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RECEIVED 15 December 2023

ACCEPTED 19 December 2023

PUBLISHED 24 January 2024

CITATION

Wang P, Chen W and Gao J (2024),
Editorial: Novel MRI biomarkers.
Front. Phys. 11:1356574.
doi: 10.3389/fphy.2023.1356574

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Editorial: Novel MRI biomarkers

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KEYWORDS

magnetic resonance imaging (MRI), imaging biomarkers, T1rho imaging, chemical exchange saturation transfer (CEST), mDixon MR, chemical exchange-sensitive spin-lock (CESL)

Editorial on the Research Topic
Novel MRI biomarkers

Introduction

Magnetic Resonance Imaging (MRI) has been available for over 40 years and has made great strides in the diagnosis of numerous pathologies. The advancements in MRI methods, pulse sequences, electronics, radiofrequency (RF) coils, and the improved magnetic fields and gradients, have continuously broadened and deepened the applications of MRI and make it the primary imaging assessment tool for many diseases and an important part in management decisions. MRI biomarkers are specific and measurable characteristics obtained from MRI scans, which can include structural, functional, molecular, or quantitative information, offering important insights into biological processes, diseases, or conditions within the body.

The goal of this Research Topic “Novel MRI Biomarkers” was to provide a platform for researchers to share findings and exchange ideas. The articles featured in this Research Topic contributed unique perspectives and innovative approaches to their fields. Here we summarize these articles in this editorial.

T_{1ρ} imaging at ultra-high field

T_{1ρ}, the spin lattice relaxation time in the rotating frame, has been used extensively to probe the relatively slow macromolecular processes, making it a practical tool for gaining information about water spin dynamics and interactions with endogenous macromolecules [1–3]. Studies have indicated that at high static fields (3.0T and beyond), chemical exchange significantly contributes to T_{1ρ} relaxation [4–6]. Therefore, at higher static fields, T_{1ρ} may improve its capability to investigate the content of labile protons associated with macromolecules. The study presented by Liu Y et al. conducted the T_{1ρ} imaging in human brain at ultra-high field (5.0T) and compared the results with 3.0T. They found that there was no significant difference in T_{1ρ} values between 3.0T and 5.0T, but the signal-to-noise ratio (SNR) was significantly improved at 5.0T, indicating the benefits of using 5.0T in investigating neurological disorders. It is worth noting that T_{1ρ} imaging at higher field strengths is prone to image artifacts arising from field inhomogeneities. There have been significant efforts previously to address this Research Topic [7–10]; another Research Topic at higher fields is the high specific absorption rate

(SAR) that potentially prolongs the imaging time. The study showed that both issues were manageable at ultra-high field 5.0T.

Correction of post-irradiation T_1 -relaxation effect in chemical exchange-sensitive MRI

Chemical exchange-sensitive MRI sequences, such as chemical exchange saturation transfer (CEST) or chemical exchange-sensitive spin-lock (CESL), are MRI techniques used to detect and visualize certain molecules or compounds in biological tissues based on their chemical exchange properties [11–14]. Both CEST and CESL techniques have been used in studying biological systems and which can offer insights into various physiological and pathological conditions. In both CEST and CESL, there is a time delay between the irradiation preparation and the imaging acquisition, during which the T_1 -relaxation can reduce the chemical exchange contrast and affect the quantification of such methods. The conventional correction method requires a separate T_1 map scan to compensate for the T_1 -relaxation effect [15], but this approach increases the total imaging time. In the paper by [Chung and Jin](#) a formula was derived from theoretical analysis to compensate for the T_1 -relaxation effect. This proposed method involves post-acquisition correction and holds potential for application in other scenarios, such as multi-slice T_1 -weighted imaging or diffusion-weighted imaging.

Ghost correction for measurements based on multi-band interleaved EPI

Multi-band interleaved EPI (echo-planar imaging) involves the simultaneous excitation of multiple slices in an MRI sequence, allowing for the rapid acquisition of multiple slices in a single imaging volume. This technique improves the speed of image acquisition, enabling faster whole-brain coverage and higher temporal resolution compared to traditional methods. Two-dimensional single-shot EPI (2D-ssEPI) is the typical MRI method used in diffusion and functional MRI because of its rapid acquisition. However, EPI suffers from Nyquist ghost artifacts caused by gradient delay associated with alternating readout polarity [16]. In the study by [Liu et al.](#), a robust 2D Nyquist ghost correction method for multi-band interleaved EPI, without the need for a reference scan and iterative calculation, was proposed. This method demonstrates promise in enhancing multiple imaging biomarkers including DWI, DTI, or multi-shot EPI.

Correction for fat quantification errors in radial multi-echo dixon imaging

Dixon imaging with multi-echo Stack-of-star radial k-space trajectories and golden angle ordering shows promise in fat quantification, specifically the estimation of proton density fat fraction (PDFF). However, imperfections in the gradient chain, such as eddy currents and system delays, might influence radial imaging and distort the estimation of fat fraction. In the work by [Zöllner et al.](#), a retrospective trajectory correction method was proposed. This method, based on a simple gradient modulation transfer function (GMTF) measurement, aims to predict and correct k-space trajectory errors

induced by the gradient chain. The results indicated that the GMTF-based k-space trajectory correction is a rapid alternative to mitigate PDFF quantitation errors caused by the gradient system. The authors validated this method using 3D radial multi-echo gradient-echo acquisitions.

Conclusion

Although a limited number of articles have been received in this Research Topic, each one offers significant insights into technical improvements addressing important Research Topic in clinical application or has important clinical implication. The future of MRI biomarkers holds immense potential. Through ongoing research and technological innovations, we can anticipate the development of even more sophisticated biomarkers that provide unprecedented levels of insight into disease processes. Moreover, the integration of artificial intelligence and machine learning algorithms is poised to further enhance the utility of MRI biomarkers. These technologies will automate data analysis, reduce diagnostic errors, and enable the creation of predictive models for disease progression and treatment response.

Author contributions

PW: Writing—original draft, Writing—review and editing. WC: Writing—original draft, Writing—review and editing. JG: Writing—original draft, Writing—review and editing.

Funding

The author(s) declare that no financial support was received for the research, authorship, and/or publication of this article.

Acknowledgments

We would like to thank all the authors and reviewers who have participated in this Research Topic.

Conflict of interest

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