Diversity of NMR Line-Shapes

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1

ChemAdder line-shape can be composed from of the following terms:

- **Lorentzian(%).**
- **Gaussian(%, global or proton specific).**
- **Asymmetry (%, global or proton specific).**
- **Dispersion (%, not very useful).**
- **Out-of-Coil (Hz), useful for benchtop and if the spectrum contains strong or broad signals.**
- **Virtual couplings (Hz, nuclei specific), if there are long-range couplings (like in steroids) the origin of which is unclear.**
- **Isotope shifts (^{13}C, Cl, Si, S) (ppm), if the H,^{13}C couplings are removed by decoupling, there remain ^{13}C isotope shifts, which may lead to a visible 1-3% shoulder at the high field (right) sides of the proton signals. Significant, for example, for glucose in biofluids.**
- **Fourier correction (33 terms) for observed-calculated difference, can be used to decrease RRMS and to reveal impurity signals under the target compound spectrum.**
- **Some essential signals, like TMS, TSP, DSS, Maleic acid, dimethyl sulfone, may have a special isotopic structure demanding a specific QM model …see QMSA Letters.**

2

Fourier correction* of observed-calculated difference spectrum:

The observed-calculated spectrum can be fitted by n-terms (max. 33/proton) Fourier function, which can be then subtracted from the observed spectrum.

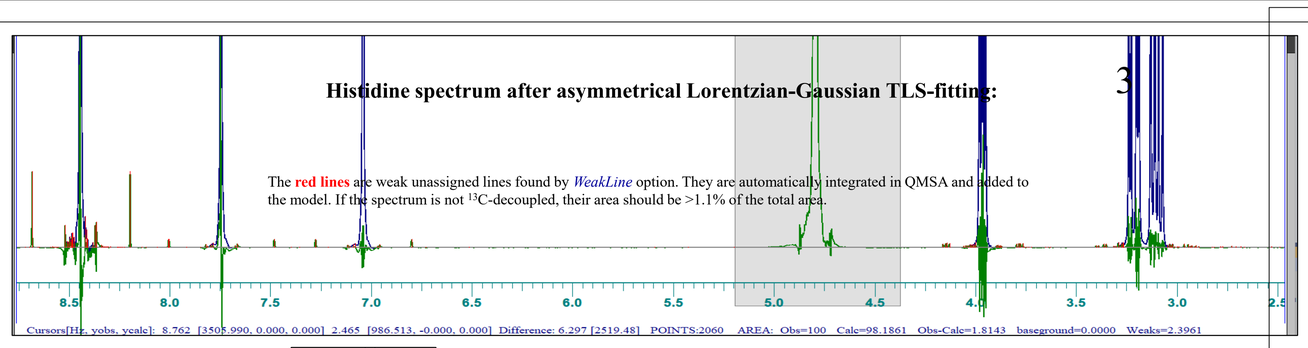
If the Fourier correction was the same for every line and the QM model perfect (= all the long-range couplings correct, the line-shape same for every line or species, etc), the subtraction should lead to zero difference! Unfortunately, this is seldom the case, but the subtraction typically leads to 40-70% decrease in eRRMS.

In principle, the subtraction should not remove impurity signals! However, if the correction is done for one multiplet, it may decrease the eRRMS by >90%, but at the same time it may remove the impurity signals hiding under the multiplet!!

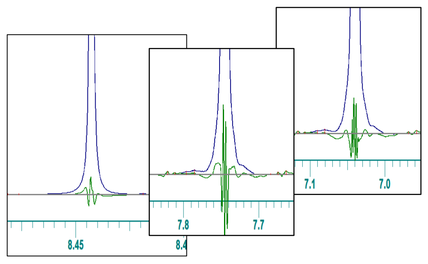
***The ChemAdder *Fourier correction*' is more than a straightforward Fourier expansion and is under tuning.**

3

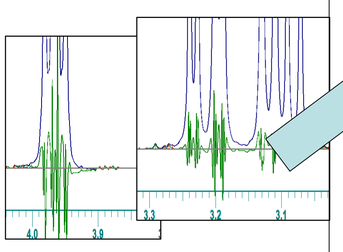
Histidine spectrum after asymmetrical Lorentzian-Gaussian TLS-fitting:



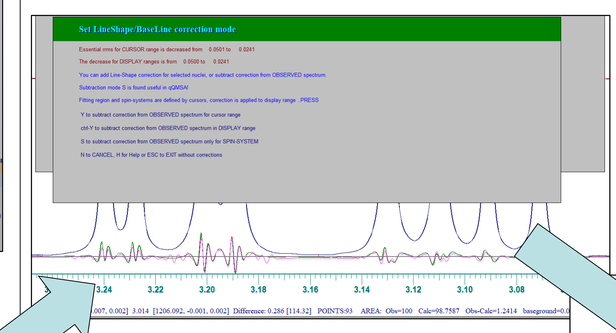
The **red lines** are weak unassigned lines found by *WeakLine* option. They are automatically integrated in QMSA and added to the model. If the spectrum is not ^{13}C-decoupled, their area should be >1.1% of the total area.



eRRMS = 0.065%



Histidine spectrum after FOURIER correction:

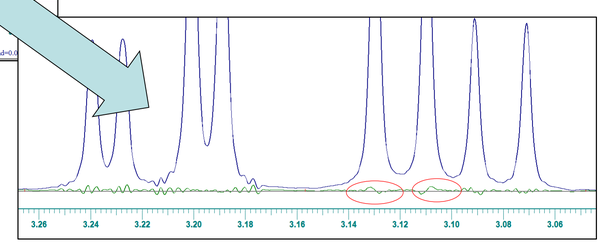


The CH_2 signals **observed-calculated difference** after line-shape optimization. The **Fourier correction** shows the fit of the **difference** with a 33 terms **Fourier function**:

The CH_2 signals and the **difference** after subtraction of the **Fourier correction**:

eRRMS = 0.024%

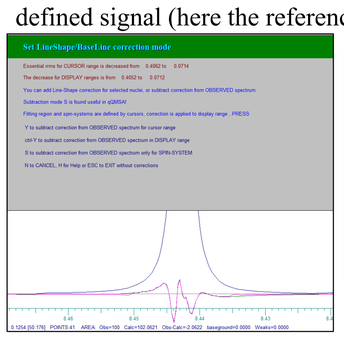
Here different Fourier functions were optimized for the two protons). The correction is somewhat proton specific.



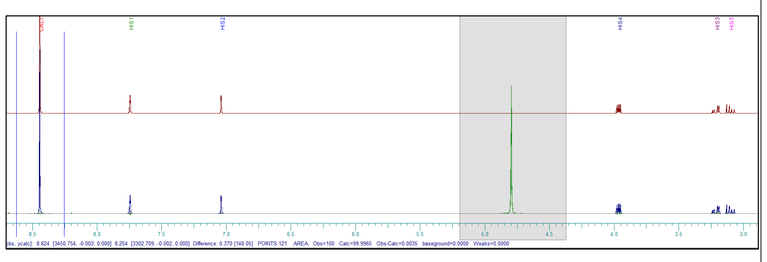
Imp? Imp?

However (next page)…

..a fair decrease of RRMS is obtained also when the **correction** is derived from a well-defined signal (here the reference signal) and then applied for all the lines:



The reference **Fourier correction:**
eRRMS from 0.40 to 0.07%



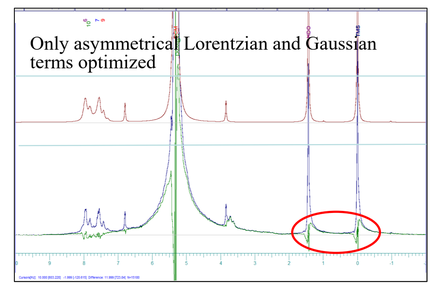
The spectrum after subtraction of the **Fourier correction** derived from the reference signal:

eRRMS decreased from 0.065 to 0.032%

Out-of-coil correction (OoC)

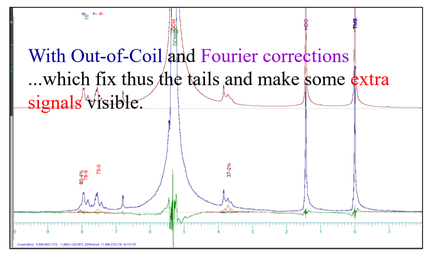
The correction is actual if the target signals lie on tails of broad and asymmetrical lines, and which cannot be satisfactorily described by the asymmetrical Lorentzian & Gaussian function. The feature can be especially important with benchtop spectra.

The **observed-calculated difference** spectrum can be fitted in ChemAdder by a N terms non-symmetrical function, which can be then subtracted from the observed spectrum. The correction compensates also a part of isotope shift shoulders.



From R. Laatikainen[a], S. Paudel[b], B. Shapiro[b], J. Zhang[c], J. Hein[c] and P. Laatikainen[a], *ChemAdderAnatomy of a 60 MHz Benchtop NMR Spectrum – Dissection*, QMSA Letters

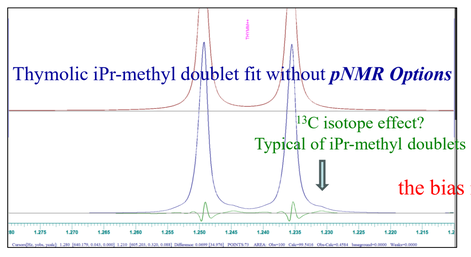
See that the correction is similar for all the three major signals:



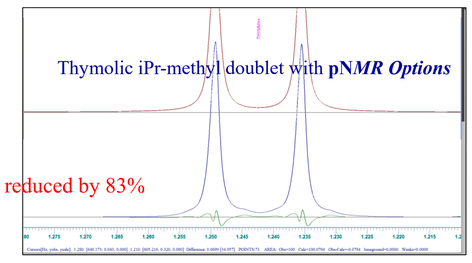
PurityNMR and IT-supported qQMSA

For example, long-range ^{13}C couplings and isotope shifts lead to structures which cannot be fitted by even the most sophisticated line-shapes. This may lead to bias of a few percent bias in PURITY%.

The ChemAdder solution is ***IT Supported qQMSA!***



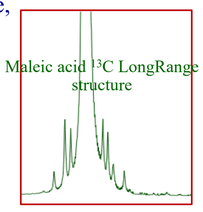
The observed-calculated area = 0.46% of the calculated area



The observed-calculated area = 0.08% of the calculated area

Isotope effects of ^{13}C, ^{29,31}Si, ^{35,37}Cl and ^{34}S

- If the H,^{13}C couplings are removed by decoupling, there remain ^{13}C isotope shifts, which may lead to a visible 1-3% shoulder at the high field (right) sides of the proton signals. Significant, for example, for glucose in biofluids.
- Some important signals, like TMS, TSP, DSS, **Maleic acid**, dimethyl sulfone, may have a special isotopic structure demanding a specific QM model …see QMSA Letters.



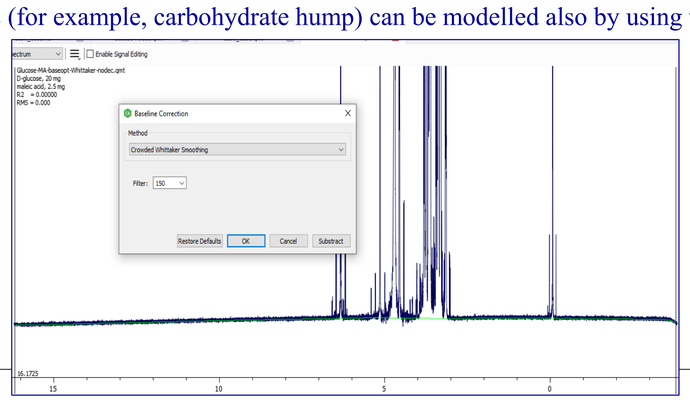
Virtual Couplings

- Virtual couplings, if there are long-range couplings (like in steroids) the origin of which is unclear.
- In ChemAdder one can define a coupling that splits all the lines of a nuclei to a regular Pascalian doublets, triplets or quartets, without defining the origin of the coupling.

Line-Shape and baseline are strongly related !

The baseline and tails of broad signals cannot be easily separated

- The baseline can be adjusted during preparation of the spectrum: in ChemAdder offers crowded Whitaker baseline correction, now with non-negativity option.
- The baseline can be optimized simultaneously with spectral and line-shape parameters: ChemAdder offers the optimizable (up to 6th order) polynomial, Bernstein polynomial and 'local cos^2' and spline baseline.
- Broad humps (for example, carbohydrate hump) can be modelled also by using the **Xtrucures**



CA

https://www.chemadder.com