

# MRS-Sim: Open-Source Framework for Simulating In Vivo MR Spectroscopy Data

J. T. LaMaster<sup>1</sup>, D. Das<sup>2</sup>, G. Oeltzschner<sup>3</sup>, J. Crane<sup>4</sup>, Y. Li<sup>4</sup>, and B. H. Menze<sup>5</sup>

<sup>1</sup>Technical University of Munich, Faculty of Computer Science, <sup>2</sup>Massachusetts Institute of Technology, <sup>3</sup>Johns Hopkins University, School of Medicine, <sup>4</sup>University of California San Francisco, Center for Intelligent Imaging, <sup>5</sup>University of Zurich, Department of Quantitative Biomedicine

**Background:** Deep learning research for MRS is a budding field with many promising applications. The greatest challenge currently is organizing enough data for deep learning (DL) models. Clinical datasets tend to be very small while DL projects can require 1E5 to 5E5 or more individual samples. Data augmentation eases this problem, but does not alleviate it entirely. A natural solution is to train on inexpensive synthetic data and apply the model to clinical data. This only works if the DL model learns a high-dimensional distribution of the training data that is similar enough to that of the clinical data. Currently this technique fails due to insufficient modeling by standard physics models of spectral components and the variation that arises during acquisition. Additionally, while there are many simulator frameworks for basis sets, there is almost nothing available for clinical data simulation meaning that they must be re-developed individually for every lab.

**Method:** Standard physics models modulate simulated basis lines, apply lorentzian line broadening and gaussian noise, and then a baseline offset. The results more closely approximate the output of a fitting model than clinical data. This framework proposes a much richer physics model, Eqn. 1, that reverse engineers the spectral fitting process. The first step is generating the basis set. This model uses MARSS[1] to simulate the basis sets. The MARSS framework generates very high quality basis lines that accurately capture the 3D nature of voxels in their simulations. Next, the modeling additions for the physics model include modeling Voigt lineshapes, zero- and first-order phase offsets, a frequency shift for metabolites and a second one for lipid and macromolecular signals, a scaling factor, B0 inhomogeneities, and a rich baseline generator. This second generator uses a smoothed, bounded pseudo-random walk function with one set of parameters for the broad, smooth baseline and another set for the more flexible, poorly defined residual water region.

$$F(\omega) = \mathcal{F} \left( e^{i(\phi_0 + \phi_1(\nu_{ref}))} e^{-i\Delta f t} * \left( \sum_n M_n e^{-2i\pi \nu_n t} e^{-t/T_2^*} e^{-i\Phi} * e^{-d_n t} e^{-g_n t^2} e^{-it\Delta\omega} + baseline + \mathcal{H}(\mathcal{N}(0, \text{snr}_0, l)) \right) \right) \quad \text{Eqn. 1}$$

Even for preprocessed spectra, including minimal amounts of these artifacts is important because no method is perfectly able to correct them, therefore, this model more accurately models the distribution of clinical data. The model can be tailored for projects addressing various artifact corrections, spectral fitting, de-noising, or simply pre-training a model with clean, realistic spectra. The ordering of the model's steps means that errors can be quantified at every stage of processing and fitting which allows for detailed error analysis of new algorithms including error propagation. Due to the modularity of the implementation, it is very easy to generate spectra for different nuclei, different applications, and to switch between the 3 major vendors. The current implementation run via command line functions and a .json config file. It is accompanied by a Jupyter notebook manual giving an overview of the model, how to use it, and how to customize the dataset. Default configuration templates are also provided.

## Examples:

**Discussion:** This work presents an open-source framework to simulate clinical MRSI data with the primary goal of facilitating deep learning research for MRS applications. This simulator uses very accurate basis lines and a rich, highly modular physics model. Parameters are sampled to optimize the performance of deep learning models. Datasets can be customized by simply modifying a provided config.json template. This framework will enable groups to explore deep learning research, even with limited clinical data. And similarly to how accurate basis spectra improve spectral fitting, accurate training data improves the performance deep learning models.

## References:

[1] Landheer, K, Swanberg, KM, Juchem, C. Magnetic resonance Spectrum simulator (MARSS), a novel software package for fast and computationally efficient basis set simulation. NMR in Biomedicine. 2021; 34:e4129. <https://doi.org/10.1002/nbm.4129>