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Developments in the evaluation of DOSY data

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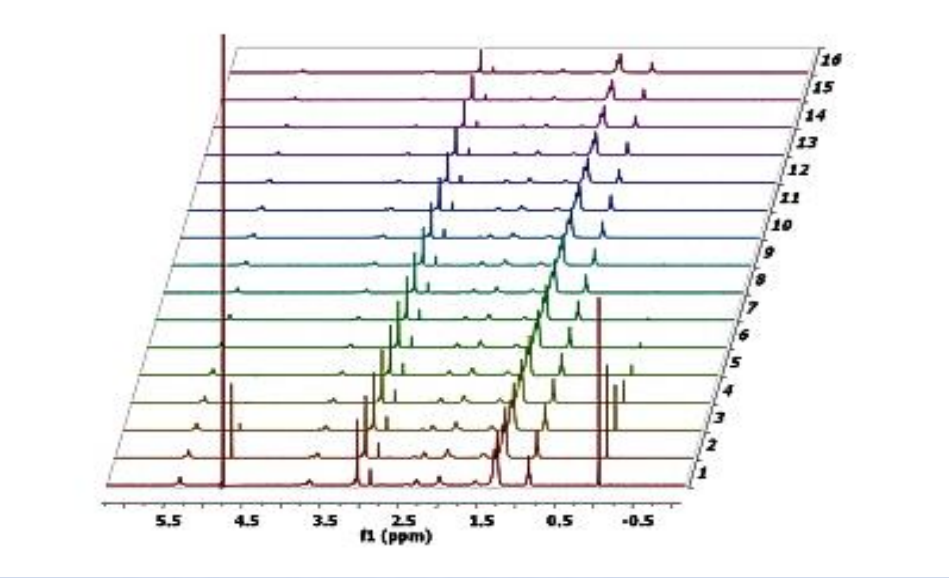
University of Milano-Bicocca
Joint congress GIDRM-GERM

DOSY: Diffusion Ordered Spectroscopy

You certainly know the principle of these arrayed-parameter experiments.
The raw data look somewhat like this:



The arrayed-parameter is a property of the used field-gradient pulse such as its amplitude (g) or duration (δ). The number of gradient settings N_g is defined by the user/operator prior to data acquisition.

Each gradient setting gives one FID and thus one 1D-spectrum

Vertical axis transformation:

from gradient settings to a universal decay variable

Example for simple Stejskal-Tanner PFG sequence:

- Decay formula (d is the diffusion coefficient, g, Δ, δ, are gradient parameters:

$$S_i(d,t_i,g,\Delta,\delta,T_2) = E_i(T_2).\exp[-d(\gamma\delta g)^2(\Delta-\delta/3)]$$

- Definition of a decay variable:

$$z = (\gamma\delta g)^2(\Delta-\delta/3) \quad \text{or} \quad z' = (\gamma\delta g)\sqrt{(\Delta-\delta/3)}$$

- Simplified decay formula in terms of d and z:

$$S_i(d,z) = E_i(T_2).\exp(-dz) \quad \text{or} \quad S_i(d,z') = E_i(T_2).\exp(-dz'^2)$$

The transformed data look the same as before, only the labels along the vertical axis change.

The advantage is that the new data set S(f,z) is independent of acquisition details, such as the used pulse sequence, or the arrayed gradient pulse parameter.

The next DOSY data evaluation step

What we want to obtain next is a 2D map
with the spectral **frequency f on the horizontal axis**, and the **diffusion constant D on the vertical axis**, digitized in N_d steps.

The numbers N_d and N_g (number of gradients settings) are independent (often $N_d >> N_g$).

D should be regulary (LIN or LOG) distributed over a user-defined interval (d_{min}, d_{max}).

We call **Dosy Transform (DT)** any algorithm that converts the raw set od difusion data to such a 2D map.

A problem that one encounters at this point is that there are various ways to achieve this goal and each of them has its own pros and cons.

Various DOSY Transform approaches.

I. Maximum Entropy Management (MEM)

Are there physically more sound approaches?

Yes, there are! For example,

a good one is the **Maximum Entropy approach**

which was used by Marc-Andrè Delsuc

It is only a pity, though, that it is **very slow**.

Various DOSY Transform approaches

II. Bayesian Dosy Transform (BDT)

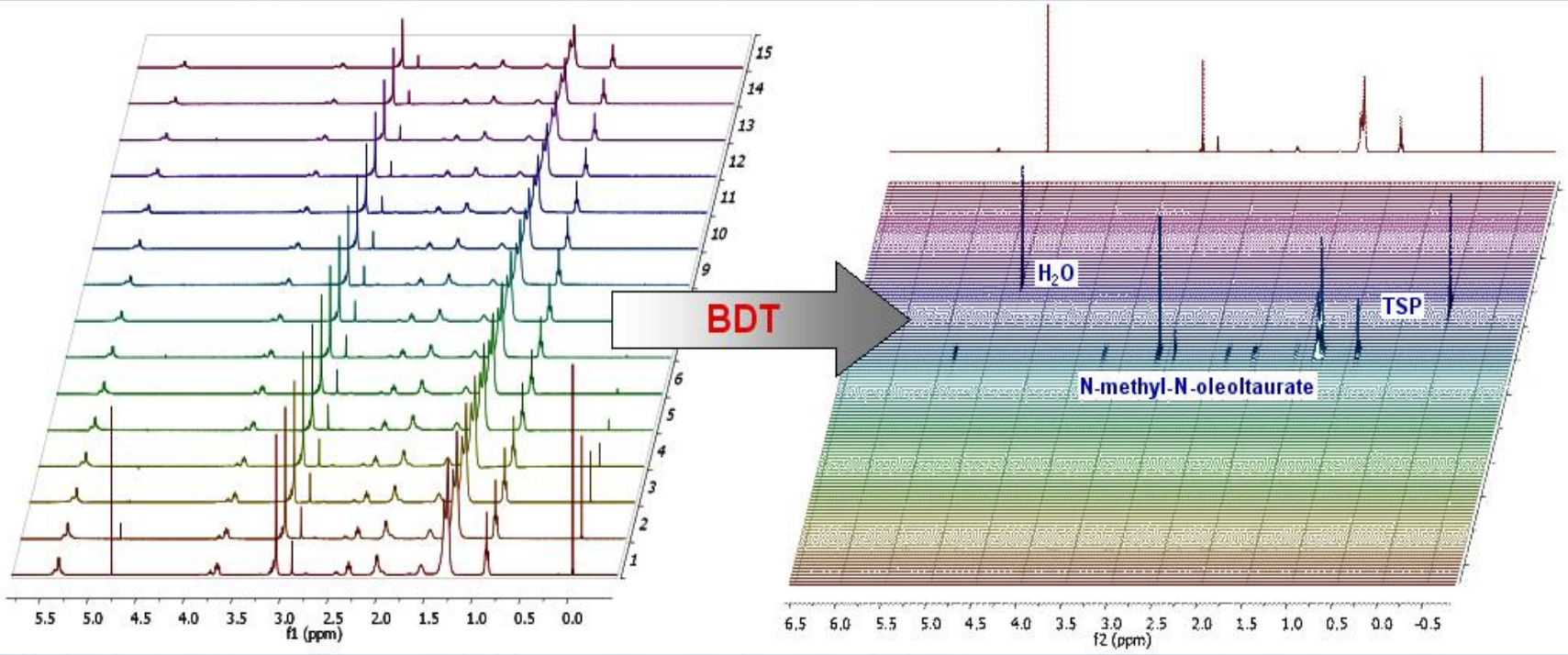
This is a pseudo-fitting algorithm due to Stan (2008)
based on a Bayesian optimization approach

It provides similar results as MEM, but it is **very fast**
(tens of seconds against hours)

Note: many people today include MEM and Bayesian approaches among the tools of AI.
Not that it matters, but we can fashionably claim that DOSY evaluation uses AI !!! Hehe!

A practical **example** of the

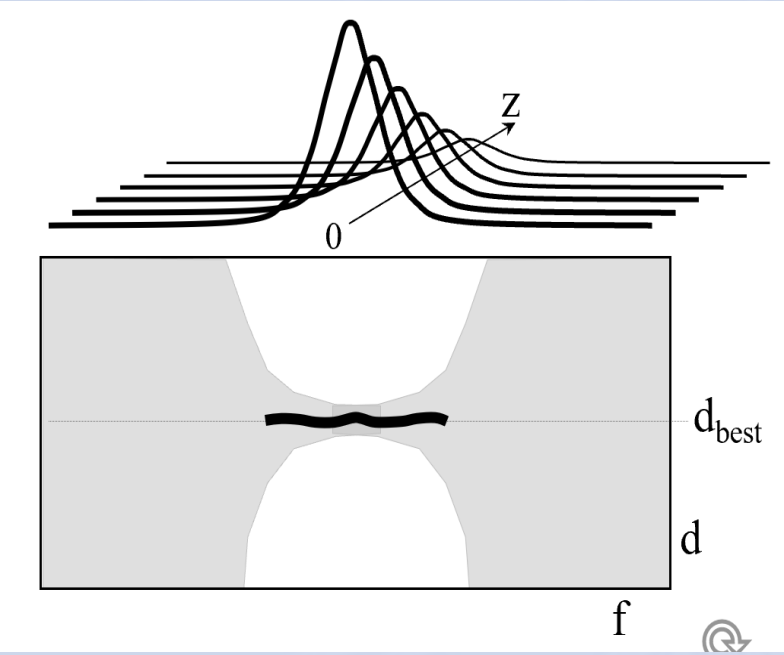
Bayesian DOSY Transform (BDT)



BDT of an aqueous solution of potassium N-methyl-N-oleoltaurate (a surfactant) with TSP at 23 C

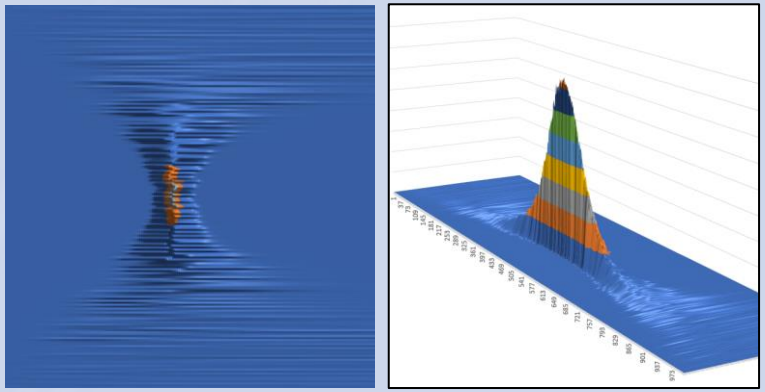
The original Varian FID file has been obtained from the *VARIAN NMR USER GROUP LIBRARY* (submitted by Brian Antalek as a sample for this DECRA algorithm)

The woes of all fitting DT methods



Confidence intervals (the gray area) in the D-dimension depend drastically on signal intensity and it is not quite clear how to represent them.

The butterfly artifact



BDT peak shapes are not circular/oval (not even the simulated ones)

- ✓ The non-intuitive DOSY peak shapes make the displays of the 2D DOSY maps non-trivial.
- ✓ There are math complications when peaks with different D-values overlap (ill-defined tasks; work in progress).

Bayesian DOSY is old stuff; enough about it …

Bayesian DOSY:
a New Approach to Diffusion Data Processing

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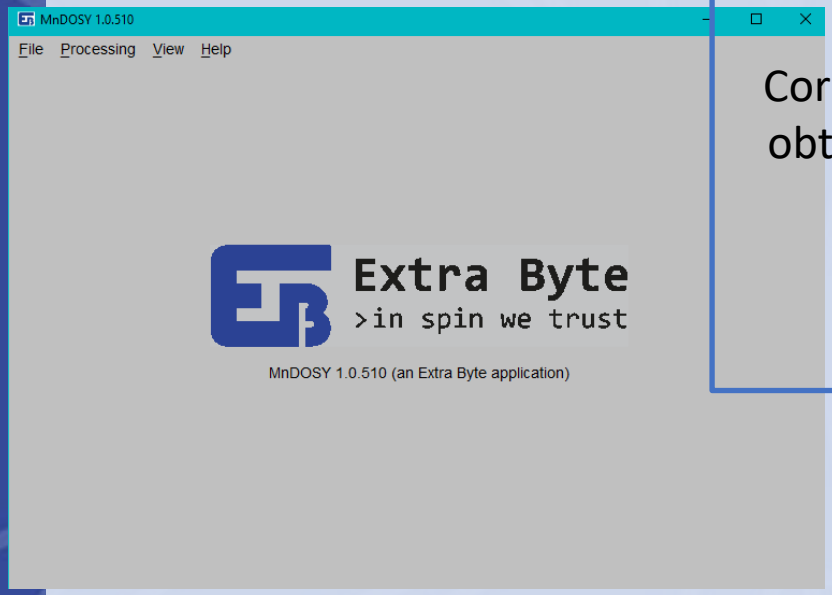
Juan Carlos Cobas Gómez, Mestrelab, Spain
www.mestrelab.com

BayDOSY

Presented at XXXVIII **GIDRM**, September 10-13, 2008, Bressanone/Brixen, Italy

Fast-forward to MnDOSY,

the **multi-nuclear** DOSY



It started from the following idea/request

(by Matthias Abele, Evonik)

Correlate two DOSY spectra of the same sample obtained observing two different nuclei such as

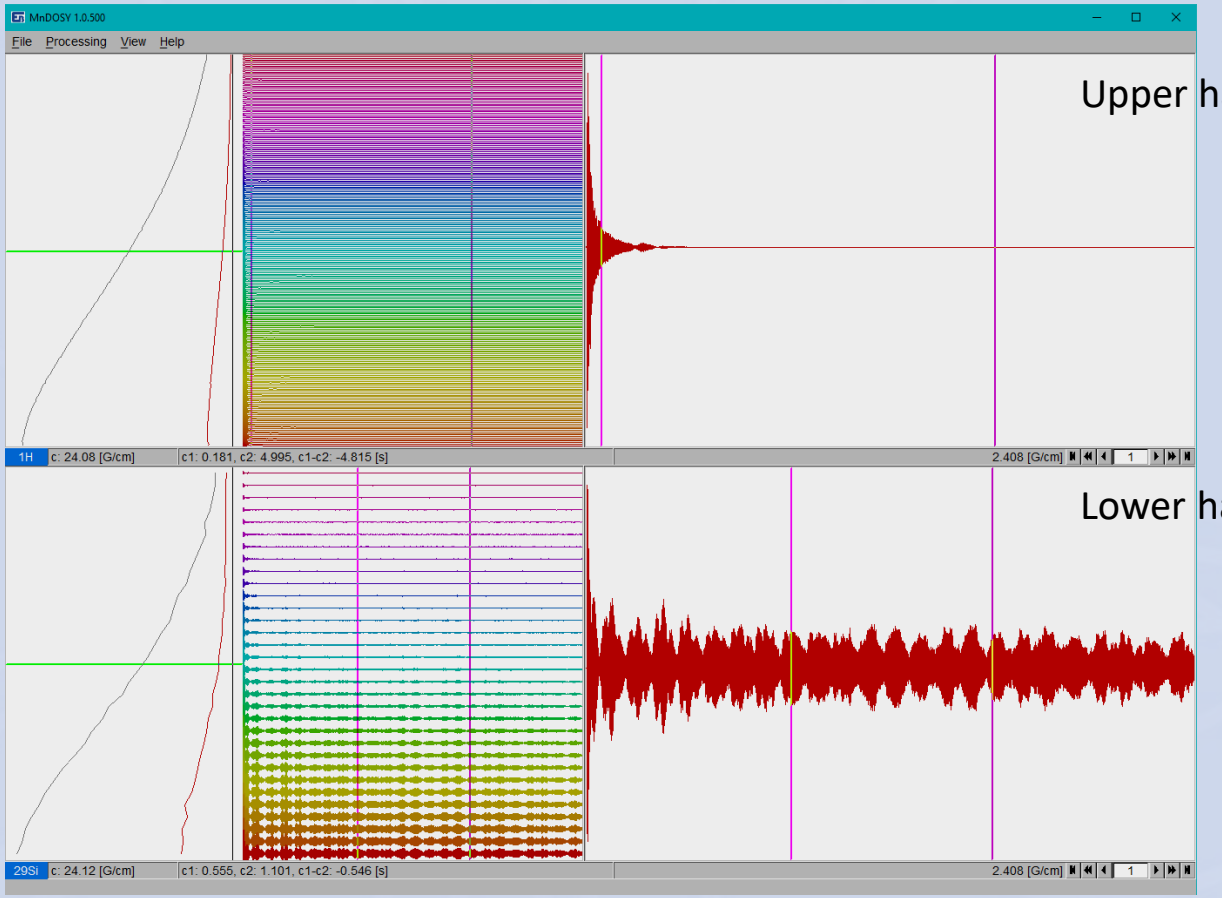
(1H, 29Si) or (1H, 13C) or (1H, 19F) or …

using a handy software tool specifically designed for the specific purpose.

The request matched the stated Extra Byte mission which is rapid development of STEM software utilities for practical tasks

Example: MnDOSY of 1H and 29Si of a mixture of oligomeric silanes

Once the two data sets are loaded, one obtains this kind of display



Upper half: 1H

Lower half: 29Si

Left panels for projection

Central panels for 2D views

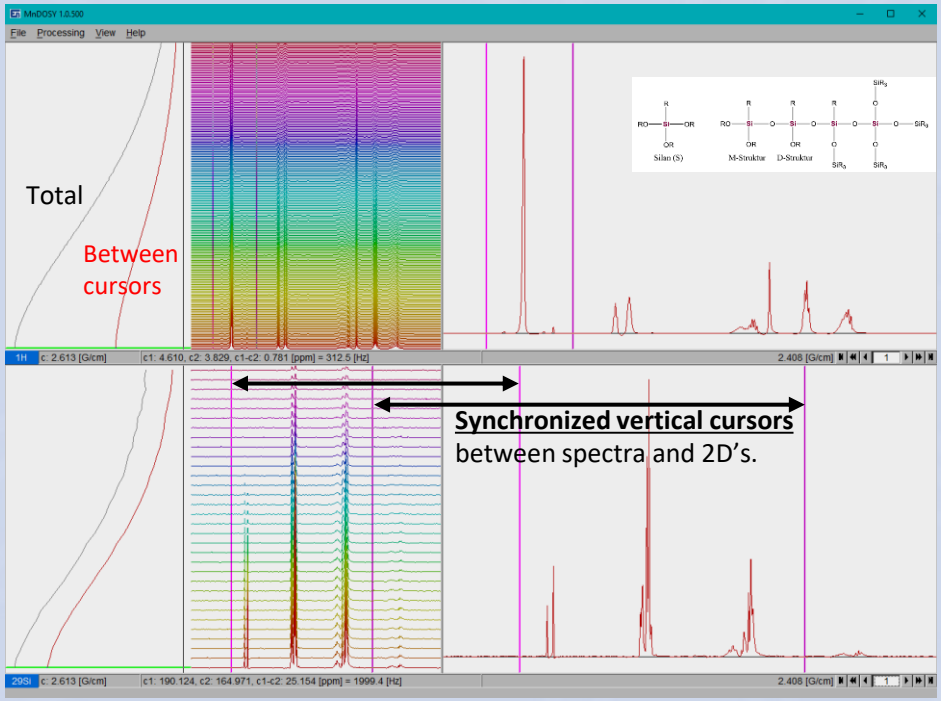
Rights panels for FID's or spectra (1st + N-th)

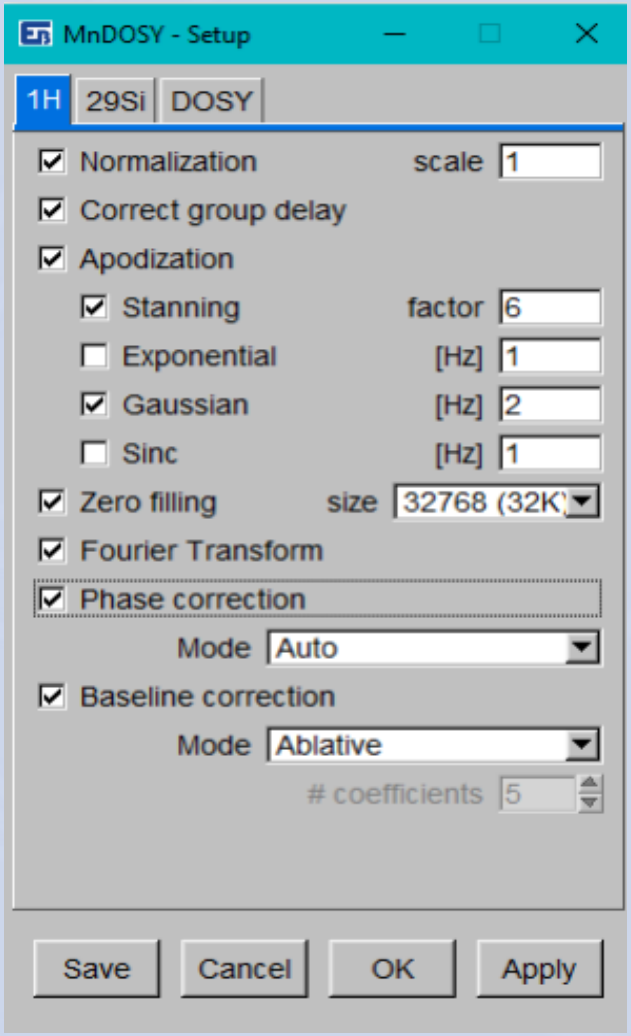
Converting FID's to spectra: once parameters are set, it is a single click!

Setting of parameters for repetitive spectra evaluations

Automation of the following processing steps:

- ✓ Vertical normalization
- ✓ Group delay handling (removes "smileys")
- ✓ Apodization functions and parameters
- ✓ Zero filling / resizing
- ✓ Fourier transform
- ✓ Automatic phase and baseline correction

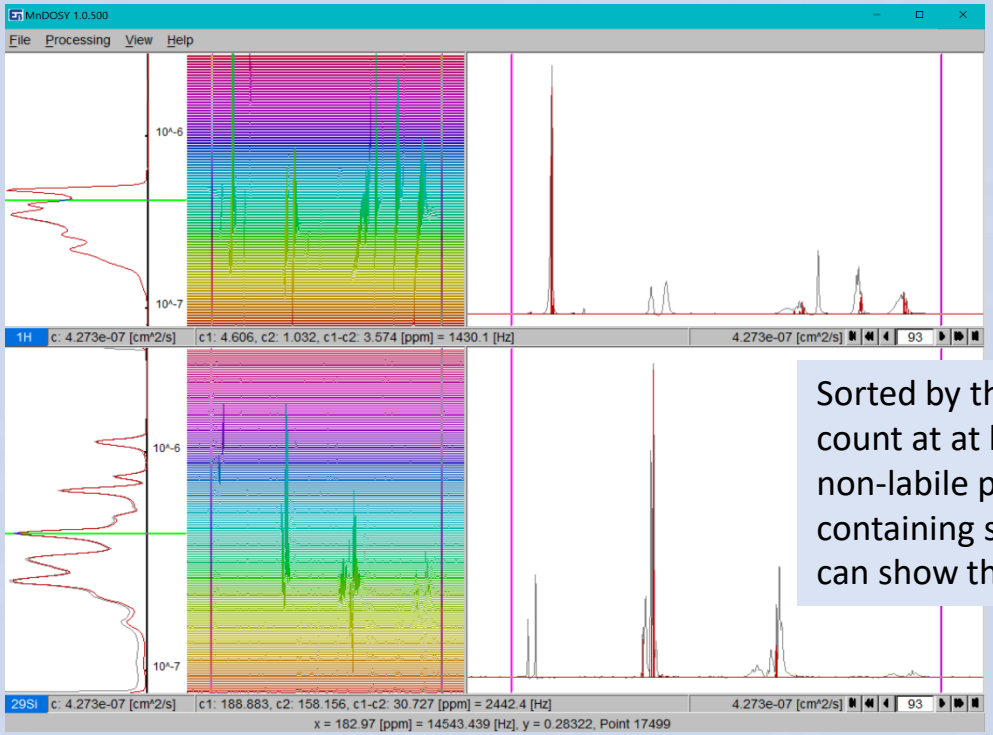


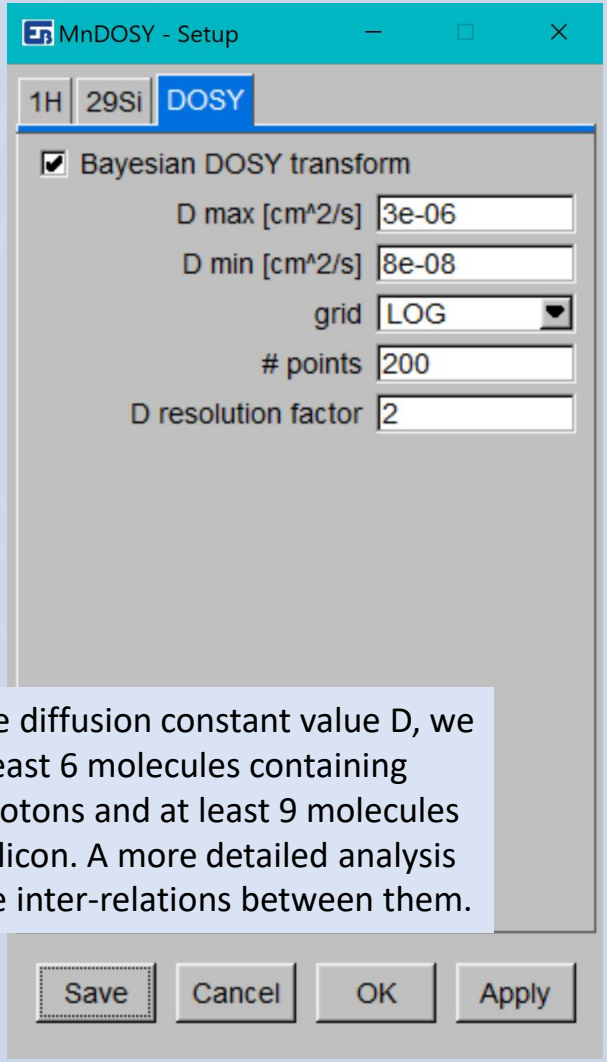


BDT: once parameters are set, it is a single click!

Salient features

- ✓ V-projections: quantitation along the D-axis.
  (total and over cursor-defined selected intervals).
- ✓ Vertical cursors: synchronized between the 1D spectra and 2D maps
- ✓ Horizontal cursors in V-projections: synchronized between the nuclei
  (see the double-ended arrow below).
- ✓ Intuitive zoom/expansion/move/reduction/remote modes.
- ✓ Readout of all coordinates on status bars.

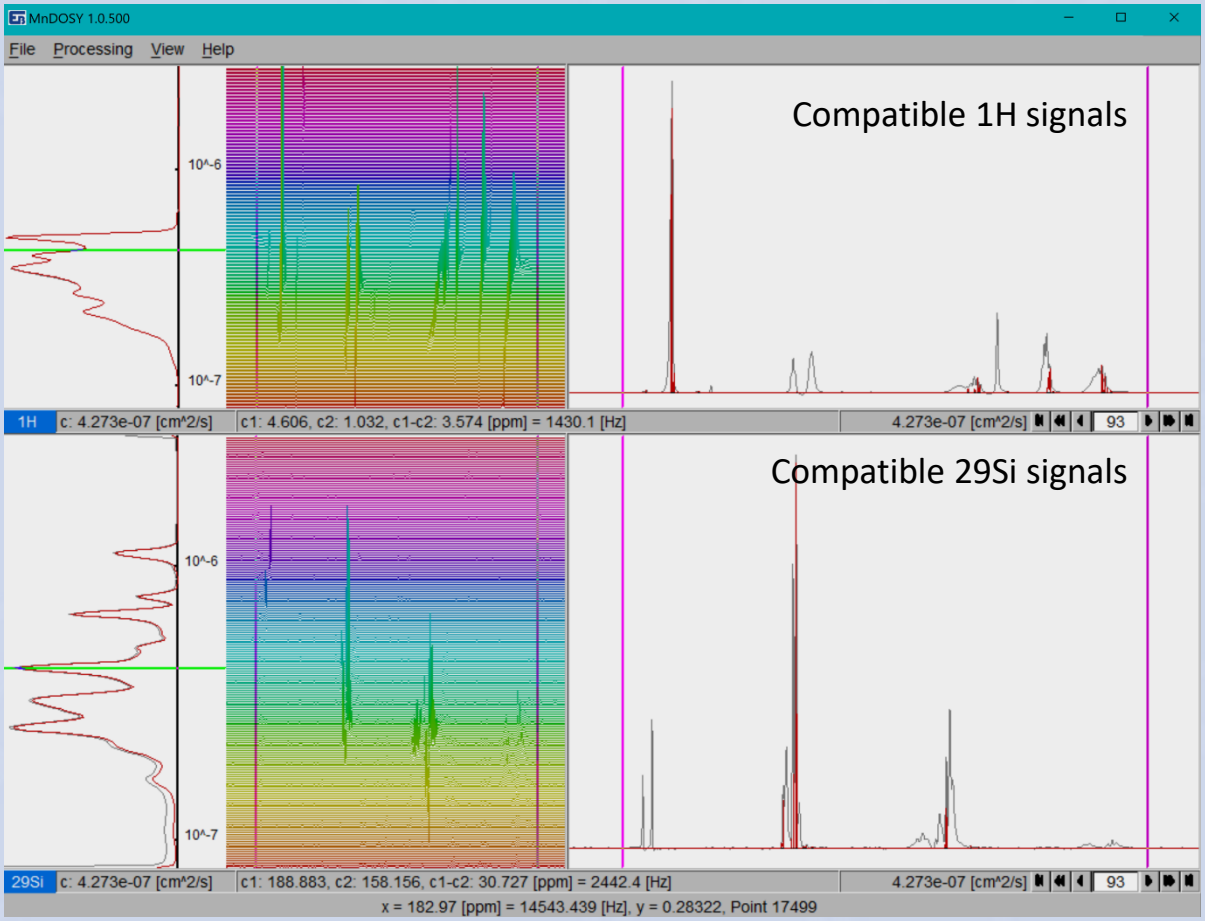




Sorted by the diffusion constant value D, we count at at least 6 molecules containing non-labile protons and at least 9 molecules containing silicon. A more detailed analysis can show the inter-relations between them.

Generic MnDOSY correlation principles:

Use the horizonatal synchronized cursors in the left panels to pick up a 29Si diffusion component. In the right-side 1D spectral trace panels one then observes as red traces the locations of the silicon 29Si signals (below) and the 1H signals (above) of the atoms that might belong to the same molecule.

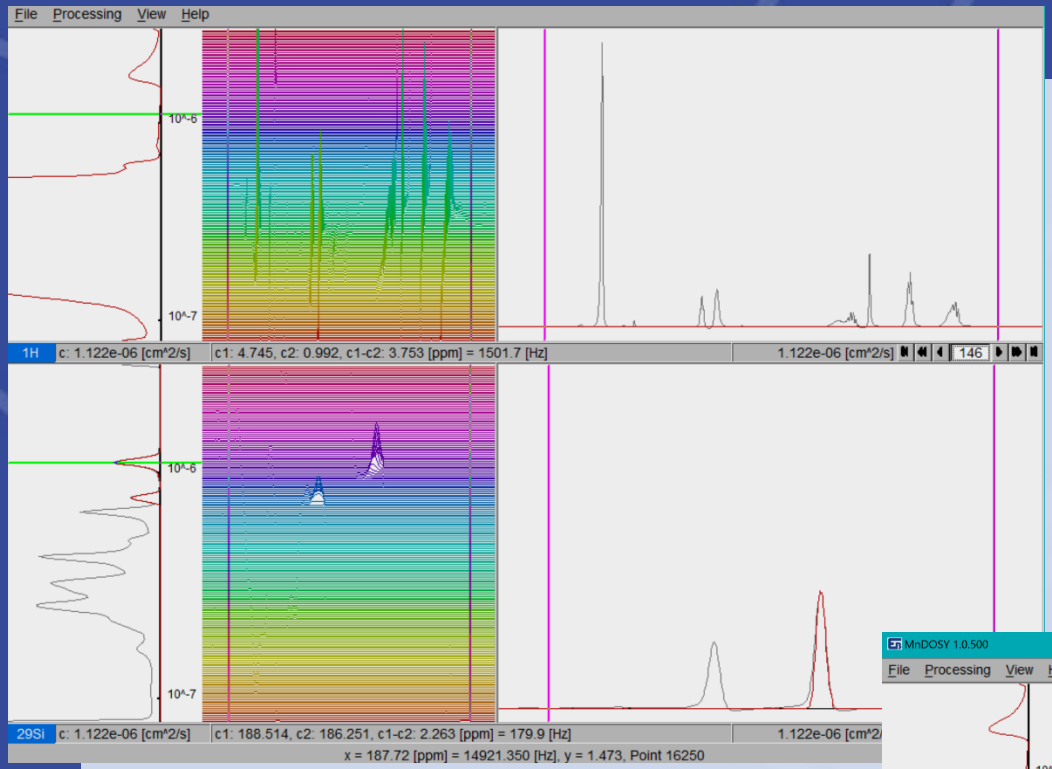


Selecting diffusion component with D = 4.273e-7 cm²/s:

The spectral panels on the right contains two traces each, one black and the other red.

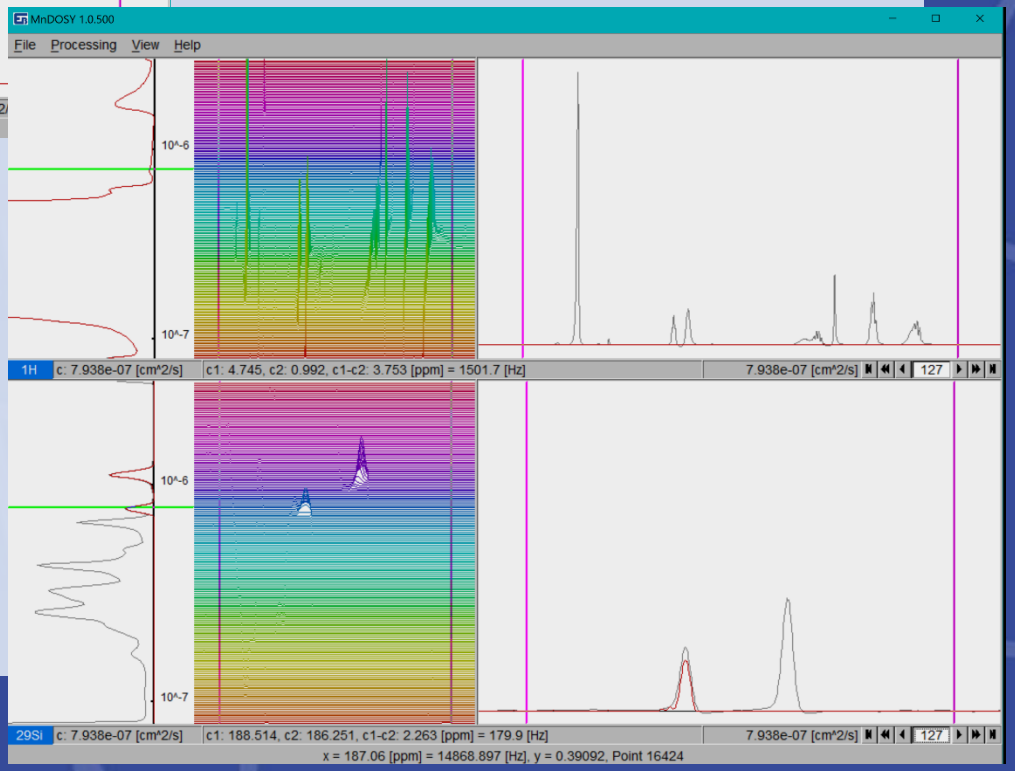
The black one is the first DOSY spectrum with the lowest gradient, used as a reference.

The red one is the DOSY trace corresponding to the left-side horizontal cursor which selects the D-value.



A simple example: the 29Si peaks at 187.13 and 187.67 ppm …

… belong to two different molecules that do not contain any non-labile protons (silicagel moieties?)



Perspectives:

We believe that MnDOSY can become a very useful tool in many applications involving mixtures of relatively small molecules containing several NMR-active nuclei.

For evident reasons,
the most important pairs of nuclei could be
(1H, 13C) and (1H,F)

Thank You for Your Attention!

Extra Byte

> In spin we trust <

The team:

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email: info@extrabyte.eu

In collaboration with

EVONIK
Leading Beyond Chemistry