

# **Fast MR Simulations with JEMRIS 2.1 - Disclosing the Secrets of MRI Sequence Development**

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## **Abstract:**

MRI simulations are needed in many cases and deliver many advantages over real systems. Safety considerations for biological tissue as well as for the MRI hardware suggest the use of simulations prior to the implementation of new processes on MRI scanners. Likewise, the efforts involved in implementing new ideas on MRI scanners may require thorough simulations. In this work, further developments of a novel, multi-processor approach to MRI simulations are presented; the package holds great promise for the sequence and hardware development community. The underlying mechanisms provide the most general and yet computationally efficient solution of the Bloch equations by means of variable time-stepping numerical integration. The presented implementation scales almost ideally with number of processors and has been implemented to run on a variety of different hardware and operating system combinations. By providing a symbolic mathematics toolbox, extensions of functionality very seldom involve programming. Parallel receive as well as transmit functionality promote the simulation of contemporary and relevant developments in the acquisition as well as excitation theory. JEMRIS is available to the MRI community as an open source project [1].

## **Introduction:**

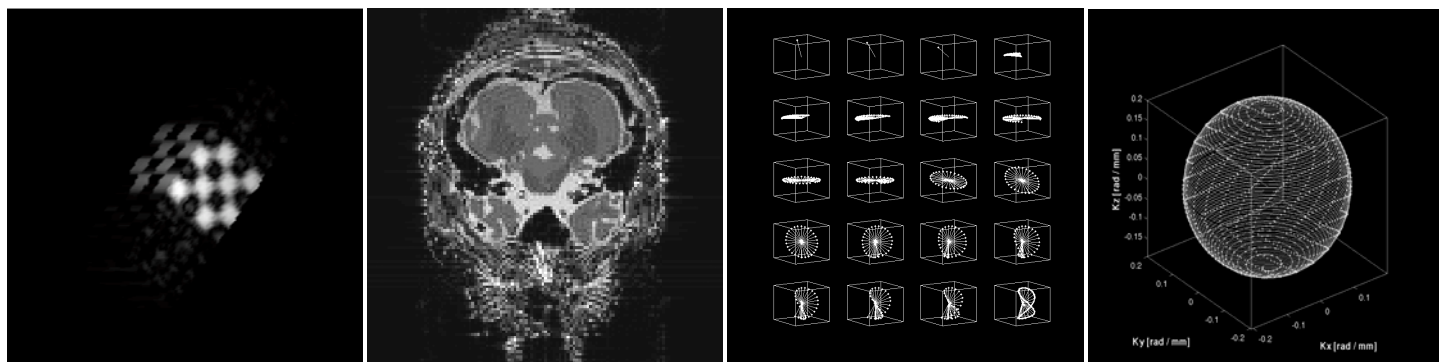
Different approaches have been suggested for the implementation of MRI software and hardware physics in the literature. The most prominent methods consider cases where analytical solutions of the Bloch equations exist [2]-[4]. But the physically most accurate simulation of slice selective excitations already requires numerical evaluation of the physics since gradient and RF pulses are applied simultaneously. This case is pushed to the utmost when multi-channel and multi-dimensional spatially-selective excitations are considered. Numerical approaches have also been suggested, in the past [5],[6]. Yet, hard- and software architectures pertaining at that time allowed only very limited simulations of small spin systems with reduced flexibility and extensibility. However, the aforementioned qualities for simulation software are crucial to adapt to future developments in the field.

## **Methods:**

JEMRIS has been written in C++ to provide extensibility of the underlying frameworks without compromising the overall performance, while intuitively reflecting the underlying physical theory. Widely available, thoroughly tested and well-documented libraries have been engaged for parallel computational functionality [7], for the extremely efficient numerical integration of the differential equations [8], for the support of symbolic mathematics [9], and to not limit the flexibility in choice of operating system and computer hardware. JEMRIS has been thoroughly tested with a variety of MRI “use-cases” on different platforms. This range includes contemporary standard notebooks up to massively parallel super computer hardware [10] with many thousands of processors. One key feature is that JEMRIS does not provide pre-defined MRI sequences and experimental setups; for instant specialised modules for EPI readout or slice selection. Instead, a few basic building modules exist, which, however, deliver huge flexibility. Nearly arbitrary complex MRI sequences can, thus, be set up from a dedicated GUI, without the necessity of any programming. This is achieved by object state observation and, where applicable, crosstalk. Parameter dependences of the interacting basic sequence modules are user-defined through analytical formulae, which are evaluated by a symbolic math library at runtime. This concept, in particular, tries to minimise limitations in sequence complexity as far as possible. For instance, the shape of gradient and/or RF pulses may be defined by the user through analytical expressions. Thus, the door is open to the formulation and simulation of MRI experiments, which may not yet be possible with the hard- and software, delivered by commercial vendors. Furthermore, a fine-grained definition of sample and traveice physics enables the operator to examine results limited merely by hardware requirements. Extensively studied and well understood software design patterns have been invested to all sub frameworks, the sequence, the physical model, the sample, the coil, and the signal for easy adaptation to the code structure for contributing software authors. And finally, the physical model is easily exchangeable to permit, for instance, simulation of phenomena associated with differential equations other than the <sup>1</sup>H Bloch equations.

## **Results:**

The following images, from left to right, show: 16-channel 5.12 ms 3D spatially-selective checkerboard excitation along a 3D spiral k-space trajectory on an ensemble of 9 million isochromats with 16 coils under the Biot-Savart regime simulated in ca.1 hour on 4096 Power6 processors; typical artefacts related to single-shot EPI sequences at ultra high magnetic fields on an MNI brain model slice simulated in ca. 20 min on a notebook with one 2-core CPU at 2GHz (or 2 min on a cluster with 16 Opteron 2-core CPUs at 1.5GHz); 8-ball spin dynamics; lastly, the implementation of a spherical navigator trajectory with symbolic mathematics.



## **Discussion:**

The presented simulation framework has proven to be extensible, easy to use, and scalable while reflecting correctly the physical phenomena associated with MRI. Further, JEMRIS provides an invaluable instrument for education. It has been used at the authors' facility in teaching undergraduate and postgraduate students of physics. JEMRIS can be easily used in advance for the implementation of theory as a proof-of-concept. Comprehensive documentation for operators as well as contributing programmers is available.

## **References:**

[1] [www.jemris.org](http://www.jemris.org). [2] Kwan et al, IEEE Med Imag 1999; 18:1085-1097. [3] Benoit-Catin et al, J Magn Reson 2005; 173:97-115. [4] Yoder et al, Magn Reson Imag 2004; 22:312-328. [5] Summers et al, Magn Reson Med 1986; 3:363-376. [6] Olsson et al, Magn Reson Med 1995; 34:612-617. [7] Jochimsen et al, J Magn Reson 2004; 170:67-78. [8] [www.mcs.anl.gov/research/projects/mpich2](http://www.mcs.anl.gov/research/projects/mpich2). [9] [www.llnl.gov/CASC/sundials](http://www.llnl.gov/CASC/sundials). [10] [www.ginac.de](http://www.ginac.de). [11] [www.top500.org/system/8835](http://www.top500.org/system/8835).