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Analysis of Image Quality Values of Signal-to-Noise Ratio (SNR) and Contrast-to-Noise Ratio (CNR) in T1 and T2 MRI Sequences of Brain Tumors

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Abstract

Brain tumors are considered one of the most serious diseases that require accurate diagnosis to determine appropriate treatment strategies. Magnetic Resonance Imaging (MRI) serves as the primary imaging modality, as it provides detailed visualization of brain structures without the use of ionizing radiation. The quality of MRI images can be evaluated using the parameters of Signal to Noise Ratio (SNR) and Contrast to Noise Ratio (CNR), both of which play an essential role in improving diagnostic accuracy. This study aims to determine and compare the SNR and CNR values of brain tumor MRI images in T1- and T2-weighted sequences, as well as to evaluate image quality based on these parameters. MRI data were obtained from publicly available online databases, followed by Region of Interest (ROI) analysis on tumor areas, healthy tissues (including white matter and gray matter), and background. SNR values were calculated as the ratio of the mean signal intensity of an ROI to the standard deviation of noise, while CNR values were calculated as the difference between the mean signal intensities of two ROIs divided by the standard deviation of noise. The Independent T-Test and Mann-Whitney U test were applied to assess differences between the T1- and T2-weighted sequences. The results demonstrated that the mean SNR and CNR values in the T2-weighted sequence were higher compared to those in the T1-weighted sequence, with statistically significant differences ($p < 0.05$). These findings indicate that the T2-weighted sequence has a greater ability to differentiate tissues and provide detailed structural visualization. Therefore, the T2-weighted sequence can be recommended as the primary choice for detailed anatomical evaluation and lesion detection in brain tumor MRI examinations.

Keywords: *Brain tumor; CNR; MRI;, SNR; T1 and T2 sequences*

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INTRODUCTION

Brain tumors represent a critical medical condition that requires prompt and accurate diagnosis to determine appropriate treatment strategies. Among various medical imaging modalities, Magnetic Resonance Imaging (MRI) is widely regarded as the preferred technique for brain tumor evaluation because of its superior soft-tissue contrast and high-resolution imaging

capability without ionizing radiation [1–3]. In clinical practice, MRI image quality plays an essential role in accurately identifying lesion location, size, and boundaries. Quantitative parameters such as Signal-to-Noise Ratio (SNR) and Contrast-to-Noise Ratio (CNR) are commonly used to evaluate MRI image quality, where SNR reflects signal strength relative to background noise, while CNR measures the ability to distinguish tissues with different intensity characteristics [4,5].

MRI technology provides various imaging sequences to highlight specific tissue properties. T1-weighted sequences are generally effective for anatomical visualization and differentiation between white and gray matter, whereas T2-weighted sequences are more sensitive to fluid accumulation and edema in peritumoral regions [6]. Previous studies have investigated the influence of acquisition parameters such as Repetition Time (TR) and Echo Time (TE) on MRI image quality. Arty et al. [7] evaluated the effect of TR and TE variations on SNR values using phantom models containing dimethyl silicone fluid and gadolinium, while Pratiwi et al. [8] analyzed TE variation effects on lumbar MRI image quality based on SNR and CNR measurements using a Philips 1.5 Tesla MRI system. Their findings demonstrated that MRI image quality is strongly influenced by acquisition conditions and sequence parameter settings. However, most existing studies were conducted using phantom models or non-cerebral anatomical regions and did not specifically compare T1- and T2-weighted sequences in brain tumor imaging.

Although several studies have examined MRI image quality quantitatively [9], limited research has directly compared the performance of T1- and T2-weighted sequences using real clinical brain tumor data. To address this gap, the present study applies a Region of Interest (ROI)-based analysis on brain tumor MRI images from the BraTS 2020 dataset using Python-based computational methods to calculate SNR and CNR values objectively. The novelty of this study lies in integrating computational analysis with clinical MRI data to quantitatively compare imaging sequences and provide a more objective basis for determining the optimal sequence for brain tumor assessment [10].

This study aims to quantitatively determine the Signal-to-Noise Ratio (SNR) and Contrast-to-Noise Ratio (CNR) in brain tumor MRI images acquired using T1- and T2-weighted sequences, and to compare the image quality produced by these two sequences. Specifically, the research seeks to address the following questions: what are the quantitative SNR and CNR values in T1- and T2-weighted MRI images, and how does the image quality differ between these sequences based on SNR and CNR analysis? The findings of this study are expected to contribute to the optimization of MRI sequence selection in brain tumor diagnosis and serve as a reference for the advancement of computational approaches in quantitative image quality analysis within the field of medical physics.

METHOD

Research Design

This study adopts a quantitative approach employing a descriptive-comparative method. The primary objective is to analyze and compare the Signal-to-Noise Ratio (SNR) and Contrast-to-Noise Ratio (CNR) values between two MRI sequences—T1-weighted and T2-weighted—in brain tumor imaging. The research does not directly involve human subjects but utilizes secondary data in the form of MRI images obtained from an online database. Computational analysis was conducted using the Python programming language to ensure transparency, reproducibility, and methodological consistency, allowing other researchers to replicate the image processing and quantitative evaluation procedures [11].

Data Source

The data utilized in this study were obtained from the BraTS 2020 (Brain Tumor Segmentation Challenge) dataset, which is publicly accessible via the Kaggle platform (www.kaggle.com). This dataset comprises MRI scans of patients diagnosed with brain tumors, categorized according to imaging sequence types, including T1-weighted and T2-weighted sequences. Each image is provided in the Neuroimaging Informatics Technology Initiative (NIfTI) format with a *.nii* file extension. A total of 40 images were analyzed in this study, consisting of 20 T1-weighted and 20 T2-weighted images. The data were randomly selected from the dataset based on consistent spatial resolution and voxel size criteria to ensure uniformity and reliability in the subsequent quantitative analysis.

Research Procedure

The research procedure was conducted systematically, encompassing several key stages: data collection, image pre-processing, Region of Interest (ROI) determination, and quantitative computation of SNR and CNR values. This study was conducted in a systematic manner, encompassing the stages from data collection to statistical analysis. All MRI data were obtained in *.nii* format from the BraTS 2020 dataset and subsequently converted into *.png* format using the Nibabel and Matplotlib libraries in Python. During the conversion process, the relative intensity distribution of the original MRI data was preserved to ensure that no significant alteration occurred in pixel intensity values. Intensity normalization was applied consistently across all images before saving them into .png format, thereby maintaining the reliability of subsequent SNR and CNR calculations. Each image was visually inspected to ensure the absence of major artifacts or image degradation that could affect the analysis quality.

The next stage involved the determination of the Region of Interest (ROI) using a manual masking approach, in which circular ROIs were placed in three main regions: the tumor area, normal tissue (white matter and gray matter), and the background area, which served as the reference for noise estimation. Circular ROIs of consistent size were manually positioned at the central and most homogeneous part of each target region to minimize partial volume effects. The tumor ROI was placed within the solid tumor component while avoiding necrotic, cystic, or hemorrhagic areas. The normal tissue ROI was positioned in visually homogeneous white matter regions contralateral to the tumor and free from visible abnormalities. All ROI placements were performed by the same observer using identical selection criteria across all MRI images to maintain consistency and reproducibility.The background ROI for noise estimation was manually positioned in a homogeneous dark region outside the brain anatomy where no visible tissue signal was present, thereby minimizing contamination from anatomical structures and imaging artifacts. The selected background regions were visually inspected to ensure uniform intensity distribution and the absence of residual signal contributions. In addition, the size and placement criteria of the background ROI were consistently maintained across all MRI images to ensure measurement reliability and comparability. ROI determination was performed using a Python-based program developed with the OpenCV and Matplotlib libraries [12].

After defining the ROIs, the Signal-to-Noise Ratio (SNR) was computed using the equation (1) [13–16]. The representative signal intensity for each ROI was calculated using the mean intensity value of all pixels contained within the ROI, rather than using the highest sampled intensity value. This approach was adopted to provide a more representative measurement of tissue signal

characteristics and to minimize potential bias in SNR and CNR estimation, consistent with standard MRI quantitative analysis methods reported in previous studies.

$$SNR = \frac{\varphi_{signal}}{\sigma_{noise}} \quad (1)$$

where φ is the average signal intensity in the ROI and σ is the standard deviation of noise taken from the background ROI [4]. Next, the Contrast to Noise Ratio (CNR) is calculated from the difference in average intensity of the two ROIs (tumor and healthy tissue) to the standard deviation of noise using equation (2) [16,17]:

$$CNR = \left|\frac{\varphi_1 - \varphi_2}{\sigma_{noise}}\right| \quad (2)$$

The calculation of both parameters was automated using Python scripts to ensure result consistency and minimize potential human error. All computed SNR and CNR values were subsequently exported to Microsoft Excel for verification and preliminary visualization. The finalized data served as the basis for statistical testing and comparative analysis between the T1- and T2-weighted MRI sequences [18].

Data Collection Techniques

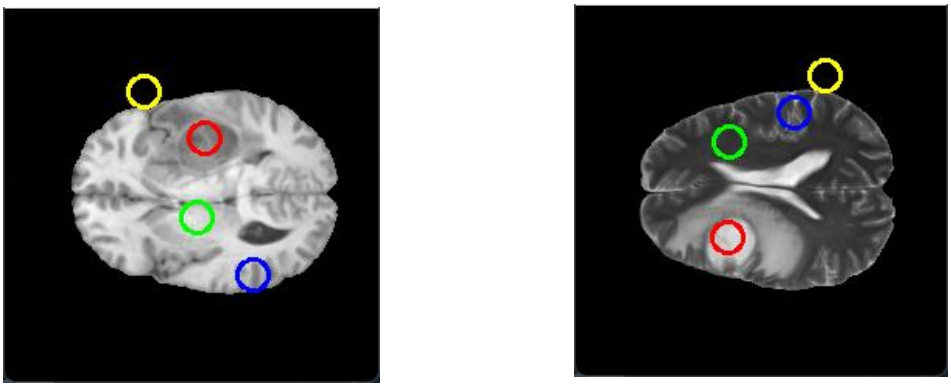
Data collection was conducted using a controlled digital observation method, wherein each MRI image was treated as an independent unit of analysis. The collection process involved no alteration or intervention in the original dataset but was entirely based on software-driven analysis. All computational procedures were executed on a laptop equipped with an AMD Ryzen 5-7520U (2.8 GHz) processor, 8 GB of RAM, and the Windows 11 operating system. To ensure transparency and reproducibility, all processing steps were systematically documented and stored in a Python-generated log file.

Data Analysis Techniques

Data analysis was carried out in two stages: descriptive analysis and inferential statistical analysis. The descriptive analysis aimed to summarize the distribution of SNR and CNR values for each MRI sequence by calculating the mean, standard deviation, minimum, and maximum values. Subsequently, the Shapiro–Wilk normality test was conducted to evaluate the data distribution. Based on the outcomes of this test, statistical analyses were performed using two distinct approaches tailored to the data characteristics. For normally distributed data, the parametric Independent t-test was employed to assess differences in the mean SNR and CNR values between the T1- and T2-weighted sequences [7]. Conversely, for non-normally distributed data, the nonparametric Mann–Whitney U test was utilized, as it does not rely on assumptions of normality [8]. This analytical framework ensured that the comparative evaluation between the two MRI sequences was conducted objectively and supported by statistically valid evidence.

RESULTS AND DISCUSSION

This study generated quantitative data in the form of Signal-to-Noise Ratio (SNR) and Contrast-to-Noise Ratio (CNR) values derived from 40 brain tumor MRI images, comprising 20 T1-weighted and 20 T2-weighted sequence images. The analysis was conducted using the Python programming language through a Region of Interest (ROI)-based approach to ensure objective and reproducible quantitative evaluation of image quality. The ROI process image on the brain tumor image is shown in Figure 1.



(a) (b)

Figure 1. ROI on MRI Images of Brain Tumors on T1 and T2 Sequences.

Figure 1 illustrates an example of Region of Interest (ROI) determination on brain MRI images with tumors for sequences (a) T1-weighted and (b) T2-weighted. Each colored circle represents differences in signal intensity values. The red circle indicates the signal intensity in the tumor region, the green circle corresponds to the white matter, the blue circle represents the gray matter, and the yellow circle marks the background area at the back of the head, which is used as a reference for noise estimation in the form of a standard deviation value [19]. For the ROIs corresponding to the tumor, white matter, and gray matter, signal intensity measurements were taken at five distinct points, and the highest intensity value among them was selected as the representative ROI value for that region [20]. After ROI analysis was performed and the intensity values for each region were obtained, the Signal-to-Noise Ratio (SNR) was calculated using Equation (1). The SNR was determined for ROIs located in both the tumor and white matter regions, resulting in two SNR values per image corresponding to each anatomical area. These SNR values were employed to assess image quality, reflecting each sequence's capability to differentiate distinct tissue characteristics. Subsequently, the Contrast-to-Noise Ratio (CNR) was calculated using Equation (2), based on the previously extracted ROI intensity values.

The analysis results indicate a significant variation in signal and noise values between the two sequences. Overall, the T2-weighted sequence tends to produce higher SNR and CNR values compared to the T1-weighted sequence.

Table 1. Average SNR and CNR values in each area of the T1 and T2 sequences.

Sequences	SNR			CNR	
	SNR Tumor	**SNR *White matter***	**SNR *Gray matter***	**CNR Tumor - *White matter***	**CNR Tumor - *Gray matter***
T1	35.45	52.53	43.04	17.08	8.09
T2	57.64	20.47	28.35	37.17	29.29

Based on Table 1, it can be observed that in the T1-weighted sequence, the average SNR value in the tumor region is relatively lower (35.45) compared to that in the white matter and gray matter regions. The CNR values between the tumor and healthy tissues also exhibit noticeable variation. In contrast, the T2-weighted sequence demonstrates consistently higher SNR and CNR values, both within the tumor area and in terms of contrast against surrounding healthy tissues. These findings indicate that the T2-weighted sequence generally produces stronger signal intensities in lesions or edema regions, enhancing the visibility of pathological abnormalities[21–23].

After obtaining the SNR and CNR values for each imaging sequence, the next step was to perform a normality test on the collected data. In this study, the Shapiro–Wilk test was employed, as it is generally recommended for small sample sizes (fewer than 50) [24]. The results of the Shapiro–Wilk normality test indicate that the data distribution across all groups is not uniform. Several data groups exhibited a normal distribution, including SNR Tumor T2, SNR White Matter T1 and T2, SNR Gray Matter T1, CNR Tumor–White Matter T1, and CNR Tumor–Gray Matter T1, with *p*-values greater than 0.05. Conversely, some data groups demonstrated a non-normal distribution, such as SNR Tumor T1, SNR Gray Matter T2, CNR Tumor–White Matter T2, and CNR Tumor–Gray Matter T2, with *p*-values less than 0.05 [18].

These variations in data distribution indicate that the assumption of normality was not fully satisfied across all datasets. The non-uniform distribution pattern has direct implications for selecting the appropriate statistical tests. For data groups with a normal distribution, the parametric Independent Sample t-test was applied to assess mean differences. Meanwhile, for non-normally distributed data, the nonparametric Mann–Whitney U test was used as an alternative [18].

Specifically, the data groups that followed a normal distribution were SNR White Matter in both T1 and T2 sequences, while those that did not follow a normal distribution included SNR Tumor (T1 and T2), SNR Gray Matter (T1 and T2), CNR Tumor–White Matter (T1 and T2), and CNR Tumor–Gray Matter (T1 and T2). The following table presents the results of the statistical comparison tests for each SNR and CNR data group. The result of the normal distribution for all data groups are presented in Table 2.

Table 2. Statistical Test Results on SNR and CNR Data for T1 and T2 Sequences.

Data Group	Statistical Test		*p-value*
	T-*Test*	U-Test	
SNR Tumor Area	-	47.0	3.705×10^{-5}
SNR White Matter	8.74	-	2.46×10^{-9}
SNR Gray Matter	-	351.0	4.68×10^{-5}
CNR Tumor - White Matter	-	33.0	6.67×10^{-6}
CNR Tumor - Gray Matter	-	27	3.06×10^{-6}

Based on Table 2, the analysis results indicate that the differences in SNR and CNR values among the tumor, white matter, and gray matter regions for each sequence exhibit high statistical significance. In the tumor region, the Mann–Whitney U test produced a value of $U = 47.0$ with $p = 3.705 \times 10^{-5}$; in the white matter region, the Independent t-test yielded $t = 8.74$ with $p = 2.46 \times 10^{-9}$; and in the gray matter region, the Mann–Whitney U test resulted in $U = 351.0$ with $p = 4.68 \times 10^{-5}$. These results confirm that the differences in image signal characteristics between tissue types and sequences are statistically significant.

In addition, the Mann–Whitney U test results for the CNR values between the tumor and white matter regions showed $U = 33.0$ with $p = 6.67 \times 10^{-6}$, while between the tumor and gray matter regions, the results were $U = 27.0$ with $p = 3.06 \times 10^{-6}$. All test results showed $p < 0.05$, indicating that there are significant differences in the SNR and CNR values among the tumor, white matter, and gray matter regions in each MRI sequence.

Furthermore, the statistical significance indicated by low p-values (e.g., $p < 10^{-4}$) demonstrates that the observed differences in SNR and CNR are unlikely to have occurred by random noise alone. In diagnostic imaging, such strong significance levels imply that signal variations across tissue types reflect genuine physiological and pathological differences rather than stochastic fluctuations. A lower p-value thus strengthens the reliability of image interpretation, enhancing the diagnostic accuracy in differentiating tumors from healthy tissues. Recent studies have emphasized that high-quality MRI images—with significantly higher SNR and CNR—are associated with improved lesion conspicuity, reduced diagnostic ambiguity, and greater positive predictive value in clinical assessment [25]. Likewise, quantitative MRI models that incorporate statistically validated image quality parameters have been shown to improve preoperative diagnostic performance in tumor classification. Therefore, in this study, the highly significant p-values reinforce that the observed SNR and CNR differences between T1- and T2-weighted sequences are not incidental but reflect systematic variations in image signal behavior—findings that hold important implications for the diagnostic precision of brain tumor imaging [25]. Beyond statistical validation, the differences in SNR and CNR values have direct clinical implications in the interpretation of brain MRI images. Higher SNR and CNR values contribute to improved lesion conspicuity and facilitate accurate delineation of tumor boundaries, peritumoral edema, and necrotic cores. Such improvements in image contrast enable radiologists to better characterize tumor morphology and heterogeneity, which are essential for determining tumor grade and guiding therapeutic interventions. Previous clinical studies have shown that enhanced quantitative image quality correlates strongly with improved diagnostic confidence and lesion detection rates in MRI examinations [26].

These results were then visualized in the form of graphs to illustrate more clearly the differences in SNR and CNR values between the T1 and T2 sequences.

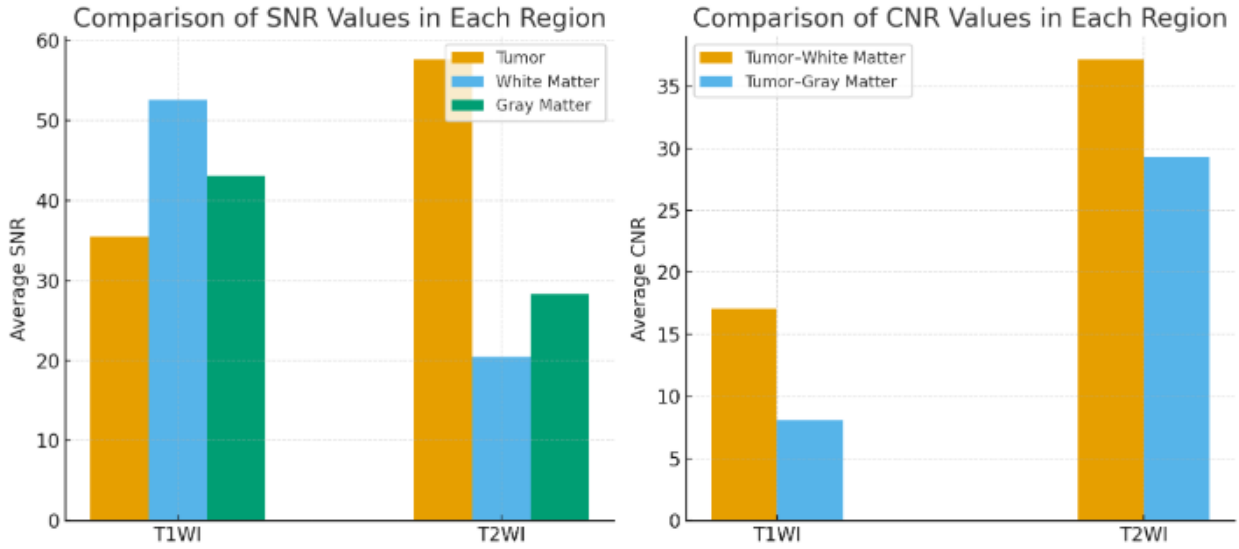


Figure 2. Comparison Chart of Average SNR and CNR Values in Each Area for T1 and T2 Sequences.

Figure 2 illustrates the comparison of mean SNR (left) and CNR (right) values in the tumor, white matter, and gray matter regions for both T1-Weighted (T1WI) and T2-Weighted (T2WI) sequences. In general, it can be observed that the T2WI sequence produces higher SNR and CNR values compared to the T1WI sequence across almost all observed regions.

In the SNR graph, the T2WI sequence shows a significant increase in the tumor region (57.64) compared to T1WI (35.45). This indicates that the T2 sequence has a better capability in capturing the signal intensity of pathological tissues. Conversely, the SNR value in white matter decreases drastically from 52.53 (T1WI) to 20.47 (T2WI), suggesting that the contrast of normal tissue diminishes as sensitivity to water content increases. The SNR value in gray matter also decreases from 43.04 to 28.35. This pattern aligns with spin relaxation theory, in which the T2 sequence emphasizes signal differences in tissues with long transverse relaxation times, such as fluids and pathological tissues, whereas the T1 sequence highlights anatomical structures with shorter longitudinal relaxation times [6]. The variations in SNR and CNR observed between T1- and T2-weighted sequences are also influenced by sequence acquisition parameters, particularly repetition time (TR), echo time (TE), and flip angle. These parameters directly affect the signal amplitude and tissue contrast, thereby modifying the overall image quality. For instance, longer TE values tend to increase the T2-weighted signal from water-rich tissues, while shorter TR values enhance T1 contrast. Studies by Karang et al. [6] have demonstrated that even slight alterations in TR and TE can substantially modify the resultant SNR, highlighting the importance of parameter optimization for diagnostic consistency.

The CNR graph shows a marked increase in the T2WI sequence, both in the contrast between the tumor and white matter (from 17.08 to 37.17) and between the tumor and gray matter (from 8.09 to 29.29). A higher CNR value indicates a stronger ability of the image to distinguish signal intensity differences between two distinct tissues. These findings support the results of Duan et al. [4] and Ningtias et al. [5], who reported that the T2 sequence is more effective in highlighting contrast differences between pathological and normal tissues due to its high sensitivity to water content and edema.

From a diagnostic perspective, these results reinforce the role of the T2 sequence as a superior modality in brain tumor evaluation. The increase in SNR and CNR in the T2 sequence indicates that lesion details, edema boundaries, and internal tumor heterogeneity are more easily identified compared to the T1 sequence [27]. From a physical standpoint, this phenomenon occurs due to the dominance of spin–spin relaxation effects, which enhance signal amplitude in tissues with high water content. The prolonged transverse relaxation time in fluids and edematous tissues allows greater differentiation between normal and pathological regions, making T2-weighted images particularly effective in detecting peritumoral edema and necrotic components. This enhanced contrast sensitivity facilitates a more accurate assessment of tumor extent and morphology, which is critical for preoperative planning and radiotherapy targeting [26–30].

Overall, these findings indicate that the T2-Weighted Imaging (T2WI) sequence provides quantitatively superior image quality for the detection and delineation of brain tumors. Thus, the results of this study reinforce the theory that increases in SNR and CNR values are directly proportional to the ability to visualize lesion morphology in MRI images, and are relevant to serve as a basis for optimizing imaging protocols in diagnostic radiology.

CONCLUSION

This study demonstrates that quantitative analysis based on the Signal-to-Noise Ratio (SNR) and Contrast-to-Noise Ratio (CNR) provides a more objective understanding of brain tumor MRI image quality, particularly in differentiating the performance of T1- and T2-weighted sequences. Through a Python-based computational approach and *Region of Interest* (ROI) evaluation, a more

systematic characterization of each sequence's capability in representing tissue contrast and signal intensity was achieved. These findings highlight the relevance of imaging physics parameters as a scientific basis for optimizing clinical MRI protocols and expanding the application of quantitative analysis in medical physics. Nevertheless, this study has several limitations, primarily due to the use of secondary data that lacked complete acquisition parameters such as repetition time (TR), echo time (TE), and flip angle, which restricted the direct evaluation of their physical influence. Furthermore, the semi-manual ROI selection process may introduce subjective variability. Future research should focus on implementing automated segmentation techniques using machine learning and integrating radiomic models to enhance analytical accuracy and efficiency. Scientifically, this study contributes to the development of physics- and computation-based methods for medical image quality assessment, serving as a foundation for future advancements in quantitative imaging, both for improving diagnostic quality and supporting further research in radiology and medical physics.

AUTHOR CONTRIBUTIONS

Ainus Sarlianto was responsible for the conceptualization, data collection, analysis, and manuscript preparation. Ainus Sarlianto, under the supervision of Pratiwi Sri Wardani and Adrianus Inu Natalisanto, jointly performed the validation and interpretation of the results. The overall study design and methodological framework were developed collaboratively by Pratiwi Sri Wardani and Adrianus Inu Natalisanto.

DECLARATION OF COMPETING INTEREST

The authors declare no known financial conflicts of interest or personal relationships that could have influenced the work reported in this manuscript.

DECLARATION OF ETHICS

The authors declare that the research and writing of this manuscript adhere to ethical standards of research and publication, in accordance with scientific principles, and are free from plagiarism.

DECLARATION OF ASSISTIVE TECHNOLOGIES IN THE WRITING PROCCESS

The authors affirm that Generative Artificial Intelligence and other assistive technologies were not excessively utilized in the research and writing processes of this manuscript.

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