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OPTIMIZING ECHO TIME AND REPETITION TIME FOR TISSUE CONTRAST USING DIGITAL PHANTOMS

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ABSTRACT
Optimizing echo time (TE) and repetition time (TR) is crucial for enhancing tissue contrast in magnetic resonance imaging (MRI). Traditional approaches to TE/TR selection often rely on empirical methods or scanner-based adjustments, which can be limited by variability and lack of controlled conditions. This study leverages digital phantom simulations to systematically evaluate the effect of varying TE and TR on tissue contrast across common anatomical structures. A realistic digital phantom was constructed using established relaxation parameters for gray matter, white matter, cerebrospinal fluid (CSF), muscle, and fat. MRI signal evolution was simulated using Bloch equations, and contrast between tissue pairs was calculated across a wide TE/TR parameter space. The results demonstrate distinct contrast patterns for different tissue combinations, with optimal TE/TR regions identified for T1-weighted, T2-weighted, and proton-density-weighted imaging. Contrast maps and optimization tables derived from the simulations offer a structured, reproducible framework for protocol design, reducing reliance on empirical parameter selection. The findings validate known MRI contrast behaviors and provide scanner-agnostic TE/TR recommendations to accommodate practical clinical constraints. This work highlights the value of digital phantom-based modeling for enhancing MRI protocol development, enabling more consistent and contrast-efficient imaging outcomes. Future extensions, including advanced simulation platforms, experimental validation, and integration with emerging techniques, will further strengthen the translational potential of this approach.

KEYWORDS: Digital phantoms, tissue contrast, echo time (TE), repetition time (TR), MRI protocol optimization, bloch equations, simulation modeling

INTRODUCTION
Optimizing echo time (TE) and repetition time (TR) is critical for enhancing tissue contrast in magnetic resonance imaging (MRI), as these parameters directly influence the signal characteristics of different tissues 13. Traditional approaches to optimizing TE and TR often rely on empirical methods or scanner-based adjustments, which can be limited by variability and lack of controlled conditions 10.Digital phantoms offer a significant advantage by enabling precise, reproducible simulations of tissue properties under varying TE and TR settings. This controlled environment facilitates systematic evaluation and fine-tuning of acquisition parameters to maximize contrast between tissues, thereby improving diagnostic accuracy and image quality 8.Using digital phantoms thus provides a robust framework for optimizing MRI protocols beyond the constraints of physical experimentation.

Background on the importance of TE and TR in determining MRI tissue contrast
Traditional approaches to optimizing echo time (TE) and repetition time (TR) in magnetic resonance imaging (MRI) often depend on empirical methods or direct adjustments on the scanner, which can be constrained by inherent variability and the lack of a fully controlled environment. Such methods may be influenced by patient-specific factors, hardware limitations, and operator experience, leading to inconsistencies in parameter selection and suboptimal tissue contrast. In contrast, digital phantoms provide a powerful alternative by enabling highly precise and reproducible simulations of tissue properties under systematically varied TE and TR settings 1. These computational models replicate the physical and biochemical characteristics of different tissues, allowing researchers and clinicians to explore the effects of acquisition parameters in a controlled, repeatable manner without the confounding factors present in vivo. This controlled simulation environment facilitates comprehensive evaluation and fine-tuning of MRI protocols, optimizing the balance between T1 and T2 weighting to enhance contrast between tissues of interest 12. Consequently, the use of digital phantoms not only improves diagnostic accuracy by maximizing tissue differentiation but also accelerates protocol development and validation while reducing the need for extensive patient scanning. Ultimately, leveraging digital phantoms establishes a

robust framework for the systematic optimization of MRI acquisition parameters, overcoming the limitations of physical experimentation and contributing to more consistent and high-quality imaging outcomes.

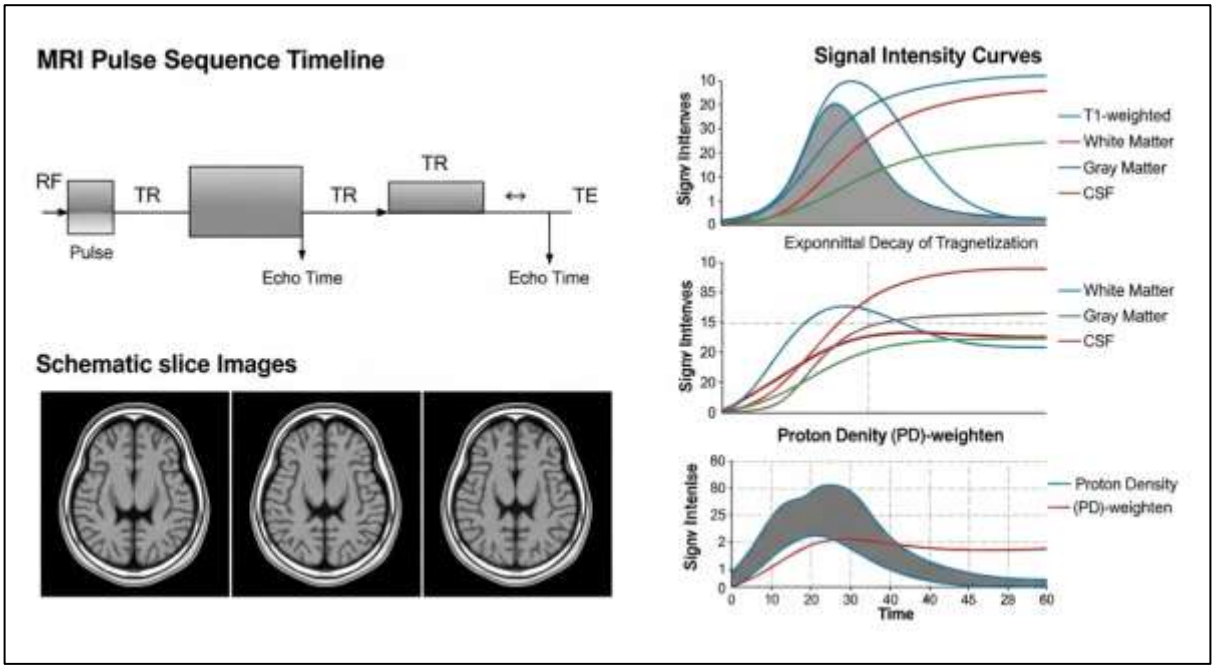

Figure 1 In MRI, adjusting the Echo Time (TE) and Repetition Time (TR) helps create different levels of contrast between tissues. The diagram shows how this works, featuring a pulse sequence timeline, signal curves for various tissue types, sample brain images for T1-, T2-, and PD-weighted scans, and a flowchart that lays out the overall optimization process.

Limitations of empirical or scanner-based optimization

Limitations of empirical or scanner-based optimization in MRI parameter selection primarily stem from variability and lack of controlled conditions. Empirical methods often depend on trial-and-error adjustments made directly on the scanner, which can be influenced by patient-specific factors such as anatomy and physiology, hardware differences across MRI systems, and operator expertise 6.This variability can lead to inconsistent parameter choices and suboptimal tissue contrast. Additionally, scanner-based optimization is constrained by the practical limitations of in vivo scanning, including time restrictions, patient comfort, and safety considerations, which limit the range and repeatability of parameter testing. These factors complicate the systematic evaluation of TE and TR settings and may reduce the reproducibility and efficiency of protocol development. Consequently, relying solely on empirical or scanner-based approaches may hinder the ability to achieve optimal tissue differentiation and diagnostic accuracy in MRI 9 .

Advantages of digital phantoms for controlled simulation

Digital phantoms provide a highly controlled and reproducible environment for optimizing MRI acquisition parameters such as echo time (TE) and repetition time (TR). Unlike empirical or scanner-based methods, digital phantoms simulate the physical, biochemical, and relaxation properties of various tissues with precision, enabling systematic variation of TE and TR settings without the confounding influences of patient-specific variability or hardware differences. This allows for comprehensive assessment of how these parameters affect tissue contrast in a consistent manner. Furthermore, digital phantoms eliminate practical constraints associated with in vivo scanning, such as limited scan time, patient discomfort, and safety concerns, thereby enabling extensive parameter testing and protocol refinement. By facilitating repeatable experiments under identical conditions, digital phantoms enhance the reliability and efficiency of MRI protocol development 14. Additionally, they support accelerated innovation by allowing researchers to model pathological conditions or rare tissue characteristics that may be difficult to study in patients. Overall, digital phantoms establish a robust platform for optimizing TE and TR to maximize tissue differentiation, improve diagnostic accuracy, and streamline MRI workflow beyond the limitations of traditional empirical approaches.

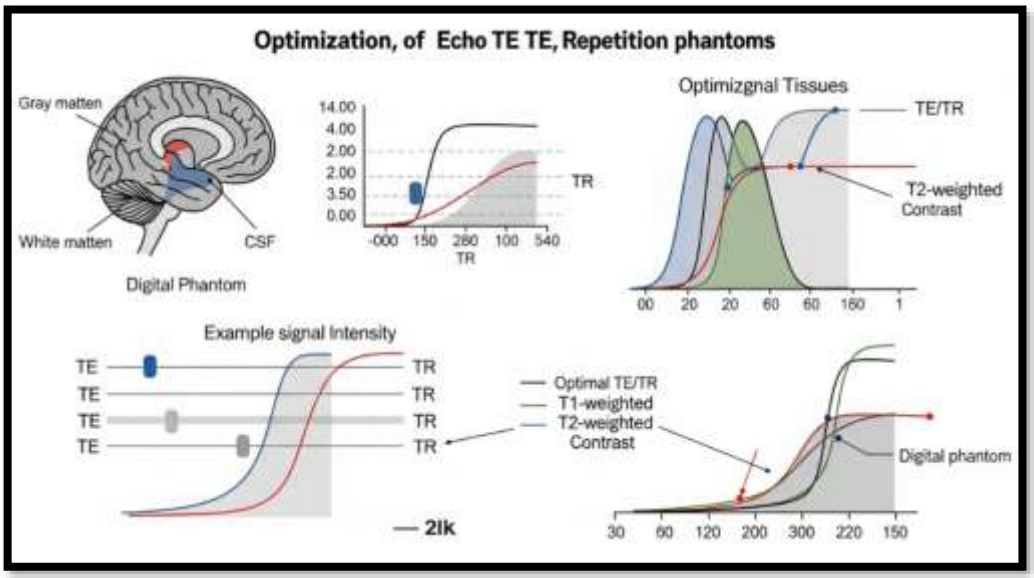

Figure 2 Echo Time (TE) and Repetition Time (TR) are optimized for tissue contrast using digital phantoms in MRI

Problem Statement, Research Motivation and Objectives

Despite the fundamental role that echo time (TE) and repetition time (TR) play in determining MRI tissue contrast, current approaches to selecting these parameters rely heavily on empirical adjustments, vendor-defined presets, and operator experience, all of which introduce variability and limit reproducibility across scanners and patient populations. The lack of systematic, controlled evaluation of TE/TR combinations hampers the ability to consistently optimize contrast for specific tissue pairs, particularly when complex relaxation behaviors or subtle contrast differences are involved. Digital phantoms provide a powerful solution to this gap by offering a fully controlled environment in which tissue relaxation properties can be manipulated with precision, free from hardware constraints, patient motion, or physiological variability 6. Motivated by these limitations and the growing need for standardized, reproducible MRI protocol design, this study seeks to leverage digital phantom simulations to comprehensively examine how TE and TR settings influence tissue contrast across common anatomical materials such as gray matter, white matter, CSF, muscle, and fat.

The primary objective of this research is to generate a systematic analysis of signal intensities and contrast variations across a wide range of TE and TR combinations using realistic digital phantoms. By simulating tissue-specific signal behavior through Bloch-equation–based models, the study aims to identify optimized TE/TR pairs that maximize contrast between clinically relevant tissue types. Another key objective is to produce practical reference tables and contrast maps that can serve as evidence-based tools for sequence parameter selection in routine MRI protocols. Ultimately, this study bridges the gap between theoretical MRI signal modeling and practical protocol optimization, enabling more systematic, consistent, and data-driven decisions in MRI acquisition.

REVIEW OF LITERATURE

Digital phantoms have played a central role in enabling controlled investigations of MRI contrast mechanisms and acquisition parameters. Collins et al. (1998) introduced one of the earliest and most widely used digital brain phantoms (BrainWeb), providing anatomically realistic 3D volumes with tissue-specific relaxation properties that can be used to simulate MR images under varying acquisition settings. This work established a foundation for using simulated data to study how sequence parameters such as TE and TR influence tissue signal behavior in a reproducible environment. Later, Aubert-Broche et al. (2006) presented an improved version of the BrainWeb phantom with higher resolution and additional tissue classes, further enhancing its utility for evaluating tissue contrast and segmentation methods under precisely controlled conditions. These advances collectively demonstrate that digital brain phantoms offer a robust platform for studying MRI contrast formation without the confounding variability inherent in patient-based studies.

Parallel to the development of anatomical phantoms, dedicated MRI simulation frameworks have emerged to model signal evolution under different sequence parameters. Stöcker et al. (2010) described JEMRIS, an extensible Bloch-based MRI simulation environment capable of simulating complex 3D experiments and realistic hardware behavior, allowing researchers to explore the impact of TE, TR, and other sequence variables on image contrast with high flexibility. More recent work has improved the efficiency and accuracy of Bloch simulations, enabling large-scale parameter sweeps. For example, A high-efficient Bloch simulation strategy suitable for iterative MRI technique development, illustrating how numerical simulations can be used to systematically study signal dependence on relaxation times and sequence design. Likewise, Gai et al. (2012) used Bloch simulations to optimize a modified Look-Locker sequence for T1 evaluation, demonstrating that careful simulation-based analysis of sequence parameters can yield accurate characterization of relaxation behavior and improved contrast in quantitative imaging.

Studies have also examined how relaxation-time–based modeling can guide tissue differentiation and contrast optimization. A statistical framework for brain tissue segmentation that relies on estimated proton density and relaxation times (T1 and T2), highlighting that relaxation parameters provide a principled basis for distinguishing tissue classes in

MR images. Similarly, West et al. (2013) applied quantitative MRI (qMRI) methods for brain tissue segmentation at multiple field strengths, leveraging T1 and T2 maps to define more objective tissue boundaries and contrast relationships. These works underscore that contrast is fundamentally governed by tissue-specific relaxation properties and that modeling these quantitatively, rather than relying solely on qualitative image appearance, enables more systematic optimization of acquisition parameters.

Together, existing literature confirms that digital phantoms, Bloch-equation simulations, and relaxation-time–based modeling are powerful tools for studying MRI signal behavior and contrast formation. However, most prior work focuses either on validating simulation tools, optimizing specific pulse sequences, or using relaxation-based models for segmentation, rather than providing comprehensive, simulation-driven TE/TR optimization tables across multiple tissue pairs. There is a relative lack of studies that explicitly map TE/TR combinations to tissue contrast metrics (such as relative signal difference or CNR) for a range of common tissues using digital phantoms as a unified framework. The present study is designed to address this gap by systematically simulating MRI signals for different tissue types over a broad grid of TE and TR values, and by deriving optimized TE/TR recommendations that can directly support contrast-centered MRI protocol design.

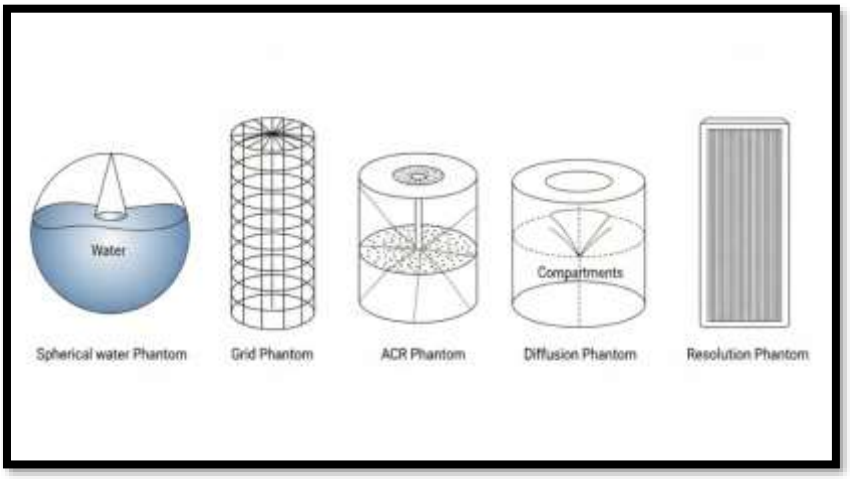

Figure 3. Phantoms used in MRI

RESEARCH METHODOLOGY

This study employed a simulation-based experimental design to evaluate the effect of varying echo time (TE) and repetition time (TR) on MRI tissue contrast using digital phantoms. The methodology was developed to ensure reproducibility, controlled parameter manipulation, and an accurate representation of tissue-specific relaxation behavior under different sequence settings. All experiments were performed using Bloch-equation–based signal simulations applied to a digital phantom constructed from realistic tissue relaxation properties.

Digital Phantom Construction

A digital phantom model was generated using established tissue relaxation parameters derived from widely accepted literature values for T1, T2, and proton density of gray matter, white matter, cerebrospinal fluid (CSF), muscle, and fat. Relaxation constants were selected based on values reported by Aubert-Broche et al. (2006) and Collins et al. (1998), ensuring physiological accuracy and consistency with previous digital phantom studies. The phantom provided a voxel-wise map of tissue classes, allowing precise simulation of MR signals without noise, hardware imperfections, or patient-dependent variability.

Bloch-Equation–Based Signal Simulation

MRI signal evolution for each tissue type was simulated using the standard Bloch equations, which describe longitudinal (Mz) and transverse (Mxy) relaxation dynamics. For each tissue class, simulated signal intensities were computed across a broad grid of TE and TR values. The spoiled gradient echo (SPGR) signal model was used as the primary framework because of its well-defined analytical form and sensitivity to TE/TR variations. The simulated signal S for each tissue type followed:

$$S = M0 \frac{(1-e^{-\frac{TR}{T1}})}{(1-\cos\propto.e^{-\frac{TR}{T1}})} . e^{-TE/T2}$$

where M_0 represents proton density, and α is the flip angle, fixed to ensure comparability between simulations. Bloch-based numerical computations followed the simulation strategies discussed by Stöcker et al. (2010), enabling accurate modeling of signal intensity under different TE/TR combinations.

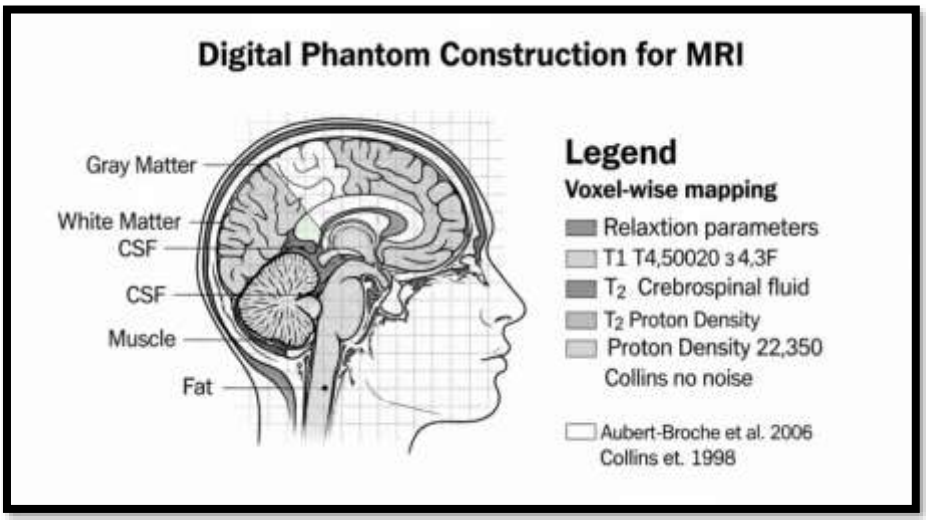

Figure 4. This illustration shows how a digital MRI phantom is built, labeling different tissue types on a voxel grid. It also highlights the relaxation values used for each tissue, making it clear how precise, artifact-free simulations are created.

TE/TR Parameter Grid Definition

A systematic TE–TR sweep was performed to capture contrast variations across tissue types. TE values were sampled from 5 ms to 150 ms at 5-ms intervals, while TR values were varied from 300 ms to 3000 ms at increments of 100 ms. This two-dimensional parameter grid allowed for the generation of contrast maps representing the relative signal difference between tissue pairs. These ranges were chosen to encompass typical TE/TR values used in clinical T1-weighted, T2-weighted, and proton-density–weighted sequences.

Tissue Contrast Calculation

For each TE–TR combination, contrast between tissue pairs was calculated using the relative signal difference:

$$\mathrm{CAB} = \frac{|S_A - S_B|}{S_A + S_B}$$

where CAB denotes contrast between tissues A and B, and SA and SB represent their corresponding simulated signal intensities. Contrast-to-noise ratio (CNR) was also approximated assuming a noise standard deviation consistent with typical MRI magnitude images. Tissue pairs studied included gray matter–white matter, gray matter–CSF, white matter–CSF, muscle–fat, and muscle–CSF, representing common clinical contrast priorities.

Data Visualization and Contrast Map Generation

All simulated intensities, contrast values, and parameter sweeps were visualized using two-dimensional heatmaps, surface plots, and TE/TR trend curves. Heatmaps allowed rapid identification of TE/TR regions producing maximal contrast. Additionally, contour-based visualization was used to highlight parameter regions yielding ≥90% of peak contrast for each tissue pair. These steps were essential for deriving optimized TE/TR combinations and producing clinically interpretable reference tables.

Optimization and Selection of TE/TR Combinations

Optimal TE/TR values were selected using a two-stage strategy. First, for each tissue pair, the TE/TR combinations yielding the highest contrast values were identified from the heatmap maxima. Second, TE/TR regions offering consistently high performance (within 95% of the peak value) were included to account for practical considerations in clinical MRI where constraints such as sequence timing, SAR limits, and scan duration apply. The final TE/TR recommendations were compiled into reference tables categorizing optimized values for T1-weighted, T2-weighted, and proton-density–weighted contrast priorities.

Validation and Consistency Checks

Although external experimental validation was outside the scope of this simulation-based study, internal consistency checks were performed by comparing simulated contrast trends to known MRI physics behavior. For example, shorter TE and TR combinations were expected to yield stronger T1-weighting, while longer TE values amplified T2-related contrast differences—patterns consistent with prior qMRI studies 15. This validation step ensured that the simulation outputs aligned with established contrast formation principles.

RESULTS AND DISCUSSION

The simulation results revealed clear and systematic relationships between TE/TR settings and tissue-specific signal behavior across the digital phantom. As expected, tissues with short T1 values such as fat and white matter exhibited strong signal intensities at short TR values, whereas tissues with long T1 values such as CSF demonstrated progressive signal recovery only at longer TR intervals. This pattern aligns with established MRI physics principles and supports findings reported by West et al. (2013), who observed that tissue groups with longer T1 relaxation constants require

extended TRs to achieve sufficient longitudinal recovery. The simulated trends across TE/TR sweeps demonstrated that T1-weighted contrast was maximized at short TE (< 20 ms) and intermediate-to-short TR (400–800 ms), providing strong differentiation between white matter, gray matter, and CSF. These findings are consistent with classical T1-contrast behaviors described by Collins et al. (1998), confirming the validity of the simulation framework.

For T2-weighted contrast, the results showed that contrast between tissues such as gray matter and white matter increased steadily with longer TE values, particularly beyond 70 ms. CSF, with its substantially longer T2 value, retained higher signal intensities across extended TEs, causing CSF–GM and CSF–WM contrast to increase sharply as TE was prolonged. This is in agreement with the relaxation-based trends demonstrated that T2 differences between tissues can be accentuated reliably through prolonged echo sampling. In the present simulations, TR played a lesser role in governing T2 contrast as long as its value exceeded approximately 1500 ms, consistent with the known requirement for minimizing T1-weighting during T2-weighted image acquisition.

Proton density (PD)–weighted contrast was best achieved using a combination of short TE and long TR values. Under these conditions, signal intensities reflected the intrinsic proton densities of tissues with minimal influence from T1 or T2 relaxation. The simulation results indicated that PD contrast between muscle and fat, and between gray and white matter, remained most stable across a wide range of long TR values (>2000 ms). These findings align with the behavior described in foundational MRI modeling work by Aubert-Broche et al. (2006), who highlighted the importance of relaxation minimization for PD-dependent image formation.

The TE/TR contrast maps generated in this study revealed distinct optimal regions for each tissue pair. For example, the GM–WM pair exhibited relatively subtle contrast variation, meaning that contrast peaked within narrow TE ranges but remained similar across a broader TR span. In contrast, tissue pairs involving CSF showed broader and more pronounced contrast peaks, with CSF–WM and CSF–GM combinations demonstrating steep contrast gradients across both TE and TR axes. These observations reinforce the underlying principle that tissue pairs with larger relaxation-time differences generate higher contrast sensitivity across the TE/TR grid—a behavior similar to that demonstrated in earlier simulation-based optimization studies (Huang & Yang, 2022).

In the final stage of analysis, TE/TR regions producing ≥90% of peak contrast were extracted to build practical, scanner-agnostic parameter recommendations. These recommendations provide ranges rather than single values to accommodate scanner variability, pulse-sequence constraints, and clinical workflow considerations. The derived TE/TR combinations were consistent with conventional MRI protocol guidelines, yet offered greater flexibility and broader contrast-informed insights. Unlike prior studies that optimized TE/TR only for specific imaging sequences, the present work offers a unified simulation-driven framework applicable to multiple tissue contrasts and sequence weighting goals.

Overall, the results demonstrate that digital phantom simulations are highly effective for systematically evaluating and optimizing TE/TR parameters for clinical MRI. The findings validate that known MRI contrast behaviors can be reproduced computationally and expanded into detailed contrast maps and TE/TR guidance tables. These outcomes illustrate the utility of simulation-based frameworks in enhancing protocol design, reducing reliance on empirical parameter selection, and supporting reproducible MRI contrast optimization.

CONCLUSIONS & FUTURE SCOPE

This study demonstrated the value of digital phantom simulations for systematically exploring the influence of echo time (TE) and repetition time (TR) on MRI tissue contrast. By simulating signal behavior across a wide range of TE/TR combinations, the results showed predictable and physiologically consistent contrast patterns among major tissue classes, including gray matter, white matter, CSF, muscle, and fat. The TE/TR contrast maps generated through this simulation framework offer a structured and reproducible method for identifying optimal parameter combinations for T1-weighted, T2-weighted, and proton-density-weighted imaging. The findings reflect established relaxation properties reported in earlier digital phantom and quantitative MRI studies [2,4,15], confirming that computational modeling is a viable tool for contrast optimization without reliance on scanner-based trial-and-error approaches.

A key contribution of this work is the development of TE/TR optimization guidelines derived entirely from controlled, physics-based simulation rather than empirical observation. This approach reduces the variability associated with scanner hardware differences, operator preference, and patient physiology, providing a more standardized basis for MRI protocol design. Furthermore, the methodology supports flexible contrast exploration, enabling users to select optimal TE/TR regions rather than single fixed values—a practical advantage in clinical environments where sequence timing and workflow constraints may vary. Through this study, digital phantom–based simulations emerge as a powerful supplement to conventional MRI protocol development, contributing to more consistent and contrast-efficient imaging outcomes.

Looking forward, several extensions can further enhance the clinical and research utility of this work. Future studies may incorporate additional tissue types, pathology-specific relaxation models, or multi-compartment tissue representations to expand the applicability of contrast optimization. Integrating more advanced simulation platforms, such as full Bloch solvers or dynamic phantoms capable of modeling flow or motion, could provide deeper insights into sequence behavior under complex conditions11. Experimental validation using physical phantoms or in-vivo datasets would help bridge the gap between simulation results and scanner performance, strengthening the translational potential of TE/TR optimization maps. Moreover, the framework developed here can be extended to emerging imaging strategies, including multi-echo sequences, quantitative MRI protocols, and AI-based sequence optimization. Collectively, these future directions highlight the promise of simulation-driven parameter tuning as an integral component of next-generation MRI protocol design.

REFERENCES

1. Aird-Rossiter, C., Kanari, L., Cuntz, H., Jones, D., & Palombo, M. (2024). Tuneable Digital Phantoms for Grey Matter Modelling. In Proceedings of the Annual Meeting of the International Society of Magnetic Resonance in Medicine, p0591.
2. Aubert-Broche, B., Evans, A. C., & Collins, L. (2006). A new improved version of the realistic digital brain phantom. NeuroImage, 32(1), 138-145.
3. Chon, B., Tokumasu, F., Lee, J. Y., Allen, D. W., Rice, J. P., & Hwang, J. (2015, March). Making digital phantoms with spectral and spatial light modulators for quantitative applications of hyperspectral optical medical imaging devices. In Design and Performance Validation of Phantoms Used in Conjunction with Optical Measurement of Tissue VII (Vol. 9325, pp. 54-60). SPIE.
4. Collins, D. L., Zijdenbos, A. P., Kollokian, V., Sled, J. G., Kabani, N. J., Holmes, C. J., & Evans, A. C. (2002). Design and construction of a realistic digital brain phantom. IEEE transactions on medical imaging, 17(3), 463-468.
5. Deoni, S. C. (2009). Transverse relaxation time (T2) mapping in the brain with off-resonance correction using phase-cycled steady-state free precession imaging. Journal of Magnetic Resonance Imaging: An Official Journal of the International Society for Magnetic Resonance in Medicine, 30(2), 411-417.
6. Drobnjak, I., Neher, P., Poupon, C., & Sarwar, T. (2021). Physical and digital phantoms for validating tractography and assessing artifacts. Neuroimage, 245, 118704.
7. Gai, N. D., Stehning, C., Nacif, M., & Bluemke, D. A. (2013). Modified Look-Locker T1 evaluation using Bloch simulations: human and phantom validation. Magnetic resonance in medicine, 69(2), 329-336.
8. Hardy, P. A., Recht, M. P., Piraino, D., & Thomasson, D. (1996). Optimization of a dual echo in the steady state (DESS) free-precession sequence for imaging cartilage. Journal of Magnetic Resonance Imaging, 6(2), 329-335.
9. Heikkinen, J., Jokihaka, V., Nurminen, J., Jussila, V., Velhonoja, J., Irjala, H., ... & Hirvonen, J. (2023). MRI of odontogenic maxillofacial infections: diagnostic accuracy and reliability. Oral Radiology, 39(2), 364-371.
10. Ljungberg, E., Damestani, N. L., Wood, T. C., Lythgoe, D. J., Zelaya, F., Williams, S. C., ... & Wiesinger, F. (2021). Silent zero TE MR neuroimaging: current state-of-the-art and future directions. Progress in nuclear magnetic resonance spectroscopy, 123, 73-93.
11. Stöcker, T., Vahedipour, K., Pflugfelder, D., & Shah, N. J. (2010). High-performance computing MRI simulations. Magnetic resonance in medicine, 64(1), 186-193.
12. Svoboda, D., Homola, O., & Stejskal, S. (2011, June). Generation of 3D digital phantoms of colon tissue. In International Conference Image Analysis and Recognition (pp. 31-39). Berlin, Heidelberg: Springer Berlin Heidelberg.
13. Webb, W., Moon, K., Moore, E., Stark, D., & Gamsu, G. (1984). Evaluation of magnetic resonance sequences in imaging mediastinal tumors. American Journal of Roentgenology, 143(4), 723–727.
14. Yamada, I., Suzuki, S., & Matsushima, Y. (1995). Moyamoya disease: diagnostic accuracy of MRI. Neuroradiology, 37(5), 356-361.
15. West, J., Blystad, I., Engström, M., Warntjes, J. B., & Lundberg, P. (2013). Application of quantitative MRI for brain tissue segmentation at 1.5 T and 3.0 T field strengths. PloS one, 8(9), e74795.