Multi-contrast Generation and Quantitative Saturation Transfer, Water, and Field Mapping using a Biophysical-Model-Free Vision Transformer (CESTFormer)

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INTRODUCTION: Saturation transfer (ST) MRI has shown promise for characterizing a variety of pathologies, targeting compounds that span a broad portfolio of proton exchange rates (e.g., aliphatic rNOE compared to glutamate-amine). Due to these marked differences, a separate pulse sequence must be acquired for each application of interest, using a specific combination of saturation pulse parameters (such as the B_1 power). As a result, multi-contrast CEST imaging is time-consuming and seldom performed in clinical settings [1]. Recently, imaging techniques combining biophysical models with artificial intelligence (AI) were suggested to accelerate quantitative ST-MRI acquisition and reconstruction [2]. However, the complexity of the multi-proton-pool in-vivo environment and the challenge of accurately modeling a large number of free tissue parameters limit the accuracy of this approach. The goal of this work was to develop a biophysical-model-free technique for automatically generating a wide variety of CEST and semisolid MT image contrasts and quantitative water relaxation, ST, and magnetic field maps from a rapid, non-steady-state-acquired single acquisition protocol.

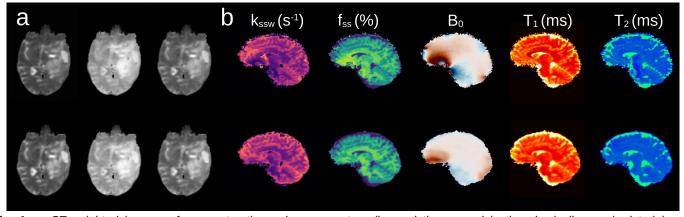


Fig. 1. a. ST-weighted images of new saturation pulse parameters (beyond those used in the physically acquired training data) generated by the proposed framework (bottom) compared to ground truth (top) from a brain tumor patient. **b.** Quantitative semisolid MT, B_0 , T_1 , and T_2 maps generated by the vision transformer (bottom) from rapidly acquired data (28.2 s), compared to ground truth reference (top). The images were acquired using a different scanner model and at a different imaging site than the training data.

METHODS: A two-step AI pipeline was designed to (i) learn the robust human tissue response to the saturation pulse excitation and (ii) exploit it for multi-parameter tissue property mapping. First, a hybrid CNN-Transformer [3] was implemented to receive pairs of pseudo-randomly acquired ST images (amide or semisolid MT) and their associated acquisition parameters. The transformer was trained to perform sequence-to-sequence prediction and accurately generate a new set of contrast-weighted molecular images in response to a user-defined unseen set of acquisition parameters. Next, an expansion of the network was realized for the simultaneous quantification of the semisolid MT volume fraction and exchange rate, water T_1 and T_2 , and T_3 and T_4 and

RESULTS AND DISCUSSION: The Al-generated whole-brain ST contrast-weighted images (**Fig. 1a**, bottom) and the quantitative molecular and water brain maps (**Fig. 1b**, bottom) were visually and perceptually similar to the reference standard output (**Fig. 1**, top). At the same time, the generated B₀ map served as a valuable means for explaining the Al results and noise removal. The acquisition time was accelerated by 94% using the proposed Al pipeline compared to alternative biophysical-model-based MR fingerprinting [2] (30 sec instead of 8.5 min). The reconstruction of fully quantitative maps (**Fig. 1b**) for the whole brain was achieved in less than 10 s. An excellent agreement was obtained between the Al-predicted quantitative brain maps and the ground truth reference (normalized root mean squared error (NRMSE) = 5-8%, peak signal to noise ratio (PSNR) = 24-30, structural similarity index metric (SSIM) = 0.81-0.92).

CONCLUSION: The proposed biophysical-model-free AI approach reduces scan time drastically while retaining the integrity and accuracy of quantitative MRI parameter maps. The suggested framework enables the rapid generation of multi-contrast CEST and semisolid MT images and may be expanded for additional contrast mechanisms.

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