The Pulseq-CEST Library: Definition of Preparations and Simulations, Example Data, and Example Evaluations

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INTRODUCTION:

Despite the prevalent use of Chemical Exchange Saturation Transfer (CEST) as an advanced MR imaging contrast technique, efforts to standardize methodology remain ongoing.[1] Maintaining consistency across studies is essential, as the individual parameters dictating RF events, gradients, and ADC events can have a heavy impact on the resulting imaging and chemical properties of high signal regions. We present the Pulseq-CEST library (https://github.com/kherz/pulseq-cest-library), a versatile repository of CEST preparation and CEST simulation definitions, to which we now add example data and example evaluation scripts. The Pulseq-CEST library provides a common basis for reproducible CEST research, and also empowers fast prototyping and idea combination, as well as generation of *in silico* training data for deep learning.[2]

METHODS:

A CEST experiment in the pulseq-CEST framework can be comprehensively understood given (i) a CEST-preparation sequence, (ii) a Bloch-McConnell parameter set, (iii) a Bloch-McConnell simulation, and (iv) an evaluation script. Using the Pulseq-CEST library, a candidate sequence or environment can be held constant while changing the other inputs, allowing for robust testing and comparison. To model CEST behavior, Pulseq-CEST utilizes the Bloch-McConnell equations, which describe nuclear magnetization over time in the presence of chemical exchange processes. Proton pool systems with a flexible number of pools mirroring *in vitro* and *in vivo* situations can be given by Bloch-McConnell parameter sets.

RESULTS:

An APTw sequence with 36 Sinc-Gaussian pulses at 3T was used to compare real and simulated data. As shown in Fig. 1, selecting a voxel within a liquid arginine sample at a concentration of approximately 20mM from a five-tube phantom produced similar results to simulated 20mM L-arginine data, matching the anticipated spectra shape and yielding local MTR_{asym} peaks at around +3ppm. The Z-spectrum for the real data also shows a CEST effect. The Pulseq-CEST Library supports similar experiments for common sequences (e.g. WASABI[3]) that can be combined with simulated data (e.g. white matter, arginine, and creatine bmsim.yaml files) to assess newly created protocols and environments.

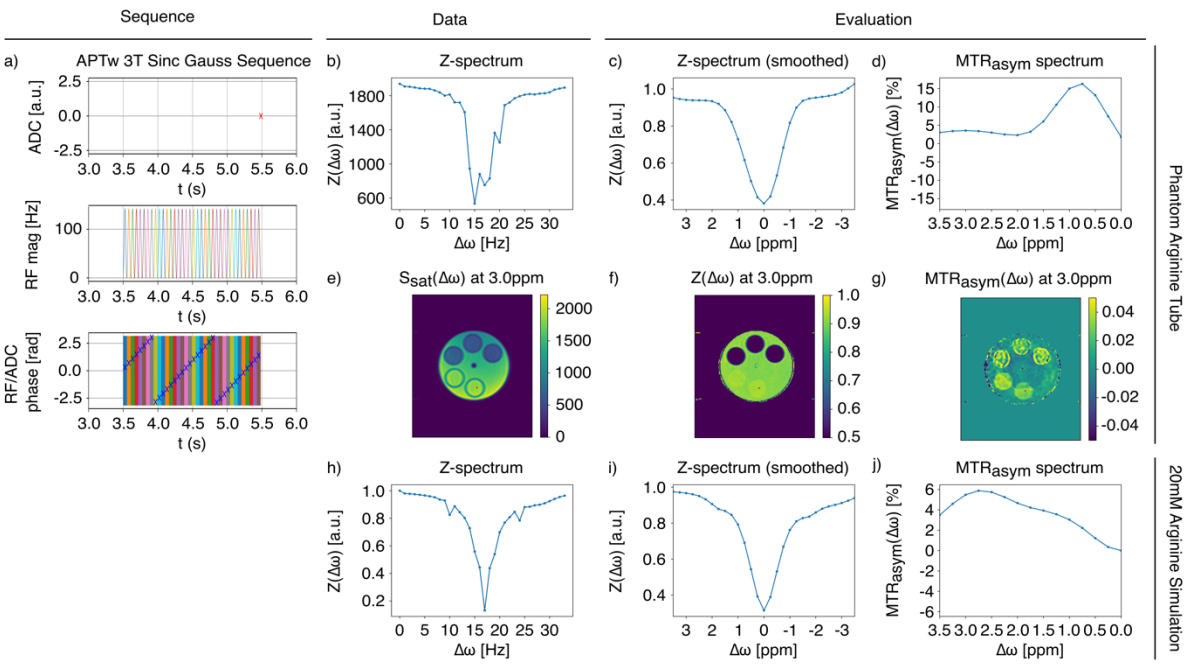

Figure 1. Pulseq-CEST comparison of real (top) and simulated (bottom) arginine data with an APTw 3T Sinc Gauss sequence

DISCUSSION AND CONCLUSION:

The Pulseq-CEST library provides a flexible tool for standardizing and prototyping of CEST sequences. Examples like the Bloch-McConnell simulation (BMsim) challenge,[4] which validated Pulseq-CEST data via an international comparison of 11 different Bloch-McConnell solvers, demonstrate the potential for collaborative development. With the capability for expansion, including the open-source incorporation of new sequences and environments, the Pulseq-CEST library accelerates the invention and spread of new CEST methods.

REFERENCES:

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