An Easy-to-Use CEST-MRF Pulse Sequence and Processing Pipeline for Bruker Preclinical Imaging

David E. Korenchan[1] , Saaussan Madi[2] , Todd Sasser[2], Tim Wokrina[2], and Christian T. Farrar[1]
[1] *Martinos Center for Biomedical Imaging, Mass General Hospital and Harvard Medical School, Charlestown, MA, USA*
[2] *Bruker BioSpin Corporation, Billerica, MA, USA*

INTRODUCTION: Magnetic resonance fingerprinting (**MRF**) offers a powerful means of rapidly quantifying multiple spin system parameters, offering flexibility in spin contrast manipulation and thereby improving parameter accuracy[1]. Combining MRF with chemical exchange saturation transfer (**CEST**) is especially beneficial for disentangling proton concentration from exchange rate and has been applied to *in vitro*, preclinical, and clinical studies[2–5]. Here we present a ready-to-use imaging sequence and processing pipeline for Bruker preclinical scanners that will expand easy access to CEST-MRF imaging.

METHODS: A previous CEST-MRF Bruker method written for Bruker ParaVision 6 was adapted to work with the newer ParaVision 360 software. MATLAB scripts were written to obtain parameter maps (proton density, T_1, T_2, proton volume fraction, exchange rate) and then report statistics (mean, standard deviation) from specified regions of interest (**ROIs**). The MATLAB code was interfaced with Python code to quickly simulate the dictionary and generate parameter maps.

RESULTS: We developed a Bruker imaging method that imports a CEST-MRF schedule from a .txt file, with the desired imaging parameters (number of acquisitions, saturation amplitude + offset + duration, repetition time (**TR**), excitation tip angle) arranged in a columnar format (**Fig. 1**). We also added a feature to perform water-resonant balanced spin-locking[8] rather than saturation when the offset = 0 Hz. For processing, the MATLAB code loads in the raw data from the "2dseq" file and the sequence parameters from the "acqp" and "method" files, then passes these and the desired dictionary simulation parameters to Python to generate the images. The user can then draw regions of interest to calculate statistics (**Fig. 1**). The average time to perform dictionary simulation (12,546,000 entries) and dot-product matching in Python for a CEST-MRF schedule with 31 acquisitions was 11m0s on a 3.2 GHz Apple M1 Max MacBook Pro with 64GB 400GB/s DDR5 memory.

DISCUSSION: The .txt read-in feature makes it very easy to generate and run a desired MRF schedule. Importantly, it also enables the Bruker method to be used for other saturation-based imaging sequences, including Quantification of Exchange *via* Saturation Power (**QUESP**) or Time (**QUEST**)[6] imaging and WAter Saturation Shift Referencing (**WASSR**) for B_0 mapping[7]. Water-resonant spin-locking generates more contrast than saturation when proton exchange is rapid[9], improving MRF quantification. The MATLAB and Python files are publicly available on GitHub (dkorenchan/cest-mrf-image-recon).

CONCLUSION: We have developed a CEST-MRF Bruker method and processing code that facilitates the implementation of MRF for chemical exchange measurement, both *in vitro* and *in vivo*. We anticipate this pulse sequence will enable more preclinical CEST studies for MRF sequence development towards more target molecules, paving the way to developing and validating a wide variety of CEST clinical imaging techniques.

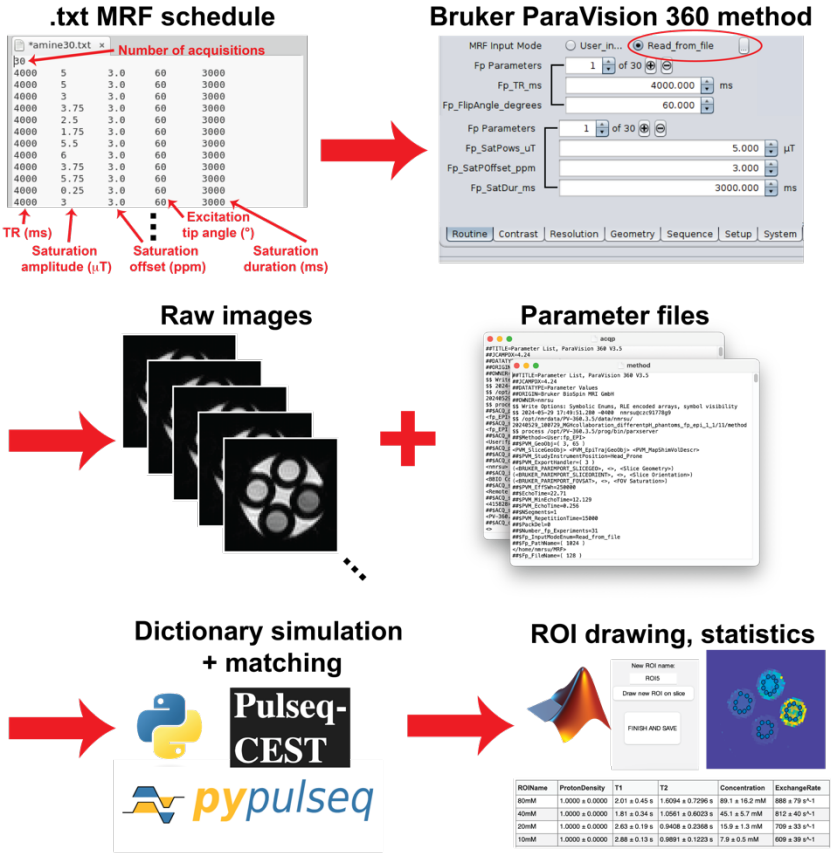

Figure 1. Graphical overview of the new Bruker ParaVision 360 imaging method and processing pipeline.

REFERENCES:
1. Ma D, *et al.* Nature 2013;495(7440):187-192.
2. Cohen O, *et al*. Magn Reson Med 2018;80(6):2449-2463.
3. Perlman O, *et al.* Nat Biomed Eng 2021;6(5):648-657.
4. Perlman O, *et al*. Magn Reson Med 2022;87(6):2792-2810.
5. Cohen O, Otazo R. NMR Biomed May 2023:e4954.
6. McMahon MT, *et al*. Magn Reson Med 2006;55(4):836-847.
7. Kim M, *et al*. Magn Reson Med 2009;61(6):1441-1450.
8. Gram M, *et al*. Magn Reson Med 2021;85(5):2771-2780.
9. Zaiss M, Bachert P. Phys Med Biol 2013;58(22):R221-R269.