imaging acquisition parameters change radiologic features [15,16], and both spatial resolution (voxel size) and gray level resolution (contrast) can affect the computation of radiomics features. These illustrate that the radiomics features is determined by imaging acquisition techniques and parameters.

Therefore, it is beneficial to establish the standardized database to analyze the big data in medical images, which will bring accurate expected data to clinical diagnosis as well as treatment. The Radiological Society of North America (RSNA), together with the National Institute of Biomedical Imaging and Bioengineering, has proposed the Quantitative Imaging Biomarker Alliance (QIBA) [17], which has represented a field in quantitative imaging. Typically, the major task is to produce medical images with descriptive deviations and variability limits, and to lower the role of image parameter differences in radiomics analyses.

However, in actual clinical practice, image acquisition and scanning protocols vary from different patients and medical institutions. Therefore, before feature extraction, preprocessing of image data is required to normalize heterogeneous imaging data. A solution for heterogeneous "spatial resolution" is to resample the voxels into isotropic pixels or voxels after co-registration of different sequences in multispectral imaging or the same imaging modality, and the solution of heterogeneous "contrast" is intensity normalization [7].

3.2. ROI segmentation

Segmentation is the key in radiomics analysis, since the segmented images can generate the feature data subsequently. Segmentation is of greater significance to measure the nodule shape, which is in contrast to the 2D texture. Moreover, it is also of critical importance in identifying the histological patterns in CNS lesion.

Image segmentation is the process in which one image will be divided into several regions with specific properties and the ROI will be extracted. Specifically, manual segmentation is possible under the hand of an experienced radiologist, and it is often regarded as the “god standard”; however, such process is very burdensome, especially for large datasets. Moreover, the inevitable high interoperability variability makes the application of this method more limited.

A segmentation method that satisfies the requirements should have four basic characteristics: accuracy, automation, consistency, and reproducibility. Recently, many automatic or semi-automatic segmentation methods have been developed, for example, image can also be segmented automatically based on the abrupt changes of the gray level (corresponded to the edges) as well as the similarity in the gray level for homogeneity measurement; nonetheless, such method is inferior to manual segmentation in terms of accuracy. We must realize that even in recent years, the development of various segmentation methods such as level set methods, graph cut methods, and growing methods, there is no universal segmentation method suitable for all types of medical images. Therefore, it is very necessary to establish a common standard for performing segmentation, and it still needs a lot of effort and experiment.

3.3. Feature extraction and quantification

Feature extraction is to select the useful information to identify various types of images. Feature extraction also requires reproducibility, and information must be informative rather than redundant [18]. Typically, the quantitative features can be automatically collected be extracted from the ROI through the high-throughput technique, so as to establish the models based on machine learning. Besides, quantitative features for radiomics analyses are the algorithms utilized for describing the local regions in one radiologic image. There are some available algorithms to this end, and the commonly seen radiomics features can be classified into several classes at present, including intensity-based, structural, texture/gradient-based, as well as wavelet. Semantic features are distinct from the radiomics ones, since the former are non-subvisual and will be directly observed and depicted by the radiologists. The above-mentioned features have been enrolled into the current review for the sake of completeness so as to establish the classifiers [19]. At present, although there are many methods of feature extraction, the method of fully automated extraction of radiomic features without redundancy is still the goal and direction of future research.

3.4. Establishment of the predictive and prognostic models

When all features are mined, various statistical models can be utilized for selecting various leading features correlated with the hypothesis-specified outcome in the process of feature selection. Specifically, selecting the leading features allows to reduce the problem dimensionality and enhance the prediction accuracy. Notably, feature selection may be performed through the univariate or multivariate statistical model. Of then, the univariate methods are only dependent on the feature association, irrespective of the redundancy; by contrast, the multivariate methods will examine the associations among various features, which would be subsequently selected following the weighing of association as well as redundancy. Generally speaking, Fisher score, Chi-squared test, as well as Wilcoxon, have been selected to select the features out of the rest statistical models. For instance, when the chi-squared test is used to select the features, the chi-squared statistics regarding each feature variable with target variable (the label/outcome) would be calculated. For target variable that is independent of feature variable, the latter will be abandoned. On the other hand, Fischer score will offer a higher rank for features displaying the higher variance (which suggests the availability of more information of the feature). Meanwhile, the Wilcoxon rank sum test would be similar to the two-sample t-test, but the former is non-parametric, which can test the null hypothesis suggesting that two populations are distributed with the same median. Moreover, features are preserved according to the confidence (statistical significance) to reject the null hypothesis.

When the optimum features have been selected, a classifier (the classification algorithm) would be established. Typically, the supervised classifier has involved the explicit training of classifier through the labeled instances, among which, the labels have represented the category of interest (such as LGG or HGG). After training, the machine classifier will be locked down and utilized for predicting the instance outcome in the test set, which has comprised the instances with no corresponding labels. Various classifiers can be utilized in prediction, such as the neural networks, random forest, support vector machines, and generalized linear models [19–21].

Moreover, higher quality prospective studies are needed to more closely assess quantitative imaging features associated with clinical outcomes to further enhance knowledge about the potential of radiomics in CNS diseases. Therefore, after building the model, we need to verify the robust performance of the model in the prospective and external setting.

Finally, due to the limitations discussed above, the use of radiomics in routine clinical practice is limited, but with the standardization of future image acquisition and experiments, and through the validation of prospective clinical trials, radiomics may be powerful in future patient management.

4. Applications of radiomics in CNS disease

We performed a literature search using both text word and MeSH strategies with the terms ‘radiomic’ and ‘radiomics’ in Pubmed database, a total of 872 related articles were identified. The titles and abstracts were reviewed, and 776 irrelevant studies were excluded. In addition, after reading the full text carefully, 16 articles were excluded. After screening, eighty articles on the application of radiomics in the CNS diseases were identified in this review. The detailed screening process is shown in Fig. 1. Additionally, the detailed of applications of these articles are summarized in Table 1.

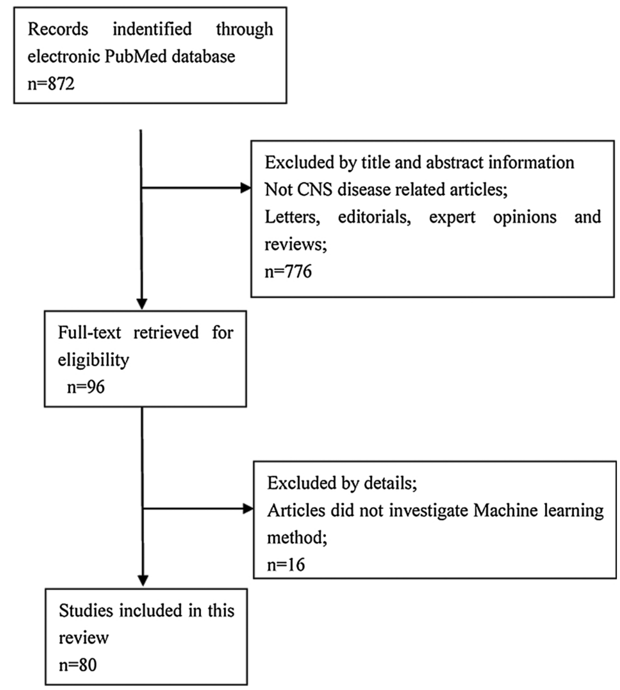

Fig. 1. Flowchart presenting the steps of literature search and selection.

4.1. Application of radiomics in the differential diagnosis of CNS diseases

Kang et al. [22] had extracted a total of 1618 radiomics features from 70 glioblastoma patients and 42 patients with primary CNS lymphoma to test the diagnostic performance. Noteworthily, the diagnostic accuracy of radiomics analysis [area under the curve (AUC) of 0.944] is better than that of traditional genomics (AUC of 0.819) as well as human reader (AUC of 0.896–0.930). Besides, the diffusion radiomics model is associated with favorable generalizability, which contributes to yielding superior performance in diagnosis to that of conventional radiomics or the single advanced MRI in terms of the identification of the atypical primary CNS lymphoma that mimics glioblastoma. Multiple studies found similar results, which suggested that the radiomics features might be utilized for effectively differentiating the primary CNS lymphoma from glioblastoma [23–25]. Artzi et al. [26] and Qian et al. [27] found that the use of radiomic machine-learning technology could help to differentiate glioblastoma from brain metastases before surgery. Kim et al. [28] and Elshafeey et al. [29] proved that radiomics model could improve the diagnostic performance of identifying the pseudo-progression in glioblastoma.

In addition, radiomics has also been applied in the differential diagnosis of CNS diseases in childhood. For instance, Fetit et al. had investigated the differential diagnosis value of MRI radiomics analysis among 134 children with posterior fossa tumors (including medulloblastoma, hair cell astrocytoma and ependymoma), which had supported that the texture features of radiomics could serve as the auxiliary diagnostic tool for brain tumors in children [30]. Similarly, Lv et al. [31] developed and validated a radiomics model to predict molecular subgroups of pediatric medulloblastoma. In the diagnosis of brain metastases, Ortiz-Ramon et al. [32] had successfully utilized the radiomics approach to accurately distinguish the two frequently-seen origins for brain metastasis (namely, lung cancer and melanoma) based on the general MRI images.

Moreover, Fan et al. [33] built a radiomics model to help neurosurgeons predict tumor consistency in patients with acromegaly before surgery. Li et al. [34] found that radiomics is a powerful tool for preoperative differentiation of malignant haemangiopericytoma and angiomatous meningioma. Lohmann et al. [35] and Peng et al. [36]

Table 1
The Applications of Radiomics in CNS Disease.

Application	Diseases	Reference
Differential Diagnosis	Distinguish glioblastoma from CNS lymphoma	[22,23,24,25]
	Distinguish glioblastoma from brain metastasis	[26,27]
	Distinguish glioblastoma pseudoprogression from tumor progression	[28,29]
	Identification pediatric posterior fossa tumor subtype	[30]
	Identification pediatric medulloblastoma subgroups	[31]
	Identification the origins of brain metastasis (lung cancer or melanoma)	[32]
	Identification the acromegaly tumor consistency (soft or firm)	[33]
	Distinguish malignant haemangiopericytoma from angiomatous meningioma	[34]
	Distinguish brain metastasis progression from radiation-related injury	[35,36]
	Distinguish AVM-related hematomas from other spontaneous intraparenchymal hematoma types	[37]
	Distinguish schizophrenia from healthy controls	[38]
	Distinguish idiopathic Parkinson's disease from healthy controls	[39]
	Distinguish Alzheimer's disease from mild cognitive impairment	[40]
	Distinguish developing normal-appearing white matter lesions (dNAWM) from non-dNAWM	[41]
Typing Diagnosis	Classification of the glioma grading	[42,43,44,45,46,47,48]
	Identification non-functioning pituitary adenomas subtypes (null cell adenomas or other subtypes)	[49]
	Prediction of cavernous sinus invasion by pituitary adenomas	[50]
	Classification of the Meningioma grading	[51,52]
	Identification the attention deficit hyperactivity disorder subtypes	[53]
Molecular Characteristics Predict	Identification IDH mutation status in glioma	[56,57,58]
	Predict 1p/19q co-deletion status in glioma	[69,70]
	Predict Ki-67 expression levels in glioma	[43,71,72]
	Predict TERT expression levels in glioma	[59]
	Predict EGFR expression levels in glioma	[73]
	Predict PTEN expression levels in glioma	[74]
	Predict POSTN expression levels in glioma	[75]
	Identification ATRX mutation status in glioma	[57,76]
	Identification TP53 mutation status in glioma	[61]
	Identification MGMT methylation status in glioma	[77,78,79]
Treatment Response, progression and Prognosis Predict	Predict prognosis and survival of gliomas	[80,81,82,83,84,85,86,87,88,89,90,91,92,93]
	Predict skull base meningioma recurrence	[94]
	Predict epilepsy incidence in patients with low-grade gliomas	[95]
	Predict intracerebral hemorrhage expansion	[96]
	Predict the edema area around basal ganglia hemorrhage	[97]
	Predict radio-chemotherapy response in recurrent malignant gliomas	[98]
	Predict somatostatin analogue response in acromegaly	[99]
	Predict prognosis of Parkinson's disease	[100]
	Predict mild cognitive impairment progression	[101,102,103]

revealed that, the radiomics method might potentially enhance the accuracy in distinguishing brain metastasis progression from the radiation-related injury. Zhang et al. [37] constructed a machine learning model based on radiomics features, which can accurately discriminated AVM-related intraparenchymal hematomas from those caused by other etiologies.

For brain functional diseases, Cui et al. [38] had proposed an effective radiomics method for diagnosing schizophrenia based on the functional connectivity, which would facilitate the objective and schizophrenia personalized diagnosis on the basis of the quantitative biomarker showing specific functional connectivity. Also, radiomics features could be used for the diagnosis of idiopathic PD [39] and Alzheimer's disease (AD) [40]. Shao et al. [41] used radiomics features to effectively identify early-stage normal-appearing white matter lesions before they developed visible white matter hyperintensities.

Taken together, the above-mentioned studies suggest that, the radiomics approach contributes to the differential diagnosis of CNS in both adults and children, so as to achieve the goals of early detection, early treatment and selection of optimal treatment.

4.2. Application of radiomics in diagnostic typing of CNS diseases

For glioma, radiomics models constructed by Tian et al. [42] had been constructed based on 30 as well as 28 optimum features to distinguish LGGs from HGGs, as well as grade III from IV, respectively. Additionally, the AUC was 0.987 in distinguishing LGGs from HGGs, while that was 0.992 in distinguishing grades III glioma from grade IV one, and they were promising compared with the use of histogram parameters as well as the single sequence MRI. Recent multiple studies have shown that glioma can be precisely graded based on the machine learning as well as feature selection technique combined with the radiomics approach; besides, the radiomic strategy put forward might contribute to clinical decision-making among glioma patients at different grades [43–48].

For pituitary adenoma, Zhang et al. [49] had used the radiomics approach to effectively and individually predict the non-functioning pituitary adenomas (NFPAs) subtypes preoperatively, which allowed to effectively distinguish the null cell adenomas (NCAs) from the other subtypes. Additionally, the radiomics predictive model (AUC: 0.852) developed by Niu et al. [50] could help to predict whether pituitary adenomas had invaded the cavernous sinus or not (distinguishing Knosp grade 2 from grade 3) preoperatively, which might thereby contribute to developing the surgical strategies. For meningioma, Zhu et al. [51] and Park et al. [52] found that radiomics model could help to noninvasively differentiate the grade of meningiomas before surgery.

For brain functional diseases, Sun et al. [53] had reported the radiomics features related to the diagnosis as well as the subtypes for attention deficit hyperactivity disorder (ADHD); meanwhile, they had established and evaluated the diagnosis and subtype classification model of ADHD based on the identified features.

Compared with the traditional imaging technology, the radiomics analysis approach can provide more valuable information to identify the different subtypes of CNS diseases, which is more conducive to disease diagnosis and clinical treatment.

4.3. Application of radiomics in predicting the molecular characteristics of CNS diseases

Compared with histological classification, gene may be a critical predictor of changes in some molecular markers associated with treatment and prognosis. The emerging radiomics techniques can not only provide the non-invasive methods to diagnose and assess lesions, but can also offer features surrounding the lesions as well as the genetic heterogeneity within lesions that cannot be obtained through laboratory examinations [54,55].

Tian et al. [56] had determined that random forest was the best machine learning approach based on radiomics to predict the isocitrate dehydrogenase (IDH) within the diffused glioma, with the AUC value of 0.931. Ren et al. found that the use of the Multiparametric MR Radiomic Features could non-invasively estimate IDH1 mutation in the low grade gliomas [57]. At the same time, a number of radiomics-based machine learning methods as well as deep learning methods have been utilized in recent years to predict the IDH genotype of gliomas, which can achieve favorable prediction results [58–68].

Han et al. [69] had developed the radiomics signature based on MRI, which allowed for the effective identification of 1p/19q co-deletion in the low grade gliomas diagnosed histopathologically, which might thus contribute to the non-invasive prediction of the glioma molecular subtype. Besides, the radiomic model built by Shofty et al. [70] could also well distinguish 1p/19q co-deletion status. On the other hand, radiomics analytics is also used in other important markers of gliomas, such as Ki-67 [43,71,72], TERT [59], EGFR [73], PTEN [74], POSTN [75], ATRX [57,76], TP53 [61] mutation as well as the MGMT methylation status [77–79].

It can reveal the tumor gene expression status through radiomic features, improve the disease prediction ability (such as brain tumors), assist in the clinical diagnosis of CNS diseases, and offer the non-invasive approach in detecting the genotypes.

4.4. Application of radiomics in predicting treatment response, progression and prognosis of CNS diseases

Nie et al. [80] used the radiomics-based deep learning approach in predicting the survival for high grade gliomas, with the accuracy of 90.66%. A number of studies have shown that radiomics analyses based on machine learning also display high accuracy in predicting the prognosis and survival for gliomas (including GBM, LGG and HGG) [81–93]. Zhang et al. [94] demonstrated that preoperative MRI-based radiomics approach can effectively predict the recurrence of skull base meningioma. Specifically, these studies will offer a potential approach for enhancing the performance in predicting the outcomes for glioma patients.

Liu et al. [95] developed and validated an effective prediction model to precisely predict the incidence of epilepsy among low grade glioma patients (with the AUC of 0.8769 for the primary cohort, and 0.8152 for the validation cohort). For cerebral hemorrhage, the radiomics model constructed by Xie et al. [96] showed high performance in predicting early hematoma expansion in patients with intracerebral hemorrhage. And the use of radiomics may be helpful in predicting edema around the basal ganglia hemorrhage [97].

Moreover, Wang et al. [98] demonstrated that, the combination of radiomics analysis with functional MRI could identify the early response to treatments of stereotactic radiosurgery combined with bevacizumab for patients with relapsed malignant gliomas in a quantitative way. Kocak et al. [99] found that the machine learning-based T2-weighted MRI could serve as a promising non-invasive approach to predict the somatostatin analogue response among acromegaly patients as well as those with GH-secreting pituitary macroadenoma.

For brain functional diseases, Rahmim [100] suggested that, adding the radiomic features into the traditional measures could dramatically improve the prognosis prediction accuracy of PD, and reduce the absolute error in prognosis prediction from 9.00 ± 0.88 to 4.12 ± 0.43. Besides, according to their results, radiomics analysis for PD images contributed to developing the potent biomarkers for predicting the prognosis for PD. Zhou et al. [101], Shu et al. [102] and Li et al. [103] found that radiomics may be a powerful tool for predicting white matter hyperintensity progression.

These studies have demonstrated that radiomics can be used for the identification of differential treatment responses, progression and prognostic assessment among patients with different CNS diseases, which has emphasized that radiomics can serve as a low-cost novel tool to improve the treatment decisions for CNS diseases. However, there exist several challenges before radiomics can reliably be integrated into main stream clinical practice. We believe that with the increasing computing power, radiomics can play an important role in the routine clinical management of CNS diseases in the future.

5. Limitations

First, interpretive challenges derived from the computed data originating from the radiomic methods cannot be ignored. Typically, such method may not obtain extensive clinical acceptance in the presence of the statistical correlations of the computed features with the clinical outcomes, until a better link occurs regarding the quantitative metric and the traditional imaging features with the potential biology. Second, the current radiomics research is a retrospective rather than prospective study, and the pixel-based analysis of existing image data requires overall lesion segmentation, which has represented the bottleneck in the research and clinical application of radiomics. Third, numerous well-documented databases are needed to develop and validate the machine learning; as a result, multidisciplinary efforts and multi-centered collaboration are necessary. Additionally, it is of great importance to evaluate the image data quality, since it will directly affect the accuracy of collective image results. On the other hand, the multiple data sources (such as different medical institutions), together with the different data types (like data for multiple imaging parameters), have made it a complex issue to share and centrally manage these data. Besides, results from radiomics research can hardly be compared due to the lack of standardized methods to guide the quantitative image analysis. Therefore, it is necessary to standardize data for different imaging protocols and parameters. Notably, the challenge of the clinical application of radiomics is the standardization of image acquisition schemes, accurate image registration and tumor segmentation. Finally, radiomics is a very large emerging field. Our review mainly introduces readers to the concepts and processes of radiomics and their application in the CNS diseases. More in-depth mechanisms and details of radiomics, as well as applications in other diseases, need to be further elaborated in the future.

6. Conclusions

This review has examined the current use of radiomics for research on CNS diseases; besides, it has also depicted the application of potential futures in clinical oncology. Up to now, radiomics is promising in the prediction of diagnosis, prognosis, as well as the best therapy for CNS diseases; specifically, radiogenomics has made the greatest contributions to bridging the gap of computer-aided prognostics with personalized medicine. In addition, the radiomics foundation for physicians has also been discussed, which has included the general methodology behind such a process. This review aims to assist the neurosurgeon, neurologist as well as radiologists in understanding and appreciating radiomics, and to encourage them to collaborate with the scientists to carry out further study in this field. At the same time, to make full use of the potential of radiomics, radiomics should be combined with other disciplines to carry out interdisciplinary research, continuously enhance the diagnostic innovation of CNS diseases, and improve the accuracy as well as personalized medical care for the entire medical community.

In conclusion, studies on radiomics have advanced the understanding towards CNS diseases through providing information for the better clinical classification and prognosis. As an emerging field, radiomics research in CNS diseases has displayed great prospects and requires further development.

Conflicts of interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

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