Neural Bloch-McConnell Fitting (NBMF): Physics-Informed Clinical CEST/MT MRF Quantification Network

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INTRODUCTION: Magnetic resonance fingerprinting (MRF)-based quantification of CEST and semi-solid (ss) MT requires a computationally demanding dictionary synthesis and matching[1] or a lengthy supervised neural network (NN) training[2]. Unsupervised learning[3] can circumvent dictionary generation, yet it still requires a lengthy training procedure and is incompatible with pulsed saturation and multi-pool imaging. The goal of this work was to develop a rapid training-set-free ssMT/CEST-MRF reconstruction method, learning directly from the acquired data via clinical-scan-compatible physical modeling and unsupervised learning.

METHODS: An efficient Bloch-McConnell ODE numerical solver was implemented over an auto-differentiation framework, chained to simulate MRF sequences and embedded within a physics-informed self-supervised learning framework, yielding the Neural Bloch-McConnell-Fitting (NBMF) pipeline (**Fig. 1**). Five healthy volunteers were scanned at two imaging sites using a 3D whole-brain ssMT/CEST MRF protocol[4] and their quantitative brain parameter maps were extracted.

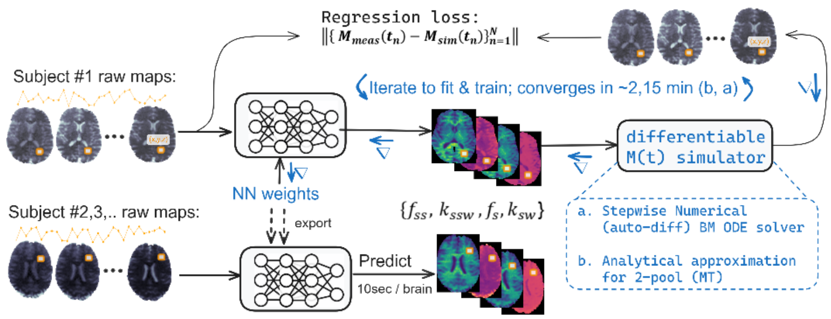

Fig. 1. Neural Bloch-McConnell Fitting (NBMF) pipeline.

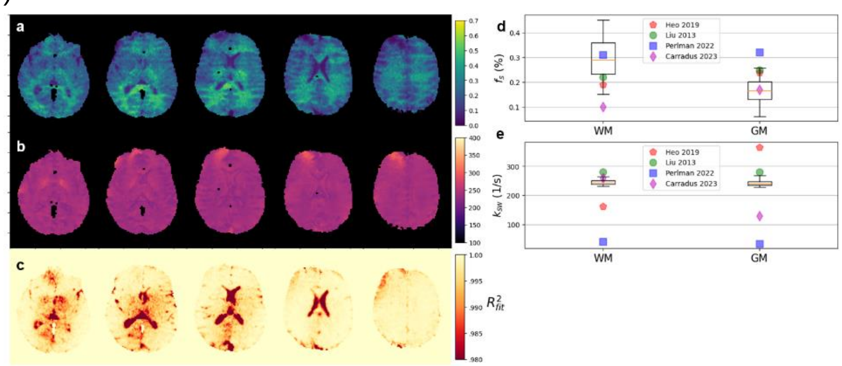

Fig. 2. **(a-b)** Quantitative CEST maps reconstructed using NBMF, alongside the residual error (**c**) and comparison to previous works (**d-e**).

RESULTS: In an amine phantom experiment, NBMF was able to reconstruct the vials' composition with similar fidelity as dictionary matching. In healthy volunteers (**Fig. 2a-c**), NBMF was able to retrieve GM/WM quantitative parameter values for the ssMT and amide in line with literature (**Fig. 2d,e**). The neural reconstructor yielded by NBMF within minutes of joint fitting & training was able to process new unseen subjects in seconds with good consistency, especially for ssMT and amide proton volume fraction quantification.

DISCUSSION: BM fitting-based reconstruction is computationally challenging even for equilibrated Z-spectra and is considered impractical for the 'general case' (non-steady-state, multi-pool pulsed-saturation) required in clinical CEST-MRF. This work presents an auto-diff numeric BM solver that enables rapid fitting for the first time (to the best of our knowledge). The same framework also jointly trains a reusable neural reconstructor, which facilitates a real-time (order of seconds) full-brain quantification when presented with additional subjects and patients.

CONCLUSION: NBMF dramatically accelerates the entire quantitative ssMT/CEST-MRF pipeline towards clinical applications, accelerating the preparation phase per new protocol and replacing dictionary generation, dot-product matching, and neural-network training with a one-stop-shop rapid alternative. The pipeline and specifically the differentiable BM simulator block can easily be modified for fitting conventional multi-B_1 Z-spectra. The innovative use of auto-diff numeric ordinary differential equation (ODE) solver could extend broadly across quantitative imaging modalities and general inverse problems involving fitting an ODE-governed model to experimental data.

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