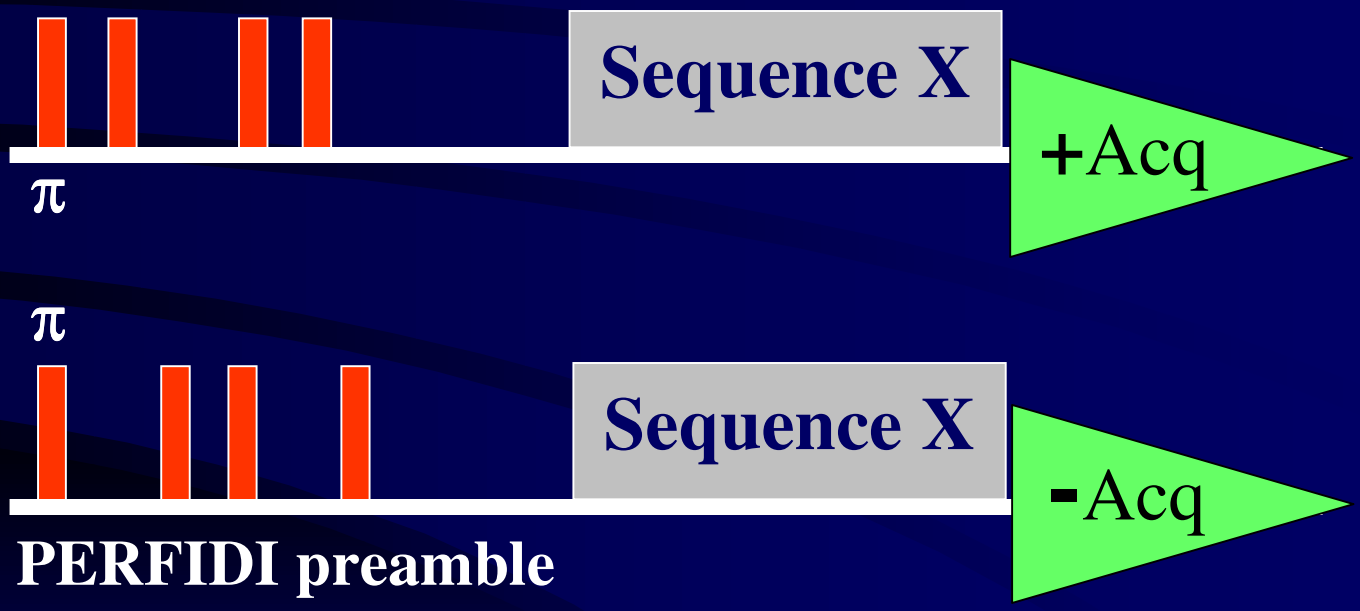
PERFIDI

Parametrically **E**nabled **R**elaxation **Fi**lters with **D**ouble & multiple **I**nversion

Stan Sýkora, Villiam Bortolotti, Paola Fantazzini

MRPM8, Bologna 10-14 Sptember 2006



Italian patent BO2005A000445, owned by the University of Bologna, Authors S.Sykora, P.Fantazzini (EU patent pending)

Inversion problems

with additively superposed components

Given: **Parameter** p,

Assumed: **Distribution density** w(p),
Single-component response s(p,t)

Measured: $S(t) = \int w(p)s(p,t)dp$

We want: w(p)

Inversion problems:

A simple-minded solution

(A) Digitize t: $t \in \{t_j, k = 1, 2, 3, \ldots, N\}$

(B) Assumed digitized p: $p \in \{p_i, i = 1, 2, 3, \ldots, M\}$

Digitization strategies: lin/log over a range; N/M (=1)

(C) The transform then becomes a matrix equation:

$$w.K = S,$$

where $w \equiv \{w_i = w(p_i)\}$, $S \equiv \{S_j = S(t_j)\}$,

and $K \equiv \{K_{ij} = s(p_i, t_j)\}$ **is the kernel matrix**

(D) Solution: $w = S.K^{-1}$

Inversion problems:

Do simple-minded solutions work ?

That depends upon the condition number C_n of the kernel matrix K which can be computed a-priori:

$$C_n(K) = \frac{< \text{largest singular value of } K >}{< \text{smallest singular value of } K >}$$

$$= \text{noise-amplification factor}$$

Example_1: $p \equiv \omega$, $s(p,t) \equiv \exp(i\omega t)$, $C_n(K) \approx 1$

Spectroscopy: Those guys are really lucky !

Example_2: $p \equiv r = 1/T$, $s(p,t) \equiv \exp(-rt)$, $C_n(K) =$ GOOGOL

Relaxometry: Bad luck !

Inversion problems:
re-conditioning ill-conditioned cases

General approach:

Narrow the set of admissible solutions

Often used methods:

- **Decrease of resolution**
- **Incorporation of a-priori knowledge**
- **Penalties on undesired features of w(p)**

Inversion is done by damped SVD or iterative fitting:

MINUIT, REPES, UPEN, …

An idea:

Why don't we avoid all the math by separating sample components before or during data acquisition ?

Separation before measurement is usually destructive

(mechanical sorting, chromatography, dialysis, biopsy, …)

We do not like that (though we often do it)

Separation during data acquisition is non-destructive and it is already an NMR evergreen

Almost all NMR spectroscopy methods separate signals according to chemical/physical parameters or coupling patterns

? What about relaxometry ?

T_1 filter precursors

From now on, the parameter p will be $r_1 = 1/T_1$

T_1 weighing in MRI:

Useful but not very selective and difficult to quantify, especially with non-ideal pulses across the sample.

Magnetization zeroing for one/more T_1 values:

Often done with 180^o pulses followed by specific delays

Drawbacks:

- **The required delays are sample-specific and …**
- **… difficult to satisfy over the whole sample.**
- **There is a drastic overall reduction of the signal**

Towards true T_1 filters

What we want to keep

We like inversion pulses, because they

- have large effect on longitudinal magnetization
- have a high tolerance to instrumental artifacts
- produce the smallest amount of offset artifacts due to transversal magnetization components
- can be improved by using composite pulses
- are compatible with trailing gradient pulses

Towards true T_1 filters

What we want to add

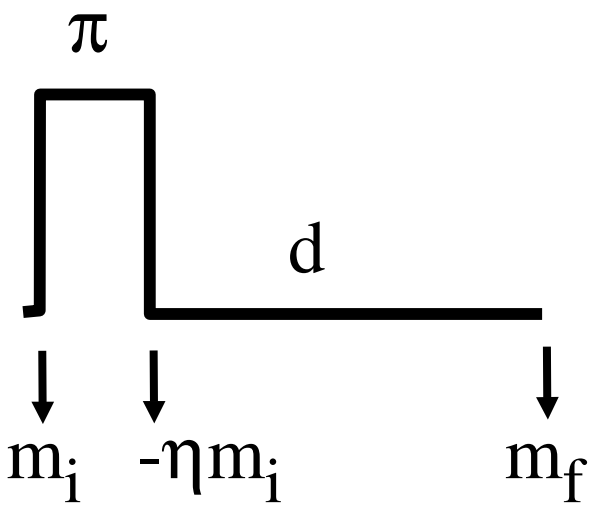
We must account for
limited efficiency of inversion pulses
in order to make our relaxation filters
work under real conditions
on real instruments

An elementary inversion

followed by a free-evolution delay interval

$$m_f = 1 - (1 + \eta m_i)\, e^{-rd}$$

where $-1 < \eta < 1$ is the **inversion efficiency factor** (typical values: 0.5 - 0.9)



Considered this as an operator $Q_\eta(d,r)$ which converts the initial magnetization m_i into the final magnetization m_f

A series of inversions

For a series of inversion pulses P_k, k = 1, 2, …, n, each followed by a delay d_k, we apply the succession of evolution operators $Q_\eta(d_k,r)$ and obtain* a recurrence relation which, luckily, has a closed-form solution

$$F(r,d_1,d_2,...,d_n) \equiv m_f =$$

$$= Q_\eta(d_n,r)\{\ldots\{Q_\eta(d_2,r)\{Q_\eta(d_1,r)\{m_i\}\}\}\ldots\} =$$

$$= 1 - (1+\eta)\Sigma_{k=0,n-1}\,(-\eta)^k \exp(-r\Sigma_{j=n-k,n}\,d_j)$$

This is a polynomial in η with r-dependent coefficients

* without any lack of generality, we have set $m_i = 1$

η*r Factorization

To obtain a good relaxation filter we must separate the effects of η from those of the relaxation rate r in order to make the filter profile the same in every part of the sample.

To do that, we need to combine several $F(r,d_1,d_2,...,d_n)$ for different settings of the d's so that the result can be written as

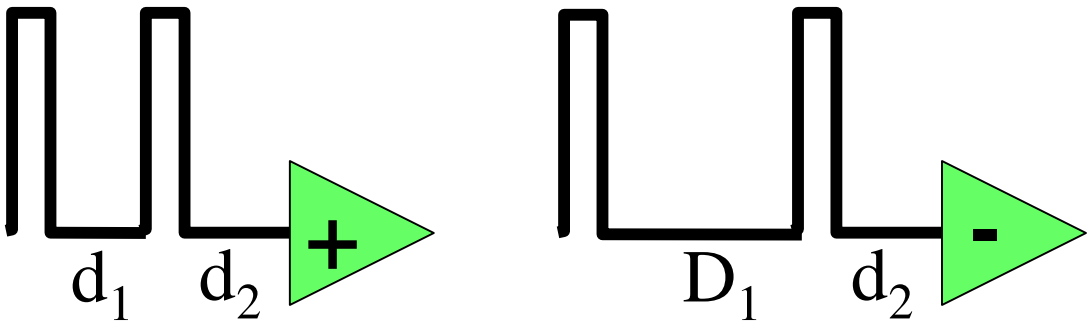
$$E(\eta).f(r,\{d_k\})$$

where $E(\eta)$ is an efficiency factor independent of η and $f(r,\{d_k\})$ is the η-independent filter profile.

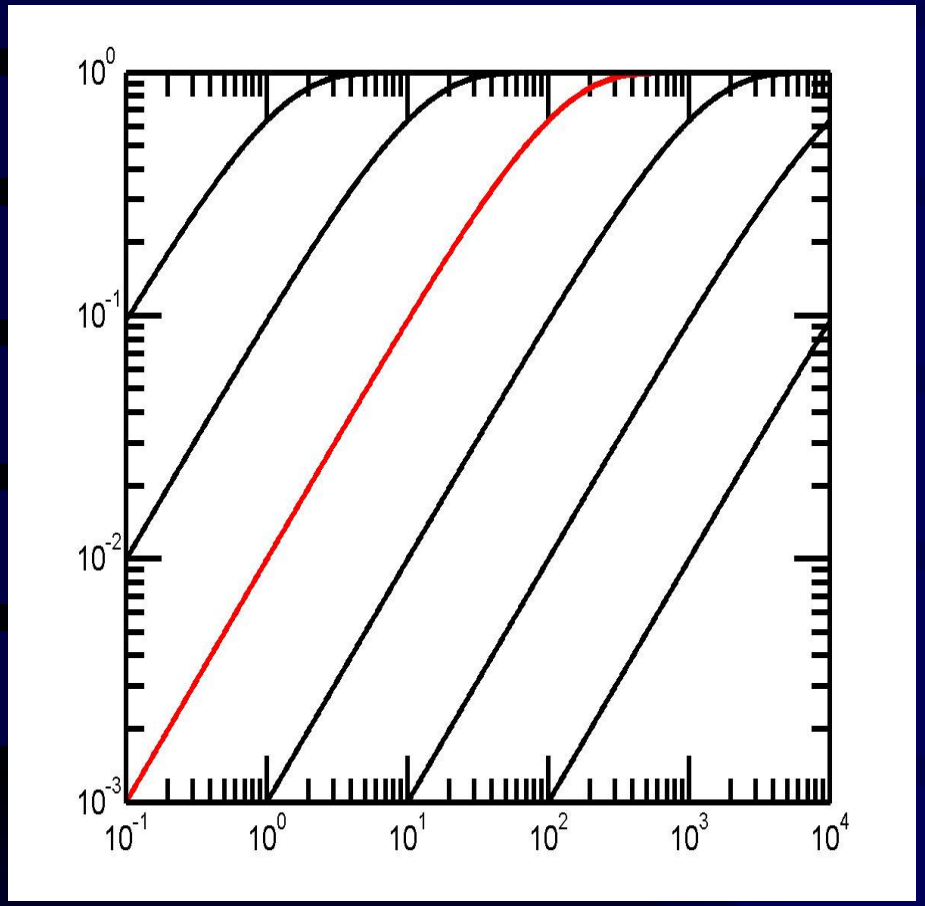
Example: 2-pulse PERFIDI

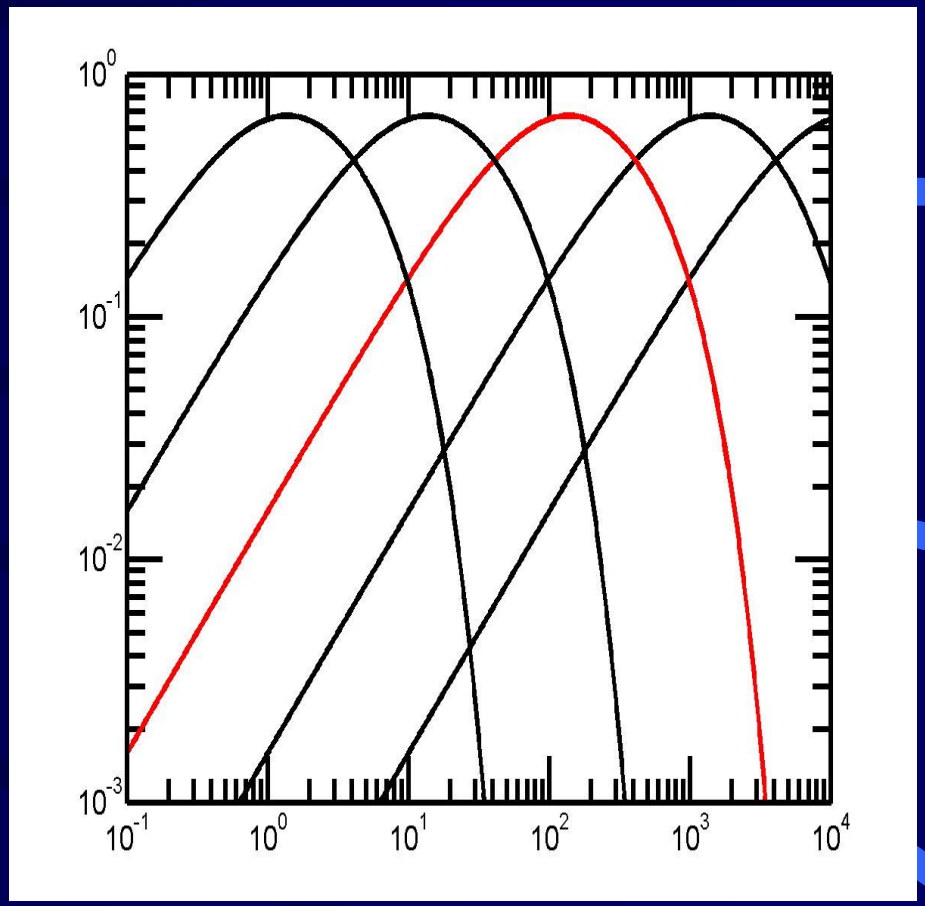
$$F(r,d_1,d_2) - F(r,D_1,d_2) = \eta(1+\eta)\,(e^{-rd_1}-e^{-rD_1})\,e^{-rd_2}$$

$$f_2(D_1,d_1,d_2) = (e^{-rd_1}-e^{-rD_1})\,e^{-rd_2}$$



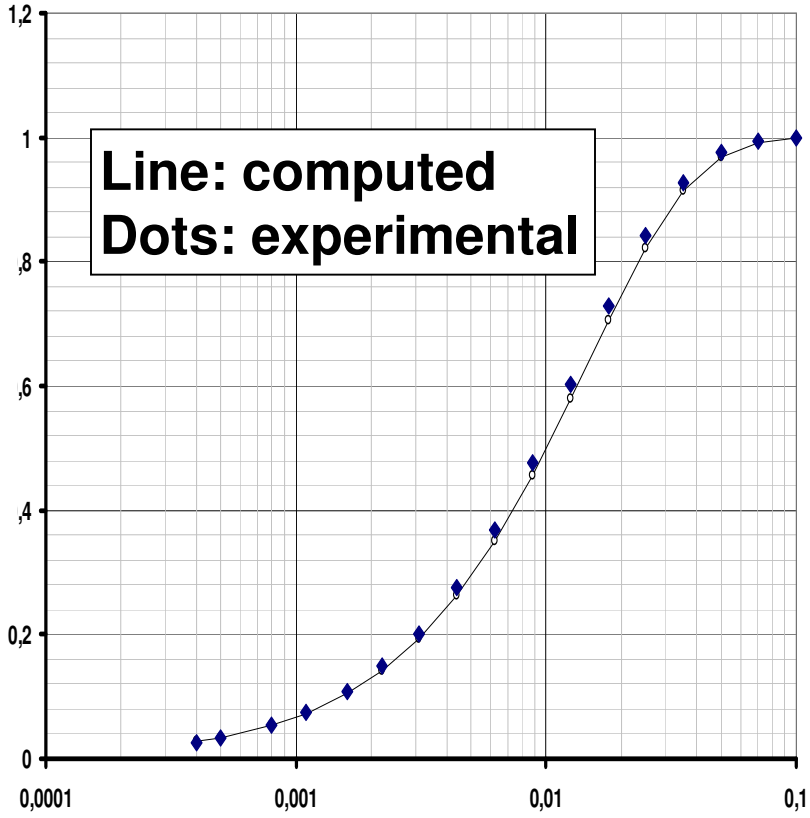
Some 2-pulse filter profiles

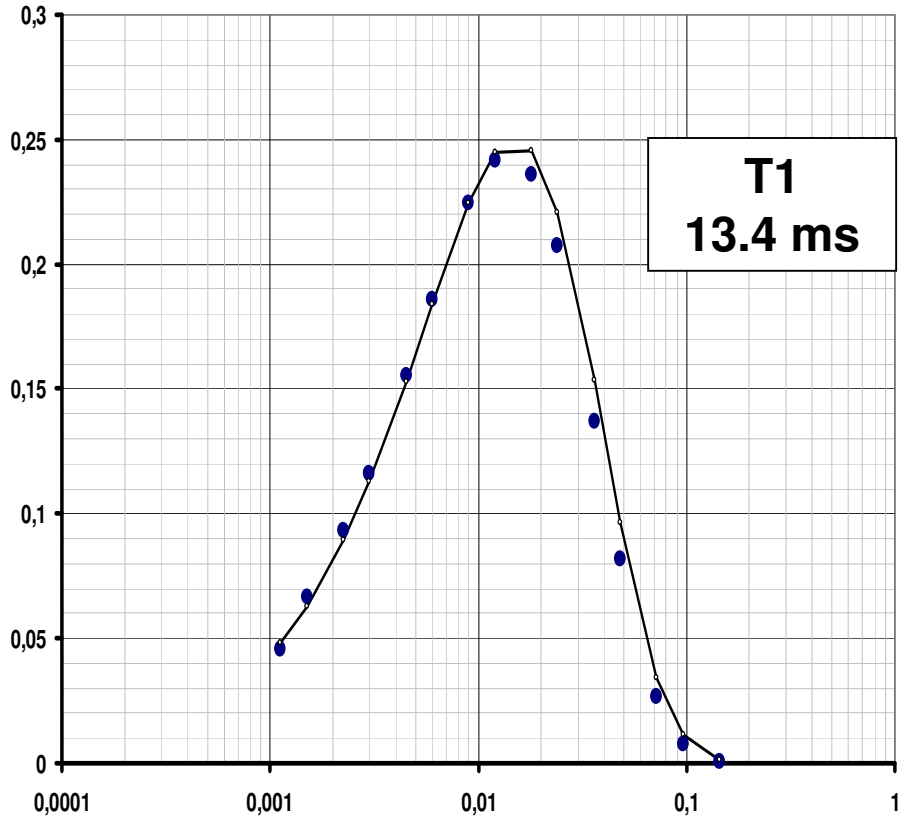




Left plot: $d_1 = 0$, $D_1 = \Delta$. **Right plot:** $d_1 = 0.15^* \Delta$, $D_1 = 1.85^* \Delta$. **Horizontal axis:** r, **Vertical axis:** attenuation (1 on top). $d_2 = 0$. Δ is 1s for the leftmost curve and decreases by 10 from left to right (the red curves correspond to Δ of 10 ms).

Experimental verification





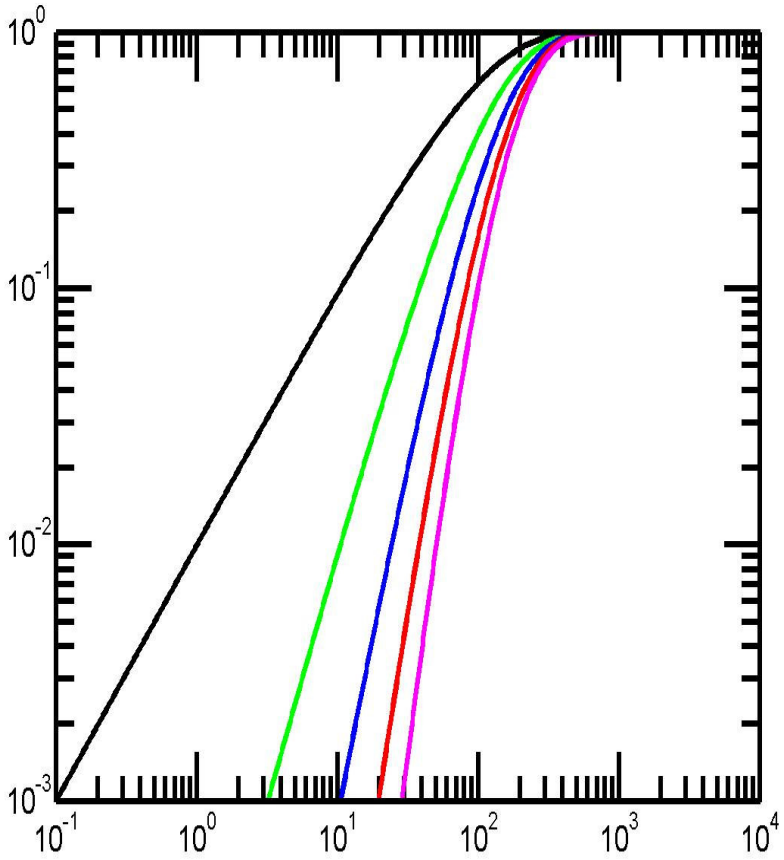
Monoexponential sample, instrument with an η of 0.85, signal sampled by a 90° pulse. In both cases $d_2 = 0$.
Left curve: $d_1 = 0$, $D_1 = \Delta$. Right curve: $d_1 = 2\Delta/3$, $D_1 = 4\Delta/3$.
Horizontal axis reports Δ, vertical axes the normalized signal.

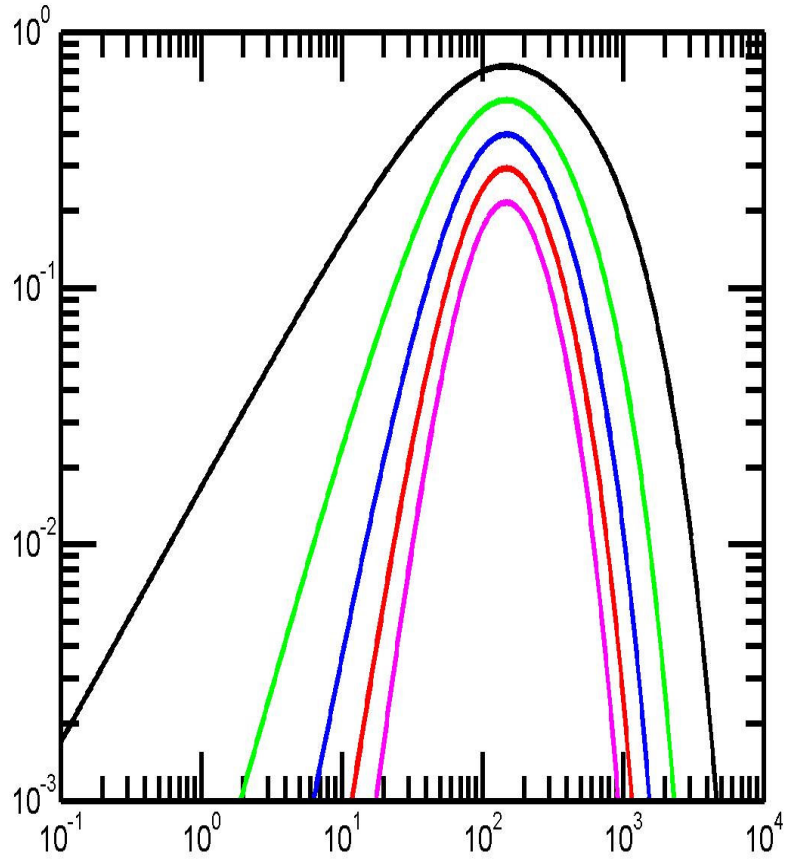
Main features of PERFIDI filters

- **Filter functions depend only upon exactly known delays and NOT at all upon sample properties or instrumental factors**
- **There is a strong analogy with electronics filters: high-pass, low-pass and band-pass**
- **Simple scaling of all delays shifts a filter function up/down the log(r) scale leaving its shape intact**
- **There are no zero crossings, just attenuations**

More filter profiles

Examples with 2, 4, 6, 8 and 10 pulses (1-5 cascaded 2-pulse filters)





The basic 2-pulse sequence parameters are the same as before.
The measurements require 2, 4, 8, 16 and 32 scans, respectively.

Exploiting PERFIDI:

PERFIDI can be used as a preamble to almost any NMR sequence

NMR spectroscopy example:

Consider PERFIDI applied to plain 1D spectroscopy

Result:

A 2D set with spectra along one dimension and T_1 along the other (a bit like DOSY but with T_1 instead of diffusion coefficient)

(WORK IN PROGRESS)

PERFIDI and MRI

MR Imaging:

- **Pre-selection of tissues according to T_1**
- **Enhanced contrast around a desired T_1 value (working on the edge of a PERFIDI filter)**
- **Synergy with contrast agents**
- **Reduced use of contrast agents**

(WORK IN PROGRESS)

PERFIDI in Relaxometry

- **Relaxation-rate interval pre-selection**
  (for example: cutting off water in biological tissues)
- **Splitting the range of r-values into smaller sub-ranges for approches such as UPEN.**
  This improves the kernel condition number.

(WORK IN PROGRESS)

The PERFIDI inversion kernel

Consider a filter $f(r,\{d_k\})$ and let $d_k = \kappa d_{0k}$, where κ is a filter scaling factor. For brevity, write $f(r,\{d_k\}) \equiv f(r, \kappa)$, considering the shape-defining delays $\{d_{0k}\}$ as given constants. The signal, sampled by a 90^o pulse at time t at the end of PERFIDI, is

$$S(t,\kappa) = \int w(r) f(r,\kappa) e^{-rt}\, dr$$

For t = 0, this leads to the inversion kernels

$$K^P_{ij} = f(r_i,\kappa_j) \quad \text{and /or} \quad K^L_{ij} = \exp(-r_i t_j),$$

of which the Perfidi kernel K^P can be made better behaved than the Laplace kernel K^L .

(WORK IN PROGRESS).

Thank you for your patience

and thanks to my wise cat Silvestro for helpful discussions

All the slides you have seen will appear on the web site

www.perfidi.net

to be dedicated to PERFIDI development, related articles, posters,

...