

# PulseqDiffusion: PyPulseq implementation of Diffusion-Weighted Echo Planar Imaging

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#### Software

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### Summary

Magnetic Resonance Imaging (MRI) acquisitions consist of a series of radio-frequency and magnetic field gradient pulses. Diffusion-Weighted Imaging (DWI) is a widely used type of MRI pulse sequence providing a key image contrast for clinical brain applications such as stroke imaging (Schellinger et al., 2010).

Developing new acquisition strategies for DWI acquisition typically requires access to and expertise on the programming environment of the MRI vendor; this limitation has been mitigated though the introduction of Pulseq (Layton et al., 2017), an open source file standard for pulse sequences that enables to deploy the exact same protocol on both Siemens/GE via TOPPE (Nielsen & Noll, 2018) and Bruker platforms, and potentially also on in-house built MRI systems. In this work we introduce PulseqDiffusion to enable open-source DWI pulse sequence programming, using PyPulseq (Ravi, Geethanath, & Vaughan, 2019; Ravi et al., 2018), a Python-based implementation of Pulseq (Layton et al., 2017). We have leveraged this tool for published research works (Fernandes, Golub, Freitas, Geethanath, & Nunes, 2020; Nunes, Ravi, Geethanath, & Vaughan, 2020).

#### Statement of need

Multiple freely available open-source image processing tools have been developed for DWI such as MRtrix3 (Tournier et al., 2019), DiPy (Garyfallidis et al., 2014), and dedicated tools in FSL, (Jenkinson, Beckmann, Behrens, Woolrich, & Smith, 2012). However, vendor-neutral open-source acquisition implementations have not been previously shared.

There has been a growing interest in developing open-source solutions for MRI, aiming to improve its accessibility (www.opensourceimaging.org). PulseqDiffusion will allow easier prototyping of DWI sequences and enable cross-vendor comparisons in clinical scanners. We also expect PulseqDiffusion to be a useful starting point for sequence development in the context of accessible low-field stroke imaging (Geethanath & Vaughan Jr., 2019).

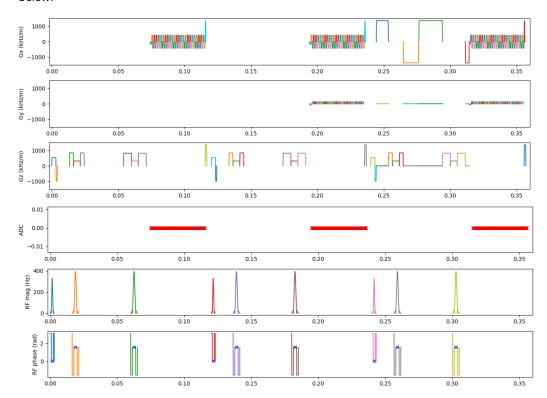
# About PulseqDiffusion

Together with the Python functions required to generate DWI sequences, we provide a tool for simulating the performance of different sequence variants considering a range of hardware



solutions (Fernandes et al., 2020). This tool predicts the signal-to-noise ratio (SNR) observed for different brain tissues (gray matter, white matter, cerebrospinal fluid - CSF) and the contrast-to-noise ratio (CNR) of an acute stroke lesion relative to those tissues, and can be found in the folder SNR\_CNR\_Study. The implemented code predicts the SNR and CNR per time unit for a spin-echo diffusion-weighted sequence, taking into account the steady-state value for the longitudinal magnetization. For that purpose, we adapted an expression used to predict the SNR per tissue per time unit for a spoiled gradient echo sequence (Marques, Simonis, & Webb, 2019). This simulation considers the possibility to use either EPI or spiral readouts and considers the impact of: B0, maximum gradient amplitude, spatial resolution and level of diffusion-weighting (comparing the achieved SNR with that of a typical 1.5T clinical scanner).

We provide Python scripts for generating example diffusion-weighted EPI sequences including single-spin echo preparation (with and without ramp-sampling during signal readout) and a doubly-refocused preparation module (Reese, Heid, Weisskoff, & Wedeen, 2003) as shown below:

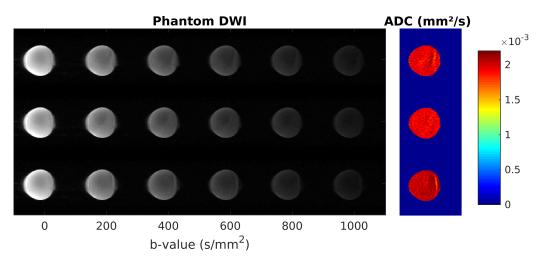


**Figure 1:** Example diffusion-weighted EPI sequence using a twice-refocused preparation module for 1 slice measuring diffusion along the readout direction using a b-value of  $500 \text{ s/mm}^2$ . The gradient waveforms applied along all three directions are shown above while the signal acquisition (ADC) and RF pulse waveforms are shown below.

The sets of diffusion gradient directions considered for pulse sequence implementation were optimised using MRtrix3 (Tournier et al., 2019).

We provide example data as well as Matlab functions for basic ghost correction and partial Fourier Homodyne reconstruction, as well as image processing. Phantom images reconstructed from the provided example k-space data, including five different levels of diffusion-weighting along three orthogonal directions, as well as the corresponding apparent diffusion coefficient (ADC) maps, are displayed:

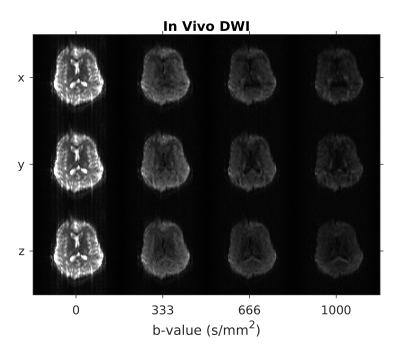




**Figure 2:** Diffusion-weighted images obtained for a doped water bottle phantom including five different levels of diffusion-weighting (200 to 1000 s/mm2) and corresponding ADC maps for three orthogonal directions.

Note that the measured ADC value is within the expected value for water at room temperature (2.0x10-3 mm2/s).

For image processing, we employ widely used open-source software tools, including the matlab toolbox for dealing with Nifti images and FSL, (Jenkinson et al., 2012) for image pre-processing and diffusion tensor estimation. In vivo images reconstructed from the provided k-space data are shown for different levels of diffusion-weighting sampled along three orthogonal directions:

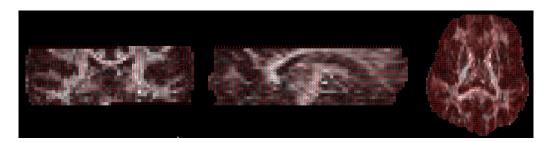


**Figure 3:** In vivo diffusion-weighted images corresponding to different diffusion-weighting levels along three orthogonal directions.

These images and diffusion maps were obtained using the process\_data matlab script (ethics approval from the local IRB and written informed consent were obtained prior to scanning).



The principal eigenvector estimated for a 12 direction in vivo data set provided as example is shown here:



**Figure 4:** Example in vivo data sampling 12 diffusion direction - principal eigenvector field in red overlaying the estimated fractional anisotropy map.

## Target audience

PulseqDiffusion is aimed at MRI researchers focusing on DWI acquisition. We envisage PulseqDiffusion to be used for replicability and reproducibility studies (multi-site, multi-vendor). The package could also serve as a hands-on teaching aid for MRI faculty and students. Users can get started with the example pulse sequences and provided phantom and in vivo data.

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