NEW UNIVERSAL NMR SEQUENCES
PERFIDI and LAPSR

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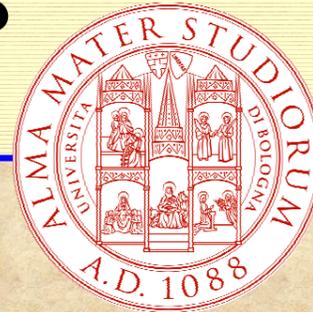
INTRODUCTION: We present two new families of sequences developed within two different projects at the University of Bologna and related by a common feature, which is the use of inversion pulses as a preamble to almost any classical NMR or MRI technique (hence the adjective **universal**). The exclusive use of inversion pulses confers these sequences insensitivity to offset-related artifacts, a property much appreciated in NMR relaxometry of large, complex samples and in MR imaging.

PERFIDI

(**P**arametrically **E**nabled **R**elaxation **Fi**lters with **D**ouble and multiple **I**nversion)

is a family of relaxation filters applicable as a preamble to almost any NMR pulse sequence. As such, it will find a wide range of applications in all branches of NMR, including spectroscopy, relaxometry and imaging. It has been designed keeping in mind complex, chemically and/or physically heterogeneous systems such as untreated body fluids, biological tissues and whole organs, porous media, etc. The patented sequences (patent BO2005A000445, University of Bologna, EU patent pending) are composed of n inversion pulses (n = 2, 3, 4, ...) and are crafted to provide (borrowing standard electronics terminology) **high-pass, low-pass and band-pass T_1-filters** of various shapes and cut-off sharpness.

Figure 1. The concept of PERFIDI
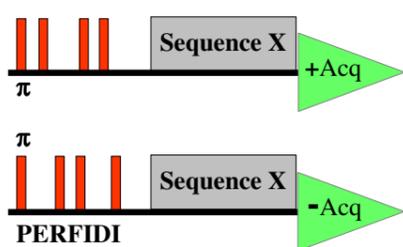
A clasical sequence X is modified by combining it with a PERFIDI preamble composed of a series of inversion pulses (typically 2 – 10) separated by suitable delays. Two or more scans with different delay settings are executed and the acquired data are linearly combined. Using theoretically derived delay settings, this has the effect of **pre-filtering the sample magnetization according to the T_1 values of individual sample components**. The filter profiles are made to depend only upon the precisely known delays and not upon sample parameters and/or inversion-pulse efficiency.

Figure 2. Examples of PERFIDI filter profiles
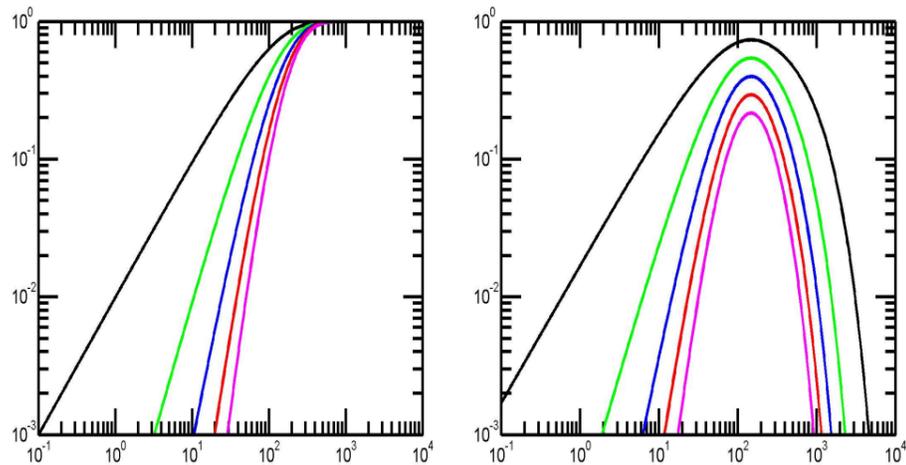
Left plot: High-pass filters. **Right plot:** Band-pass filters.
Horizontal axis: Longitudinal relaxation rate $r_1 = 1/T_1$. **Vertical axis:** Attenuation (1 on top).
The profiles regard 2 (black), 4 (green), 6 (blue), 8 (red) and 10 (violet) pulse filters. The respective measurements require 2, 4, 8, 16 and 32 scans, respectively. The profiles can be shifted up/down the $\log(r_1)$ scale simply by applying a common scaling factor to all delays present in the PERFIDI preambles.

Applications of PERFIDI

In NMR Spectroscopy of complex samples:

➤ **Consider PERFIDI applied to plain 1D spectroscopy. The result is a 2D set with spectra along one dimension and T_1 along the other (somewhat like DOSY but with T_1 instead of diffusion coefficient).**

➤ **Further 2D and 3D examples of this type are numberless.**

In MR Imaging:

➤ **Pre-selection of tissues according to T_1**

➤ **Enhanced contrast around a desired T_1 value (using the edge of a PERFIDI filter)**

➤ **Synergy with the action of contrast agents**

➤ **Reduced use of contrast agents**

In MR Relaxometry of complex, polydisperse samples:

➤ **Relaxation-rate interval pre-selection (e.g.: cutting off water in biological tissues)**

➤ **Splitting the range of r-values into smaller sub-ranges prior to an inverse Laplace transform evaluation by mathematical methods such as UPEN** [1]

➤ **Sampling of broad r_1 or T_1 distributions with no/reduced mathematical mediation**

➤ **Replacing the Laplace inversion kernel with a better behaved PERFIDI kernel**

PERFIDI web site and references

For more details about PERFIDI, please consult the web site **www.perfidi.net**

1) G.C.Borgia, R.J.S Brown, P.Fantazzini, *Uniform Penalty Inversion of Multiexponential Decay Data*, *J.Magn.Reson*. 132, 65 (1998).

2) S.Sykora, V.Bortolotti, P.Fantazzini: *PERFIDI: Parametrically Enabled Relaxation Filters with Double and multiple Inversion*, Magnetic Resonance Imaging, proceedings of the 8th International Bologna Conference on Magnetic Resonance in Porous Media*, in print.

LAPSR

(**L**ogarithmically distributed **a**-**P**eriodic **S**aturation **R**ecovery)

is one of a family of **SMS** (**S**ample **M**agnetization **S**uppression) sequences

which aim at **suppressing as fast as possible the nuclear magnetization of all components of a sample** with particular attention being paid to samples with extremely wide distributions of relaxation times, offsets, and nutation angles (B_1 inhomogeneity).

### The development of SMS sequences started from these observations:

(i) Classical NMR relaxometry methods, such as **inversion recovery** (IR), are slow because they require reaching the equilibrium magnetization before every scan and they often fail in situations where sample complexity combines with severe instrumental imperfections (ex-situ NMR, large samples, severe B_1 inhomogeneity, insufficient transmitter power, etc.).

(ii) The alternative is to use the **saturation recovery** (SR) sequence or the **APSR** sequence (train of 90° pulses with linearly decreasing delays), possibly in tandem with gradient pulses. The goal is to achieve zero-magnetization state and do so as fast as possible. Compared to IR, the results are encouraging but usually still far from ideal and free of artifacts.

These observations prompted us to carry out an extensive series of **theoretical simulations** in order to answer objectively the question of *how fast and how well can one suppress the magnetization of complex samples using standard pulse sequences*. The interesting results, obtained applying integrated Bloch equations to multi-component virtual samples, were then compared with experiments. It turns out that the best saturation sequences are composed of about 20 **inversion pulses** with **logarithmically distributed delays**. Relaxation curves can be measured **about 3 times faster** than with IR and remain **meaningful even under very imperfect experimental/instrumental conditions.**

Figure 3. Example of the theoretical residual magnetizations

just after the saturation sequence, computed for a virtual phantom with 81 components covering all combinations of nine T_1's (3000, 1000, 300, 100, 30, 10, 3, 1 and 0.3 ms), three offsets (0, 650 and 1300 Hz) and three B_1 inhomogeneity settings (RF-amplitude variations of –20, 0 and +20%). The LAPSR sequence contained **20 pulses with geometrically decreasing delays**, the last of which was 50 µs.

Relative residual magnetizations plotted against the first delay (in seconds) between the saturation sequence pulses

The same plotted against the common nutation angle of the pulses (in degrees). The first delay was 2 s.
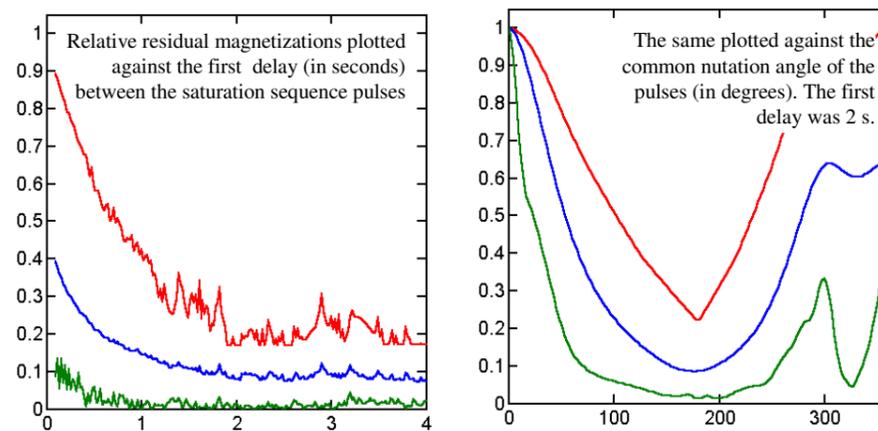
Vertical axes: **relative residual magnetization** m_r of the worst-case single component (**red**), the mean-square value of m_r over all components (**blue**) and the plain average of the magnetization over all components (**green**). Though only the latter quantity can be measured, the ideal would be to zero all three quantities in order to exclude any contamination of T_1 relaxation curves by refocused transversal components. The shortest-duration sequence which gets close to this ideal uses 180° pulses and first delay of 2 s.

Figure 4. Experimental relaxation curves

measured on a large relaxation phantom with three-components (3.6, 60 and 480 ms) using different saturation sequences and a rather low, inhomogeneous B_1. In these conditions the traditional APSR sequence, suitable for narrow T1 distributions, was found even more inefficient than the textbook SR sequence. As expected from theoretical simulations, LAPSR with 180° pulses gives the least residual magnetization at $\tau = 0$ (% values shown in the parentheses) and the smallest pseudo-noise at small τ–values due to undesired echoes.

- SR (20.3%)
- APSR 90 (70.8%)
- LAPSR 90 (4.9%)
- LAPSR 180 (3.3%)