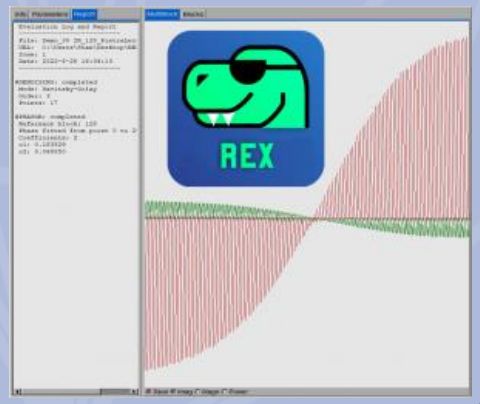
More NMR software Utilities from Extra Byte
(see www.extrabyte.eu/products)

REX

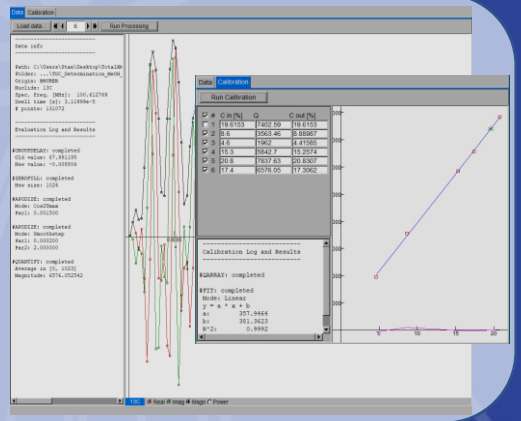
Complete software support for NMR relaxometry in any of its forms. Complete coverage from FID analysis to discrete and continuous ILT of relaxation curves, to NMRD and/or VT profiles analysis. With our help adapts to data from any vendor.



TotalXMR

Quantitative NMR analysis of chemical elements. Calibration support for total assays by either low-field or high-field NMR.

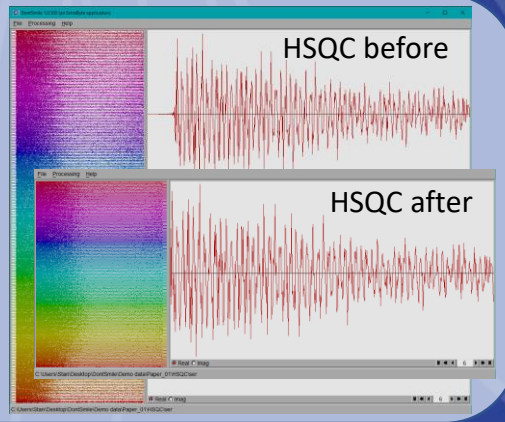
Discrimination modes: none, solid/liquid, aromatic/aliphatic (where applicable), isotopic.



DontSmile (free)

Expertly removes the annoying *smileys/frownies* artefacts due to receiver group delays from Bruker NMR spectra.

Just correct the *fid* or *ser* files and then process them as you like, with any software you like. The smileys will be gone!



Extra Byte

> in spin we trust

We are physicists & programmers,
and we specialize in rapid development of
STEM software applications,
particularly (but not only) in the area of
Magnetic Resonance (MR).

We also provide **MR consulting** and
software/hardware feasibility studies.

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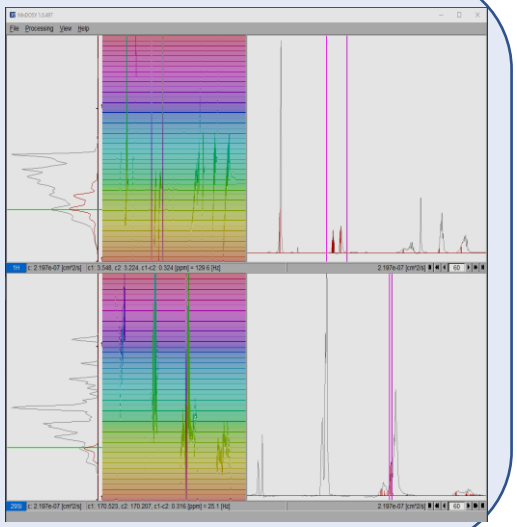
MnDOSY

Multi-nuclear Diffusion-Ordered NMR Spectroscopy

A novel NMR Spectroscopy software tool that goes a step beyond the standard DOSY

- ✓ Correlates DOSY spectra of two nuclei obtained from the same sample (for example 1H, 29Si)
- ✓ Boosts the capability of DOSY to analyse mixture components
- ✓ Simplifies the assignments of functional groups
- ✓ Evaluates also traditional single-nucleus DOSY spectra

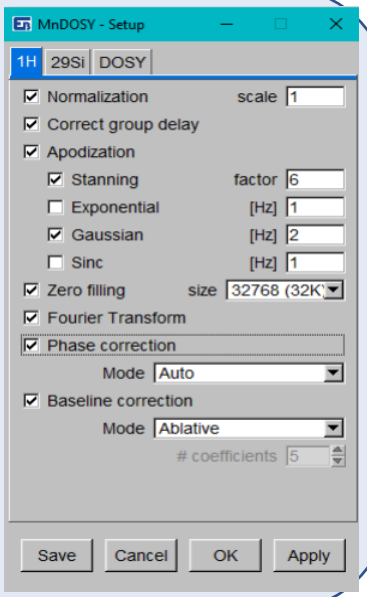


Setting of parameters for repetitive evaluations of spectra

Automation of the following processing steps:

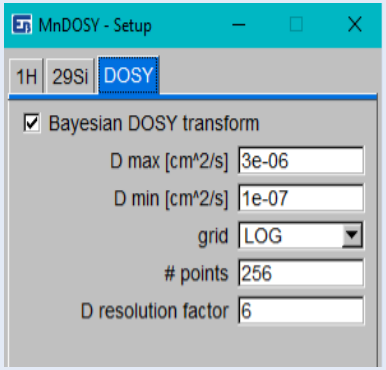
- ✓ Vertical normalization
- ✓ Group delay handling (removes “smileys”)
- ✓ Apodization functions and parameters
- ✓ Zero filling / resizing
- ✓ Fourier transform
- ✓ Automatic phase and baseline correction
- ✓ DOSY transform

Distinct parameter sets for different nuclides. The settings can be saved to a file and reused in a next session.



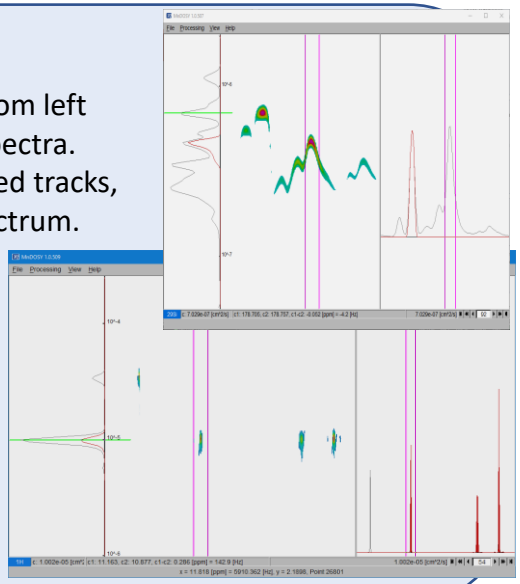
About the DOSY transform

- ✓ Uses a Bayesian algorithm (BDT) developed in 2008 by Stan Sykora.
- ✓ Presently assumes mono-exponential decays, but behaves reasonably always.
- ✓ Is lightning fast (16K x 256 BDT under 1’).
- ✓ User may set the diffusion constant (D) range and type (LIN/LOG), as well as a “resolution factor” parameter.



Salient features

- ✓ Three canvasses for each nucleus; from left to right V-projection, 2D map, 1D spectra.
- ✓ 1D spectra: browse & explore selected tracks, together with the 1st (strongest) spectrum.
- ✓ 2D map: stacked / bitmap / contour
- ✓ V-projections: quantitation along the D-axis (selected versus total).
- ✓ Vertical cursors: synchronized in the 2D map and the 1D spectra.
- ✓ Horizontal cursors in V-projections: Synchronized between the nuclei.
- ✓ Intuitive zoom/expansion modes.
- ……



Current limitations:

- ✓ Reads only Bruker data
- ✓ Combinations of nuclei so far tested: (1H, 29Si) and (1H,13C)

Collaborate with us on other combinations and/or other data and get a discount on your start-up license!

What is ahead

- ✓ Compatibility with data acquired on spectrometers from different OEM’s
- ✓ Bi-exponential DOSY transform to suppress signals overlap problems
- ✓ Integration od Mn-DOSY with high-resolution relaxometry

Purchase a renewable one-year license today and enjoy any advances at no extra cost!