# A hardware-independent environment for MR acquisition and simulation

Kelvin Layton[1], Stefan Kroboth[1], Jochen Leupold[1], Huijun Yu[1], Feng Jia[1], Sebastian Littin[1], Tony Stöcker[2], and Maxim Zaitsev[1]
[1]*Medical Physics, University Medical Center Freiburg, Freiburg, BW, Germany,* [2]*German Center for Neurodegenerative Diseases, Bonn, NRW, Germany*

**TARGET AUDIENCE** Researchers with an interest in rapid sequence development and prototyping for any hardware platform.

**PURPOSE** Implementation of pulse sequences is an arduous task for students and researchers. Despite extensive development environments provided by MR manufacturers, sequence programming typically involves low-level programming with C, C++ or even custom programming languages. These environments may be suitable to develop product sequences for use in a clinic; however, they often inhibit researchers whose focus is to quickly test new ideas, demonstrate novel physics or compare different sequences. In this work, we present an open, hardware-independent sequence programming environment ideal for rapid prototyping through simulations and measurements.

**METHODS** The key components to our environment, depicted in Fig. 1, include (1) the open-source JEMRIS project[1] for sequence programming and simulation, (2) a new hardware-independent low-level sequence format[2] and (3) hardware-dependent interpreter sequences. **JEMRIS**: The MRI simulator provides a drag-and-drop sequence programming interface. The code was modified to output a low-level sequence file for execution on various hardware platforms. Additionally, hardware constraints such as maximum gradient strength, gradient rise time and maximum $B_1$ amplitude are incorporated into the programming console. **Sequence format**: The new sequence format was developed to be human-readable, compact, vendor independent and low-level. The resulting text file is hierarchical consisting of a timing table, which references 'event' objects, which in turn can reference compressed 'shape' objects. The resulting files contain no loops but a simple list of instructions, moving much logic to the console. This is simpler than existing paradigms and made possible by the increased memory of the microcontroller hardware used in modern scanners. **Interpreter sequence**: The interpreter sequence implements the sequence file on specific hardware. We have currently implemented interpreter sequences for Siemens, Bruker and in-house gradient hardware[3,4]. Each interpreter must account for hardware-specific requirements. For example, the gradient 'raster' time on the Siemens system is 10μs, so gradient pulses must be resampled to this grid such that the area (for phase encoding) or amplitude (for frequency encoding) is preserved.

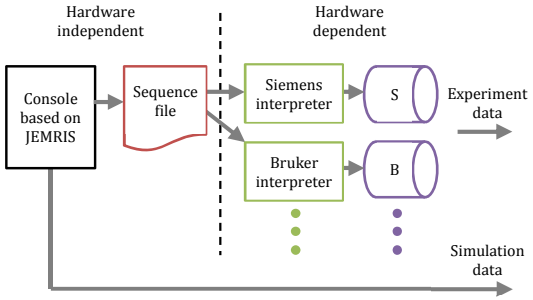


**Fig. 1** Block diagram of the development environment. The (left) JEMRIS-based console can simulate data or generate hardware-independent sequence files, which can be executed by (right) arbitrary hardware platforms to produce experimental data.

**Experiments**: Two experiments were performed to demonstrate the setup. Datasets encoding $T_1$, $T_2$, proton density and $B_0$ inhomogeneity were acquired at a resolution of 256×256 from a contrast phantom using a 3T Siemens scanner. Quantitative maps were obtained by nonlinear fitting to the appropriate signal equation and then interpolated to a resolution of 512×512. These high-resolution maps were used to simulate a 2D spin echo (SE) sequence with FOV=210×210mm, resolution=64×64, $T_E$=15ms, $T_R$=100ms, flip angle=50°, slice thickness=3mm. The simulations are based on the Bloch equations and include arbitrary RF excitation, spin dephasing, relaxation and $B_0$ inhomogeneity to accurately represent the physical environment. The sequence was then executed on the scanner (using the same sequence file) to obtain experimental data for comparison. In a second experiment, we defined a single-slice gradient echo (GRE) sequence with FOV=80×80mm, resolution=256×256, flip angle=20°, slice thickness=3mm. A 60mm phantom containing plastic tubes was measured with a Siemens 3T human scanner and a Bruker 9.4T animal scanner using the same sequence file.

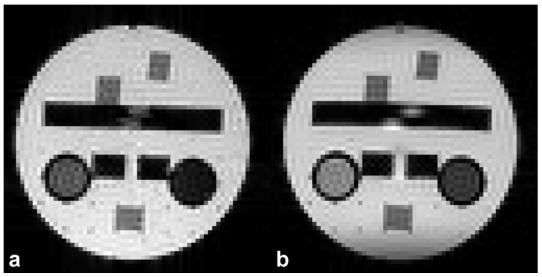


**Fig. 2** Phantom with regions of various $T_1$, $T_2$ and proton density. The same spin-echo sequence file was (a) simulated with the Bloch equations and (b) measured on a Siemens 3T scanner.

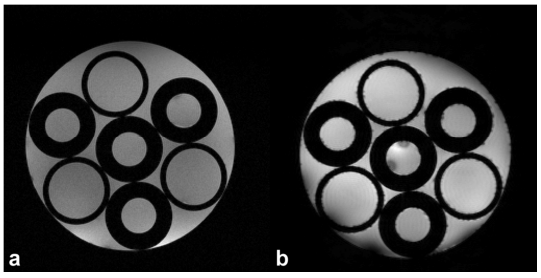


**Fig. 3** Phantom with plastic tubes acquired with (a) Siemens 3T human scanner and (b) Bruker 9.4T animal scanner using the same gradient-echo sequence file.

**RESULTS & DISCUSSION** The new hierarchical sequence format compactly represents arbitrary sequences. Using this format, the SE sequence is compressed to 71KB, which is 0.3% of the size of the uncompressed sequence. Likewise, the GRE sequence is 86 KB (0.5% of the uncompressed size). **Simulation**: Fig. 2 illustrates the similar contrast of the SE sequence obtained through simulation and experiment. Using the same sequence file for both datasets improves the consistency between simulation and experiments. This allows for accurate and rapid sequence prototyping with reduced time at the scanner, representing a substantial cost saving. **Hardware-independence**: Fig. 3 displays images from the same GRE sequence acquired on a 3T Siemens and 9.4T Bruker scanner. Images differ slightly due to different RF coil characteristics and increased inhomogeneity at the higher field strength. The platform independence can be advantageous for institutions with multiple scanners and also aid in the sharing of sequences between institutions.

**CONCLUSION** A consistent interface for simulation as well as measurements across hardware platforms could dramatically reduce training costs for MR practitioners, increase prototyping efficiency, and improve teaching of MR physics. The proposed environment also promotes vendor-independence and openness across institutions.

**REFERENCES** [1]Stöcker et al. 2010 MRM 64:186–193 [2]To be published online on *MRIunbound* [3]Yu et al. ISMRM 2014 #4821 [4]Jia et al. ISMRM 2013 #666

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