Holistic QMSA+CTLS

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The purpose of hQMSA is to describe every very detail of the spectrum

Holistic quantitative QMSA + CTLS
(CTLS = Constrained Total-Line-Shape)

A spectrum data may contain the 5 different type NMR signals :

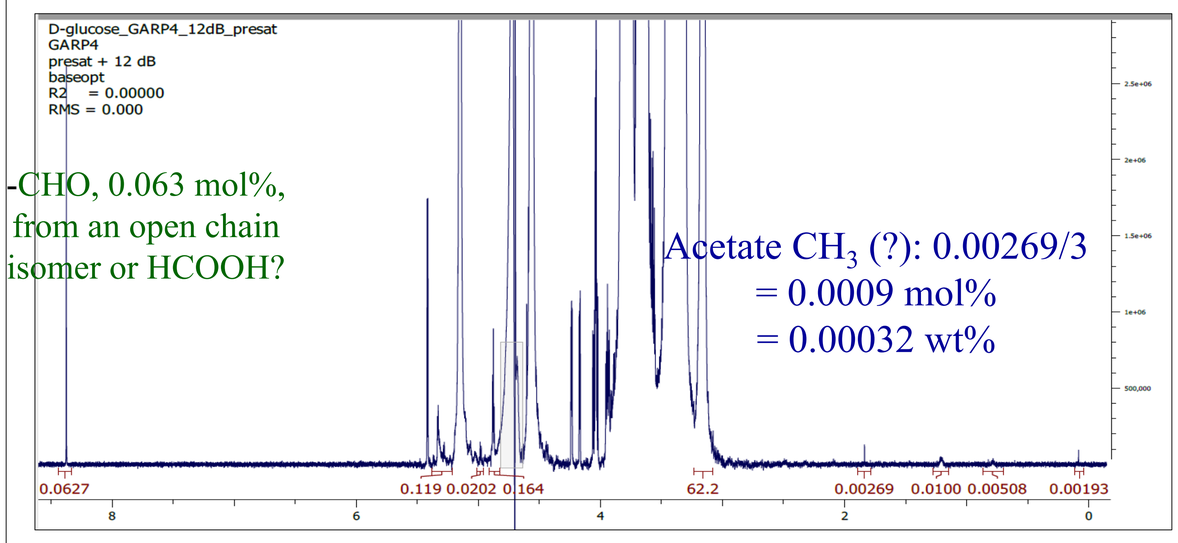
- 1. *Quantum Mechanically modellable signals*
- 2. *Xtructures* (singlets, multiplets), like polymer and lipoprotein signals
- 3. *Xpectrals*, like albumin spectrum
- *4. Xpurities,* unassigned weak signals
- 5. *Integrals*, none of the above

The common point is that the signal area/nucleus is the same:

Total area = QM + Xtructures + Xpectrals + Xpurities + Integrals

All the species can be handled in one model by ChemAdder !

The mol%'s of of impurities can be determined by integration or CTLS, …here using the B2-proton signal as the quantitative reference:



B2-proton, mol% = 62.2% (= β-glucose mol%)

T2 edited serum spectrum with three types of *xtructures*

- Singlets
- Regular Pascalian (here doublet)
- Multiplets with varying line-intensities, constant line-spacings and line-widths (lipoproteins, CH_2 and CH_3). In the less regular multiplets, either line-spacings, intensities and/or line-widths are allowed to vary.

Biofluids ..XPECTRALS.

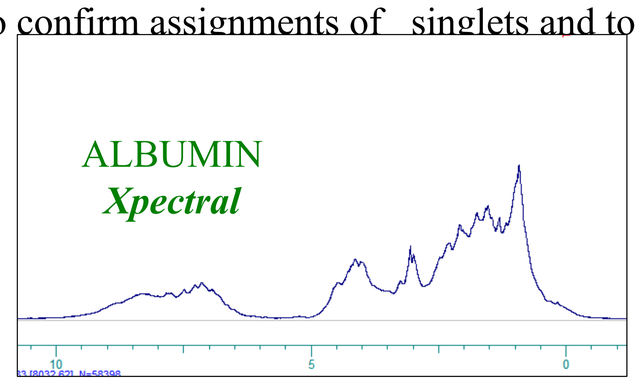
^{1}H NMR of serum = *QM-spectra* + *Xtructures* + *Xpectrals*

QM-spectra: glucose and other small molecule metabolites

Xtructures: lipoproteins

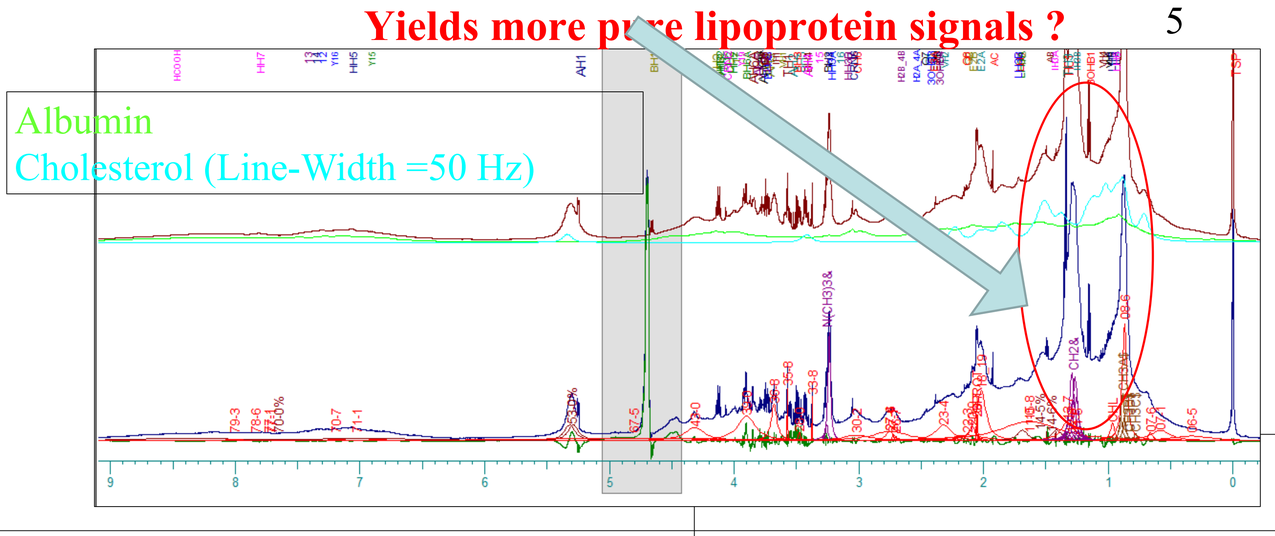
Xpectrals: albumin, cholesterol

Spiked QMSA (spkQMSA) …to confirm assignments of singlets and to compensate RF bias!



The **spectral xtructures** can be singlets, regular (Pascalian). In the less regular (several options) multiplets, either line-spacings, intensities and/or line-widths are allowed to vary.

QM-spectra + Xtructures + Xpectrals
Yields more pure lipoprotein signals ?



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XPURITIES

- A spectrum may contain weak well-defined signals like **^{13}C satellites** or **peaks arising from unknown impurities**.
- In not ignored QMSA, the weak signals are added to the baseline and, thus, lead to a positive bias - too high a purity !
- The **xpurities** can be found automatically, added to the model and subtracted from the major spectrum.
- The peak areas give an estimates of the impurity concentrations and more accurate picture about the sample purity.