

NMR practical course

1st 2021.6.15

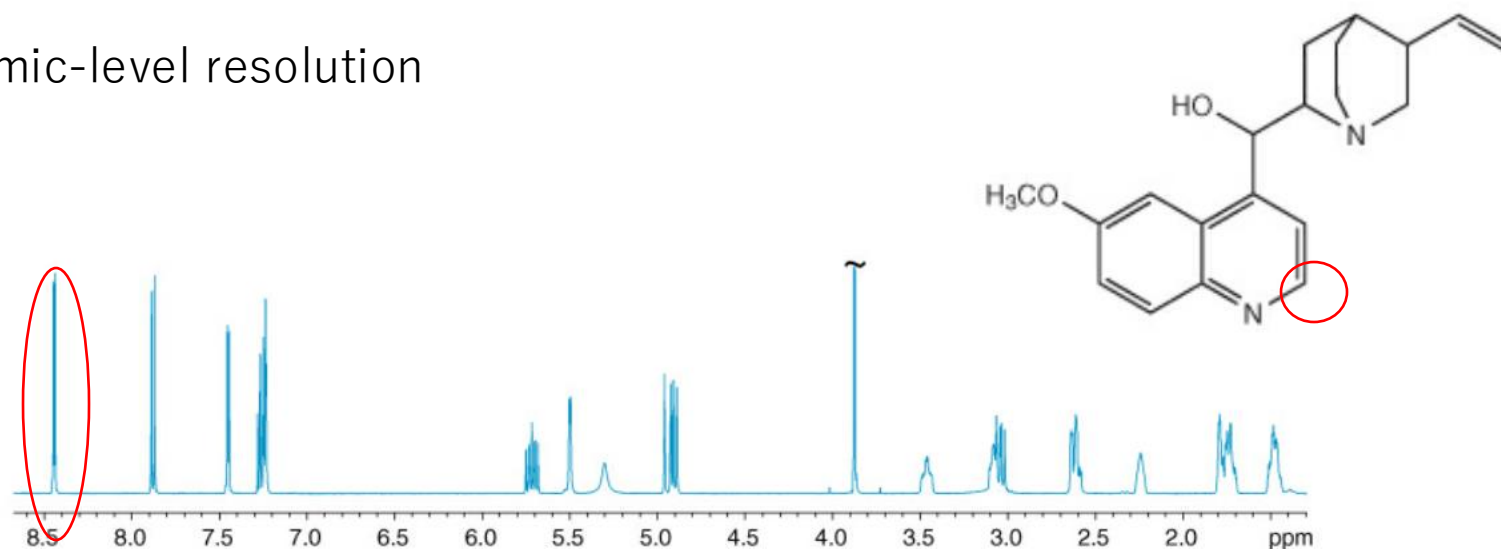
last updated 2021.7.9

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Advantage of using NMR

Atomic-level resolution



The chemical structure and ^1H -NMR spectrum of 'quinine' in CDCl_3 solution. The hydrogen atoms in the red circles in the structure are observed in the red circles in the spectrum.

The hydrogen atoms in the structure can be observed in pieces.

Disadvantage of using NMR

Worst sensitivity in the industry
Expensive equipment and maintenance costs



UV spectrometer : ¥1,000,000~
Detectable from pM order
Measurement time: a few seconds



NMR : ¥50,000,000~
Detectable from uM
Maintenance cost per year
: ¥1,000,000

Measurement time:
several minutes to hours



CT scan
a few seconds



MRI scan
More than 30 mins

NMR applications

Structure determination of small molecule compounds

Structure determination and
acquisition of structural information of biomolecules

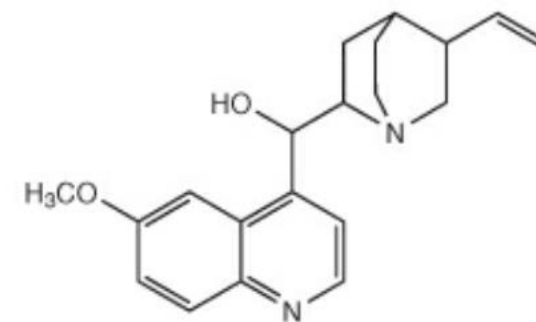
Quality control

Drugs, proteins, lipids, rubber, plastics, etc.

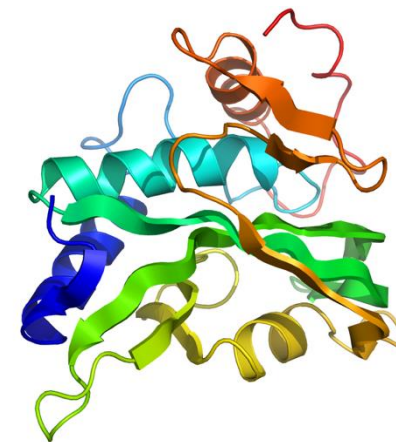
Regardless of the state of matter (liquid, semi-solid, solid).

Metabolomics of wine

Know the raw materials, the region, the domaine,
even the year of production! (No need to be a sommelier)



Quinine



Protein glutaminase

<https://www.bruker.com/ja/products-and-solutions/mr/nmr-food-solutions/wine-profiling0.html>

NMR can tell us a lot of things !

Sample preparation – for small molecule compounds

Use a deuterium ($^2\text{H}=\text{D}$) solvent
 D_2O , CD_3Cl , $\text{d}_6\text{-DMSO}$ ($=(\text{CD}_3)_2\text{SO}$), CD_3OD , etc.

Not interfere with the observation
of proton signals in the compounds.

Volume : $500\ \mu\text{L}$

Dissolve a few mg of sample.

**** Solubility is important. ****

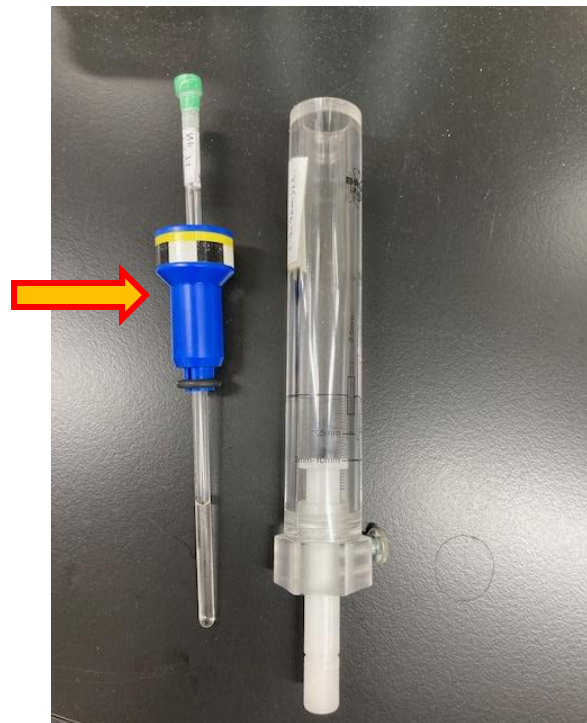
The solvent height is at least 4 cm.



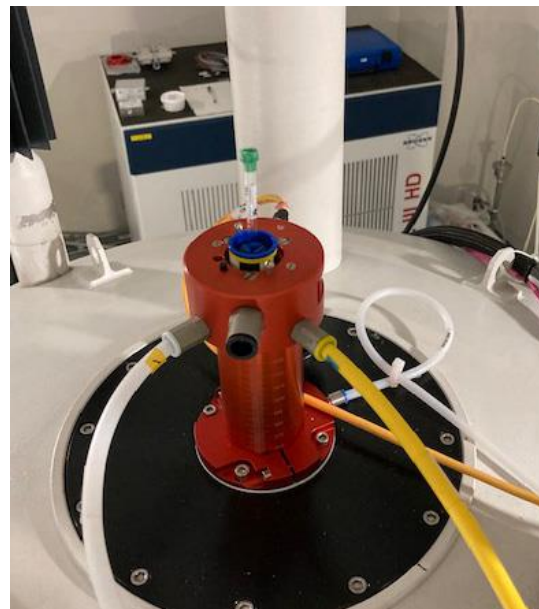
5 mm NMR tube and
human right hand.

Sample tube insertion to NMR magnet

Holder
(spinner)



Adjust the sample position
with a gauge.



Float the sample with air.
Insert the sample by closing the air valve.



Procedures after sample insertion

1. Lock
2. Tuning
3. Shimming
4. Parameter setting

For students in the practical course,
4 is a term you can easily understand.
2 is a term you may have encountered somewhere before.
But 1 and 3 may be new to you.

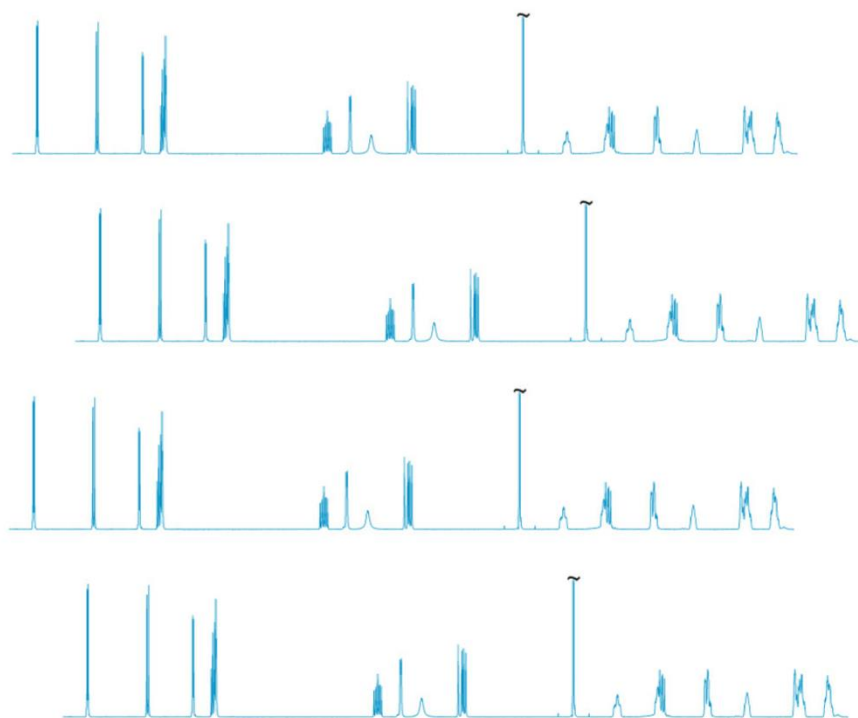
1. Lock

Lock is applied using the frequency of deuterium in the solvent.

Worst sensitivity in the industry => Needing stack of scans

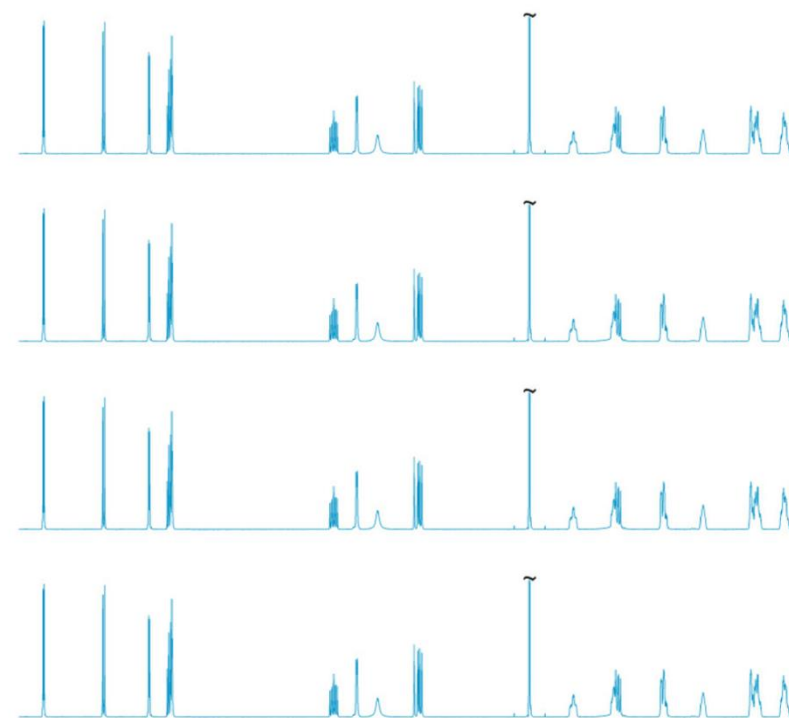
Atomic-level resolution => NMR frequency accuracy required for correction

ロックをかけないと毎回ずれる



Lock off

ロックをかけると揃う



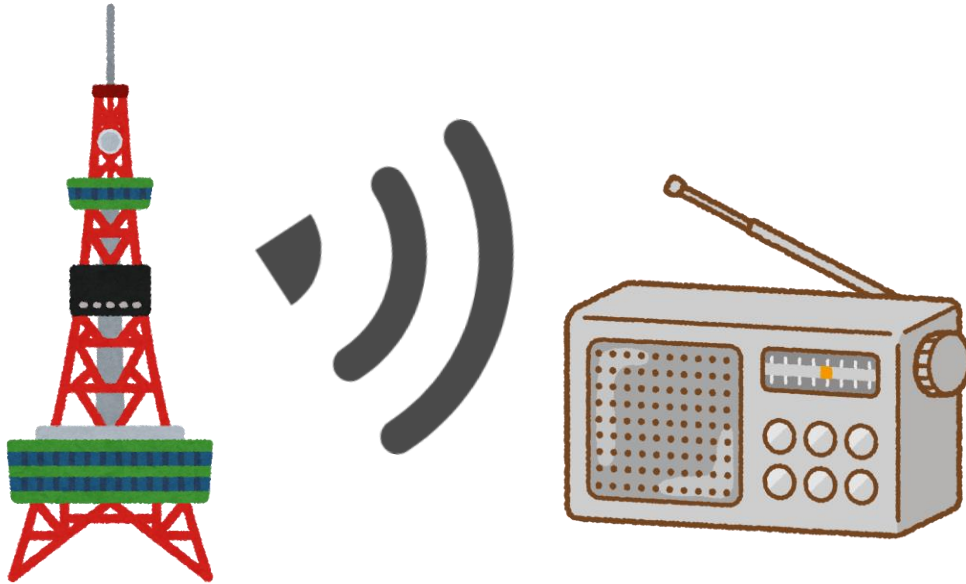
Lock on

2. Tuning

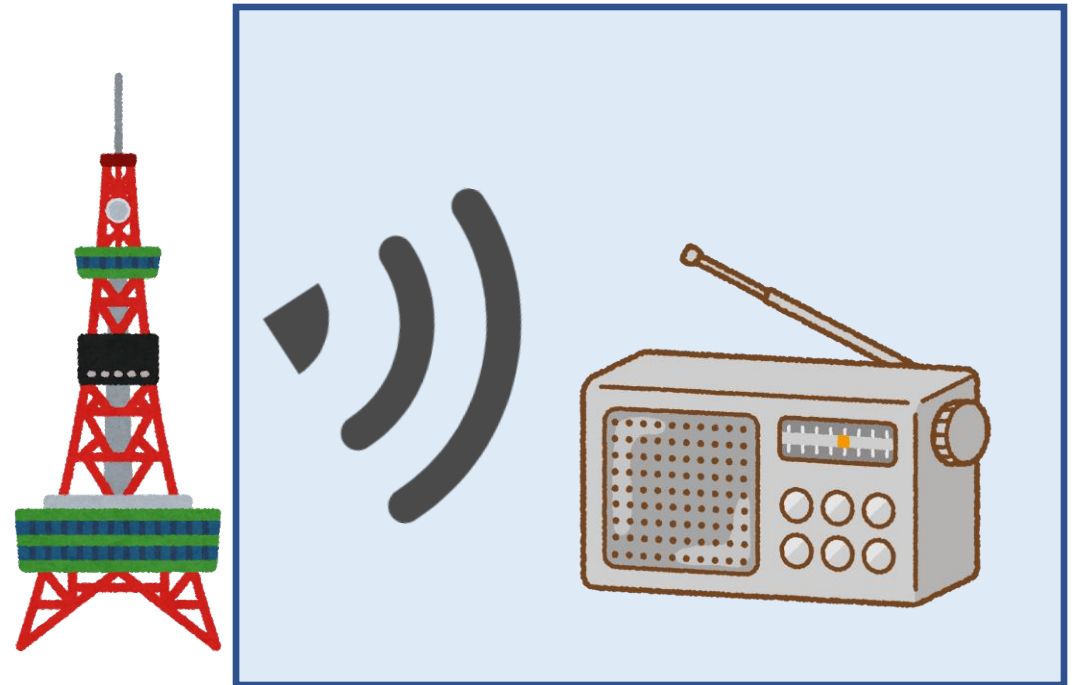
Almost the same meaning as tuning a radio.

To tune the frequency to the channel (nuclear type) you want to listen to.

To make a clear sound (input pulse or output signal).



Almost constant as it passes through the air



Since it passes through a solution and glass of tube, fine adjustment is required if the sample change.

3. Shimming

To improve the uniformity of the magnetic field.

The electromagnet coil for adjusting the uniformity is called “shim coil”.



The magnetic field is easily disturbed at the gas-liquid interface.

=> Keep at least 1 cm away from the detection area.

Detection area (about 1.6 cm).

The magnetic field is also easily disturbed at bottom of the NMR tube.

=> Keep at least 1 cm away from the detection area.

4. Parameter setting

OK by default setting

There are too many unfamiliar terms,
so do not change the settings until you have a deep understanding of these terms.

The screenshot displays the Bruker TopSpin software interface, specifically the 'AcquPars' (Acquisition Parameters) window. The window title is '210506_yuzawa_01_Sal 1 1 C:\Data\kumeta'. The 'General' tab is selected, and the 'Channel f1' section is expanded. The parameters are organized into two columns, with the right column providing descriptions for the values in the left column.

Parameter	Value	Description
PULPROG	zg30	Pulse program for acquisition
TD	65536	Time domain size
SWH [Hz, ppm]	12019.23	Sweep width
AQ [sec]	2.7262976	Acquisition time
RG	203	Receiver gain
DW [μsec]	41.600	Dwell time
DE [μsec]	6.50	Pre-scan-delay
D1 [sec]	1.0000000	Relaxation delay; 1-5 * T1
DS	2	Number of dummy scans
NS	16	1 * n, total number of scans: NS * TD0
TD0	1	Dimension of accumulation loop
SFO1 [MHz]	600.1337060	Frequency of ch. 1
O1 [Hz, ppm]	3706.05	Frequency of ch. 1
NUC1	1H	Nucleus for channel 1
P1 [μsec]	9.48	F1 channel - 90 degree high power pulse
PLW1 [W, -dBW]	12	F1 channel - power level for pulse (default)

Acquisition parameters in the simplest 1D-proton NMR experiment.

Demonstration

Step	command
0. Sample Insertion	ej/ij
1. Lock	lock CDCL3
2. Tuning	atma
3. Shimming	topshim 1d rga
4. Parameter setting	edc
5. Acquisition	zg

Procedures after acquisition

1. FT
2. Phase correction
3. Analyse

1. FT, Fourier Transform

generate the spectrum from FID data



FolderName (Sample Name)

ExpNo (Experiment Number)

ProcNo (Process Number)

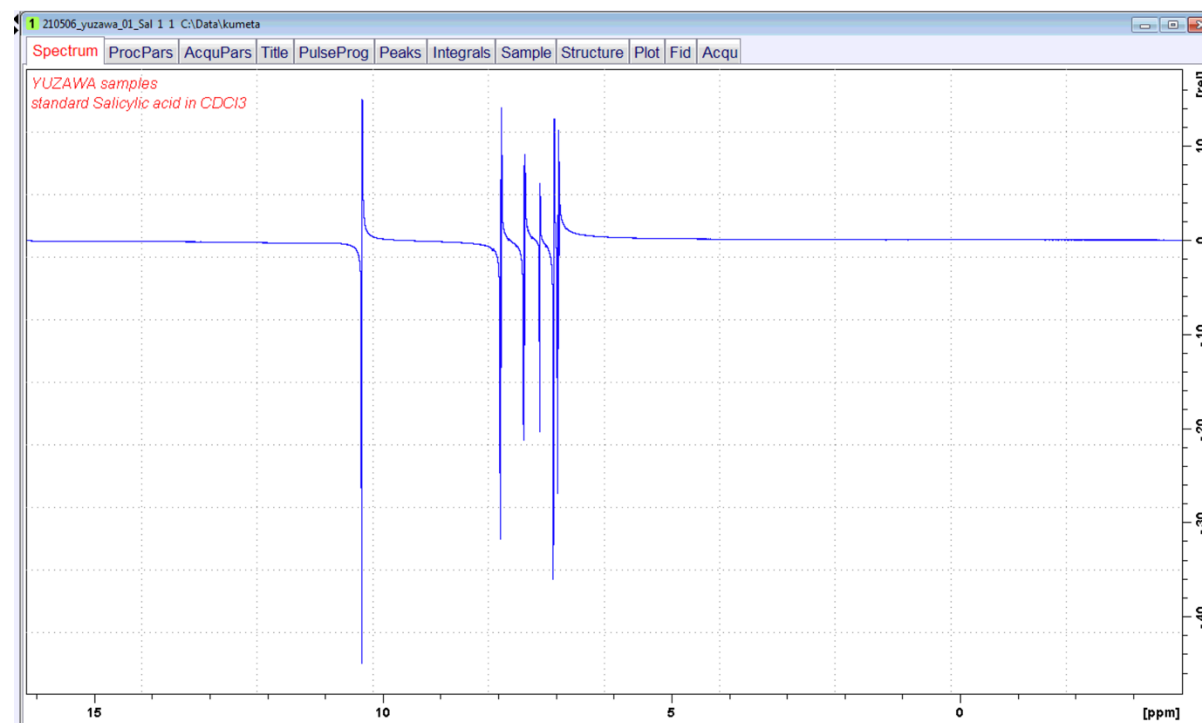
Double click on ProcNo

efp FT with exponential window function

.all show full spectrum

There is a signal in negative region.

= "Phase" not aligned
need to compensate



2. Phasing

"Phase correction" to get the "absorption" spectrum.

apk0 Zero-order automatic phase correction
.ph Change to phase correction mode
.sret Return, and save spectrum

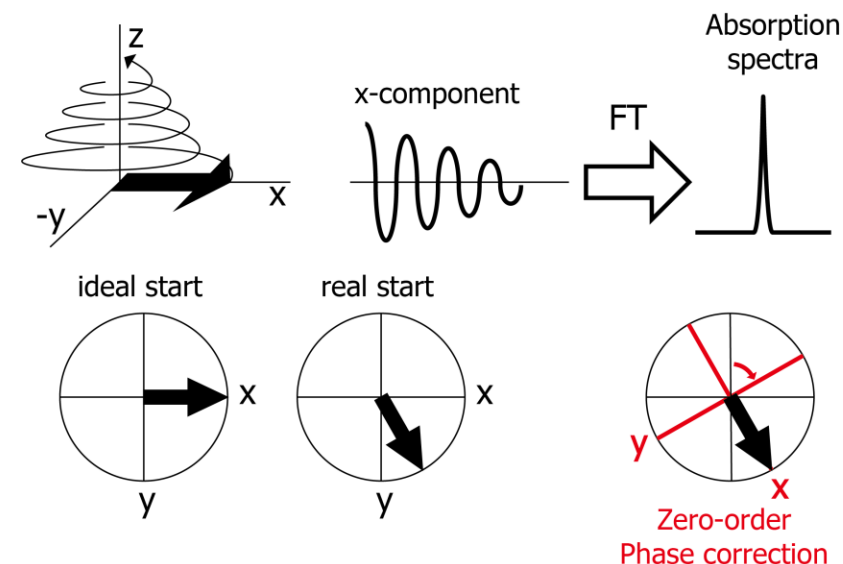
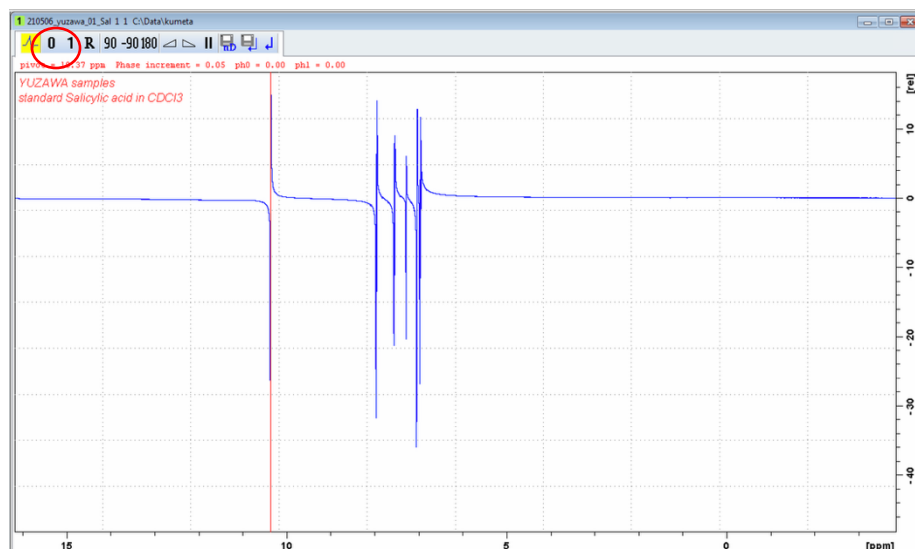
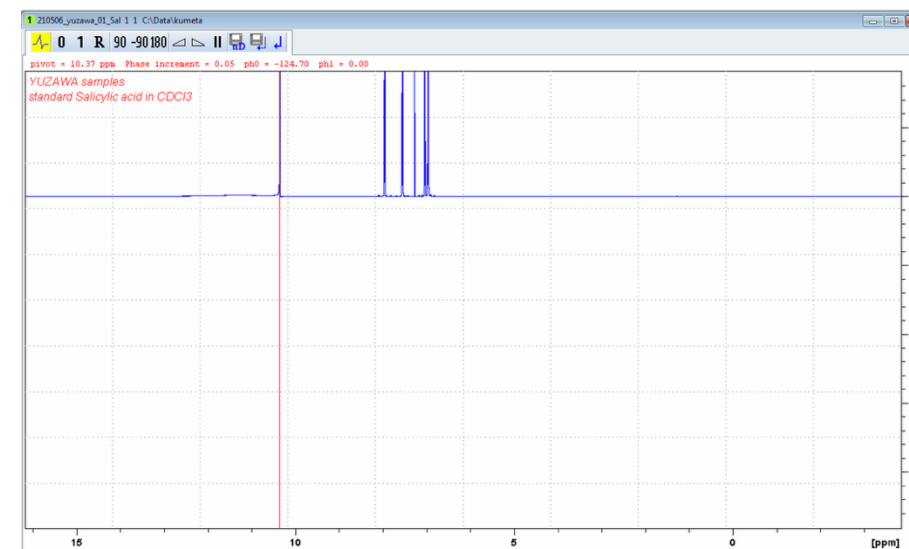
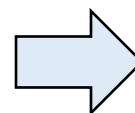


Image of zero-order phase correction

Drag the "0" icon, and mouse up and down.



"dispersion" spectrum



"absorption" spectrum

3. Analyse

Overlay and compare spectral data

.md Change to multiple spectrum mode

Demonstration

1. FT

efp

2. Phase correction

.ph / .sret

3. Analyse

.md