NMR Training Course (Operation)

JEOL Ltd.
Taiwan
陳國豐 Edward Chen

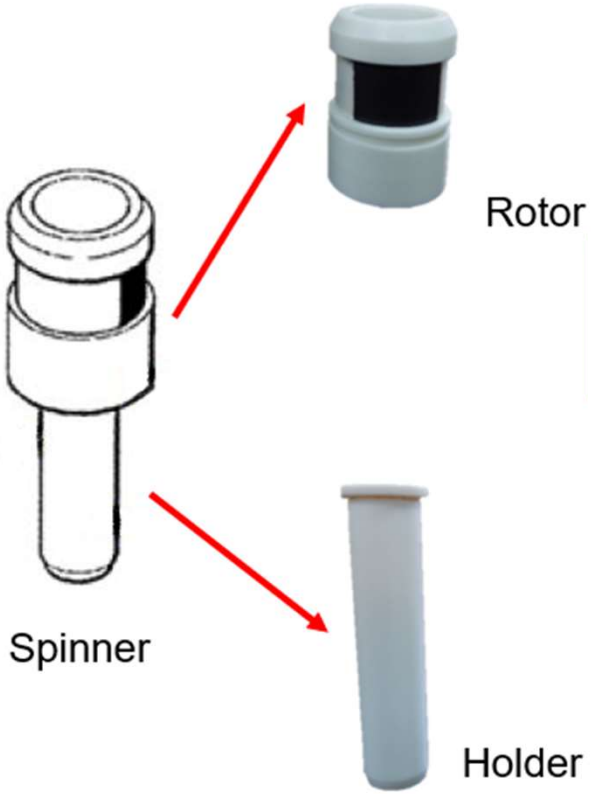
Precaution

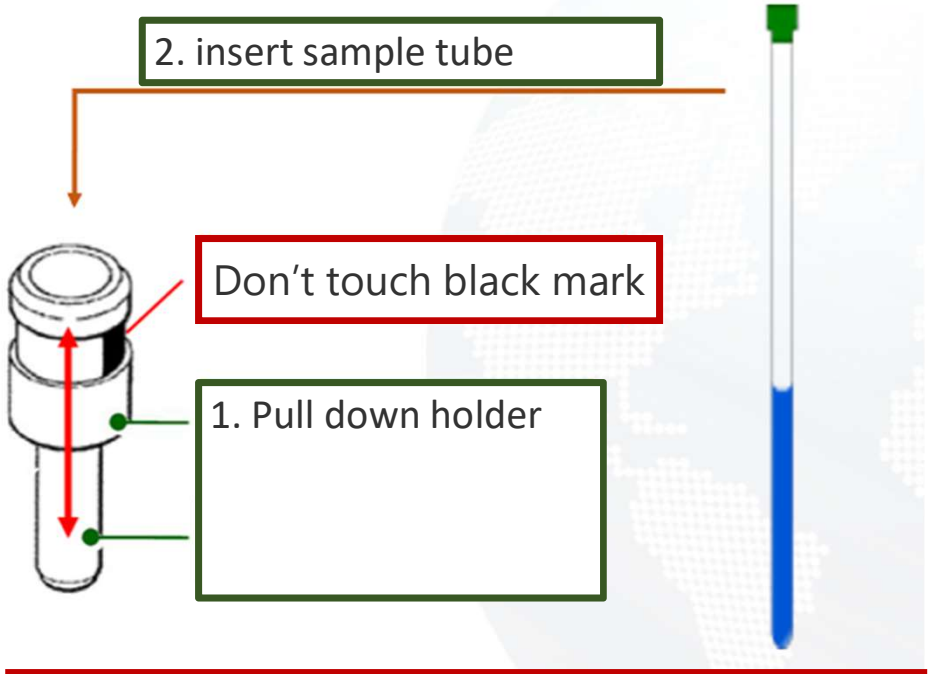
- Do not insert anything other than the Spinner and Tube into the SCM
  Special attention: Please be especially careful with bracelets, necklaces, items in your pockets, and other loose metal objects.
- In the event of a magnet quench, immediately notify everyone and evacuate the laboratory.



ref: https://www.youtube.com/watch?v=d-G3Kg-7n_M&ab_channel=SebastianSteiner

Sample preparation

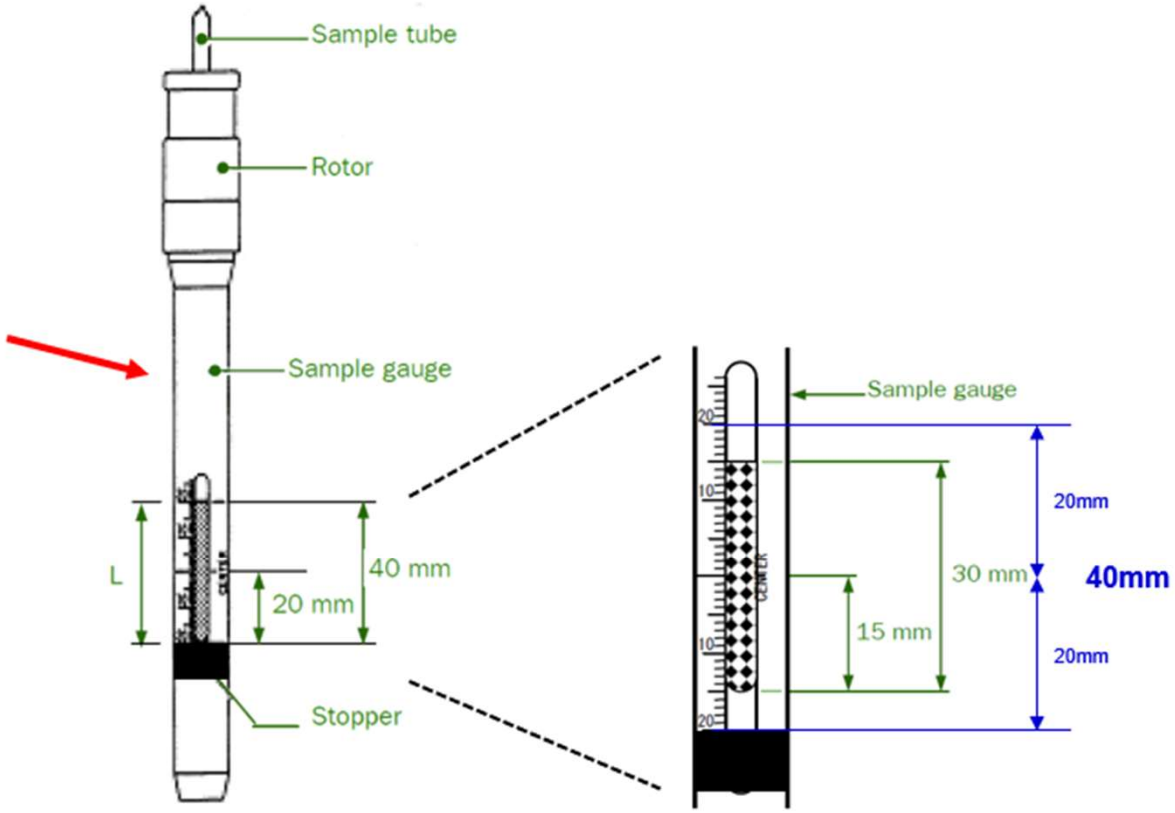




Please clean your tube before insert it!!!!

Sample preparation





- To ensure proper operation of the gradient shim, a sample height of **4 cm** is recommended.
- The sample must be **completely dissolved**. If the sample contains solid particles, they may significantly affect the homogeneity of the magnetic field.
- The minimum sample height is **3 cm**.

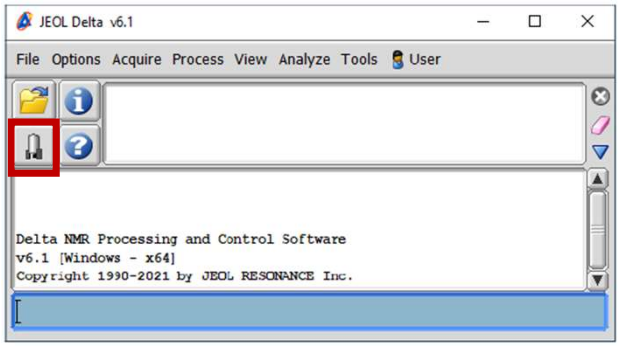
  If the sample height is **3–4 cm**, adjust the bottom of the Tube to **–17 mm**.
- Before inserting the Tube, make sure that the **Spinner has been fully extended upward and downward**.

Do NOT use the gauge to measure the sample position and then move the Spinner up or down.

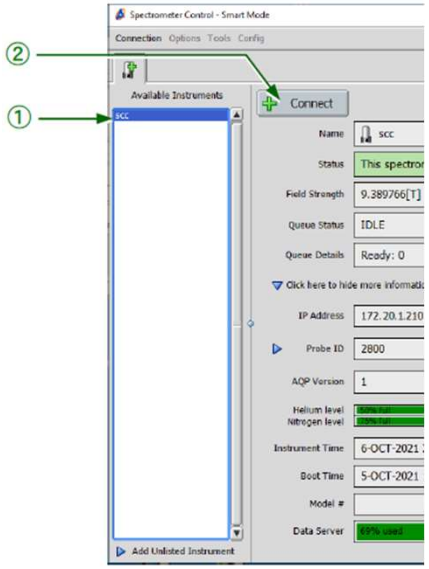
Starting the Delta program



1. Double click Delta icon.



2. Click instrument icon.



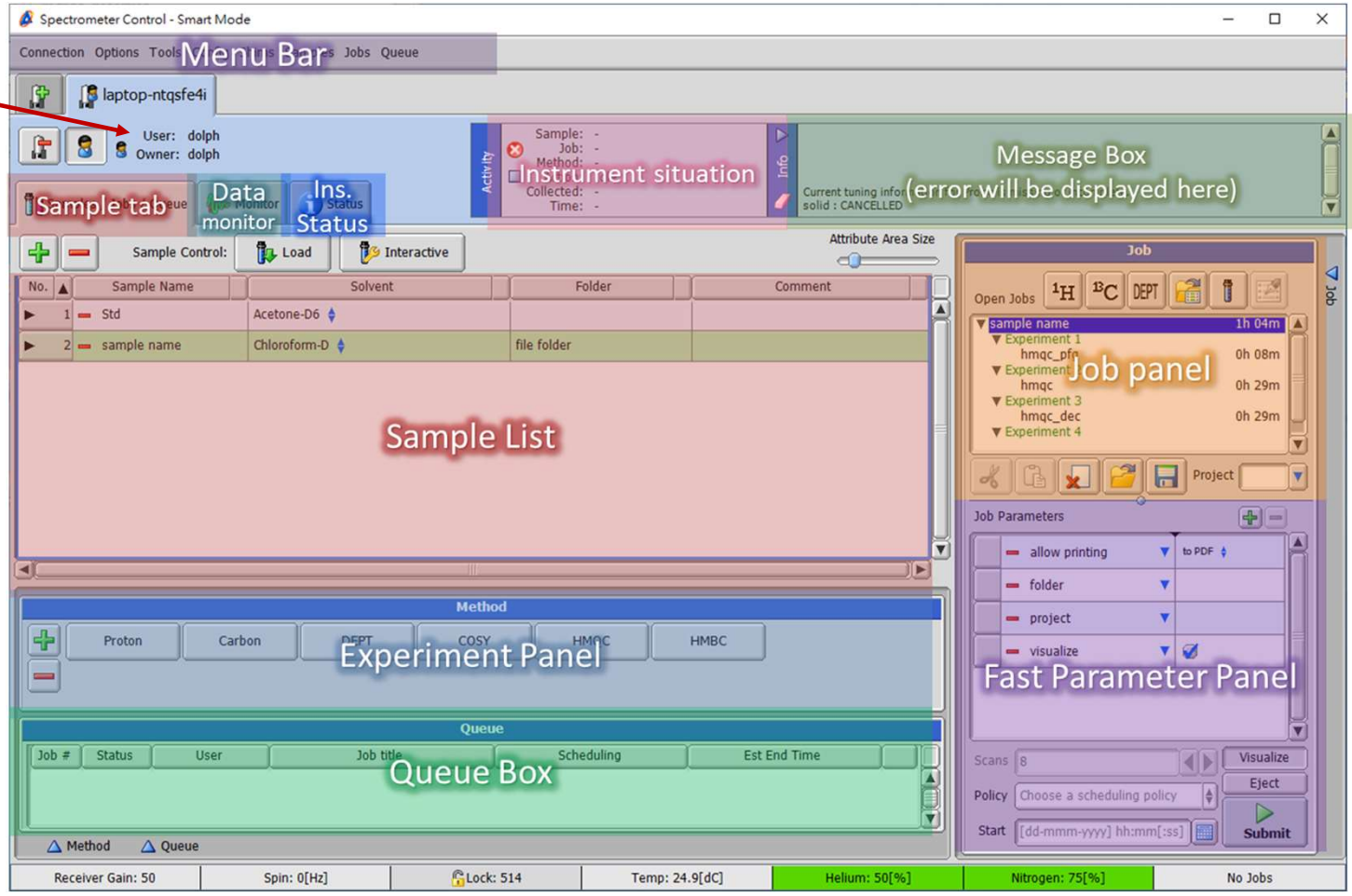
3. Select “scc” and click Connect.



4. Input user name and password then click “Own”.

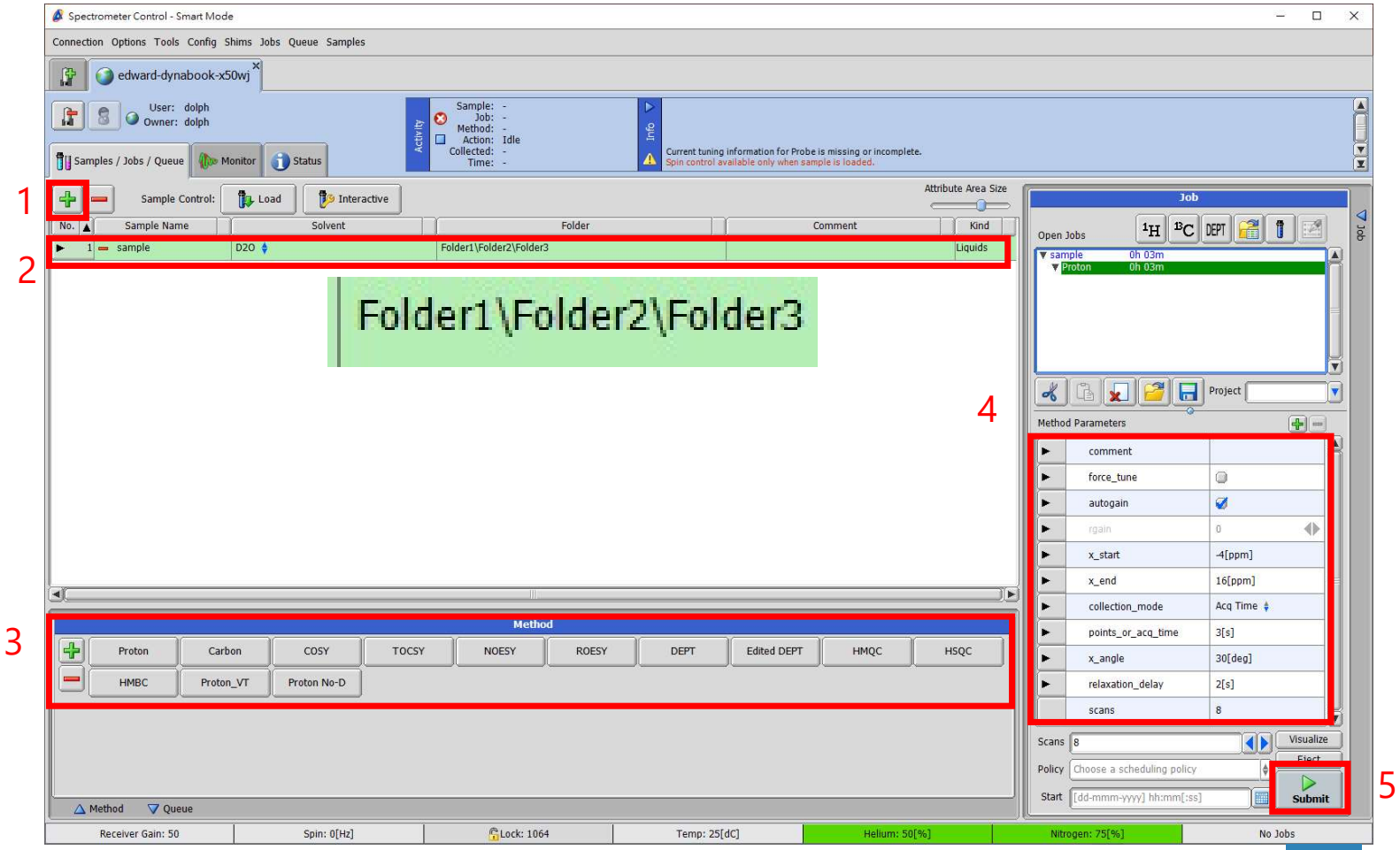
Control Window

Please confirm that you are the owner

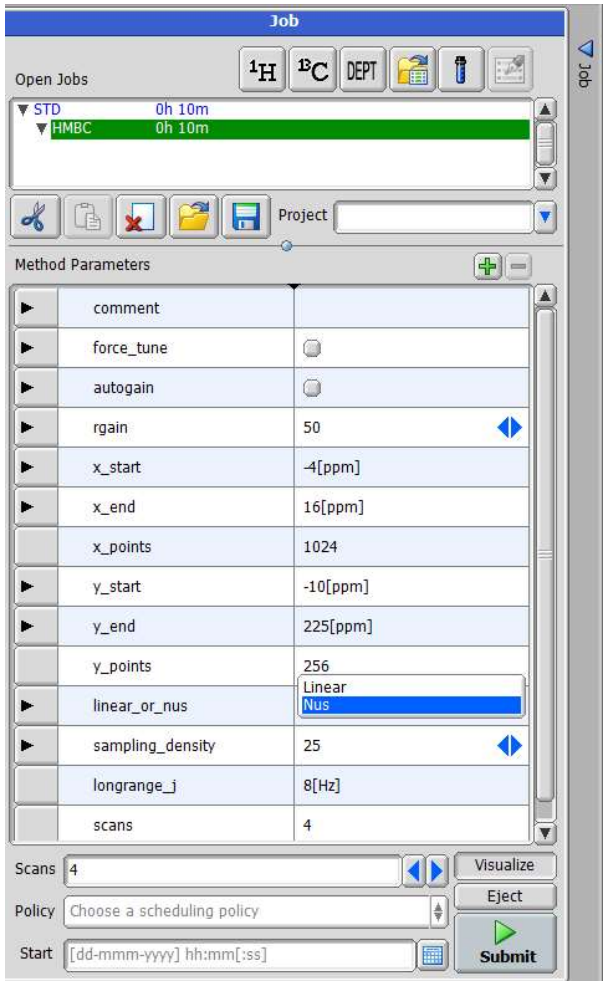


Quick experiment flow (with automation experiments)

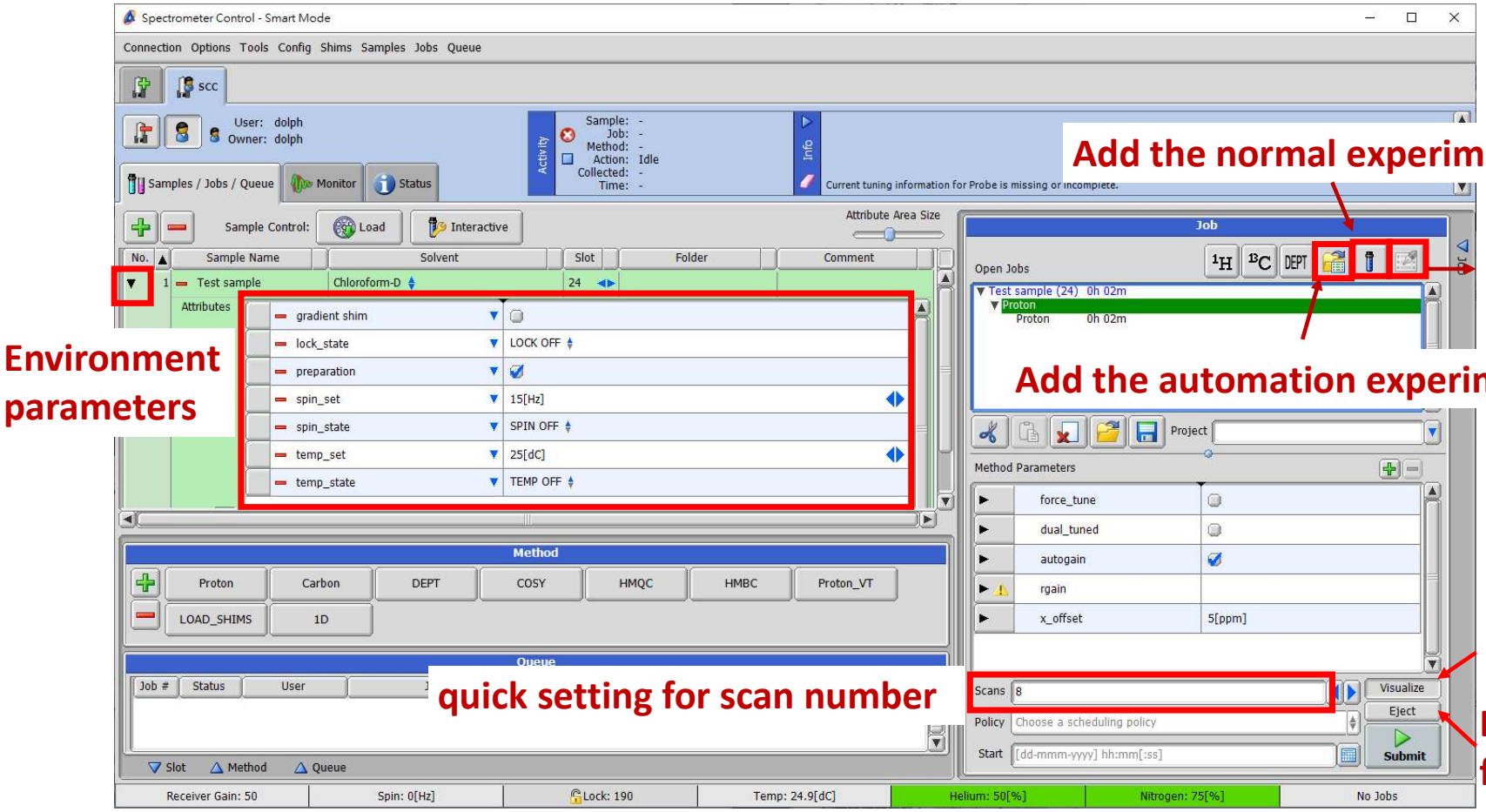
1. Add a sample row.
2. Input sample information.
3. Select the experiments.
4. Modified parameters.
5. Submit your job.



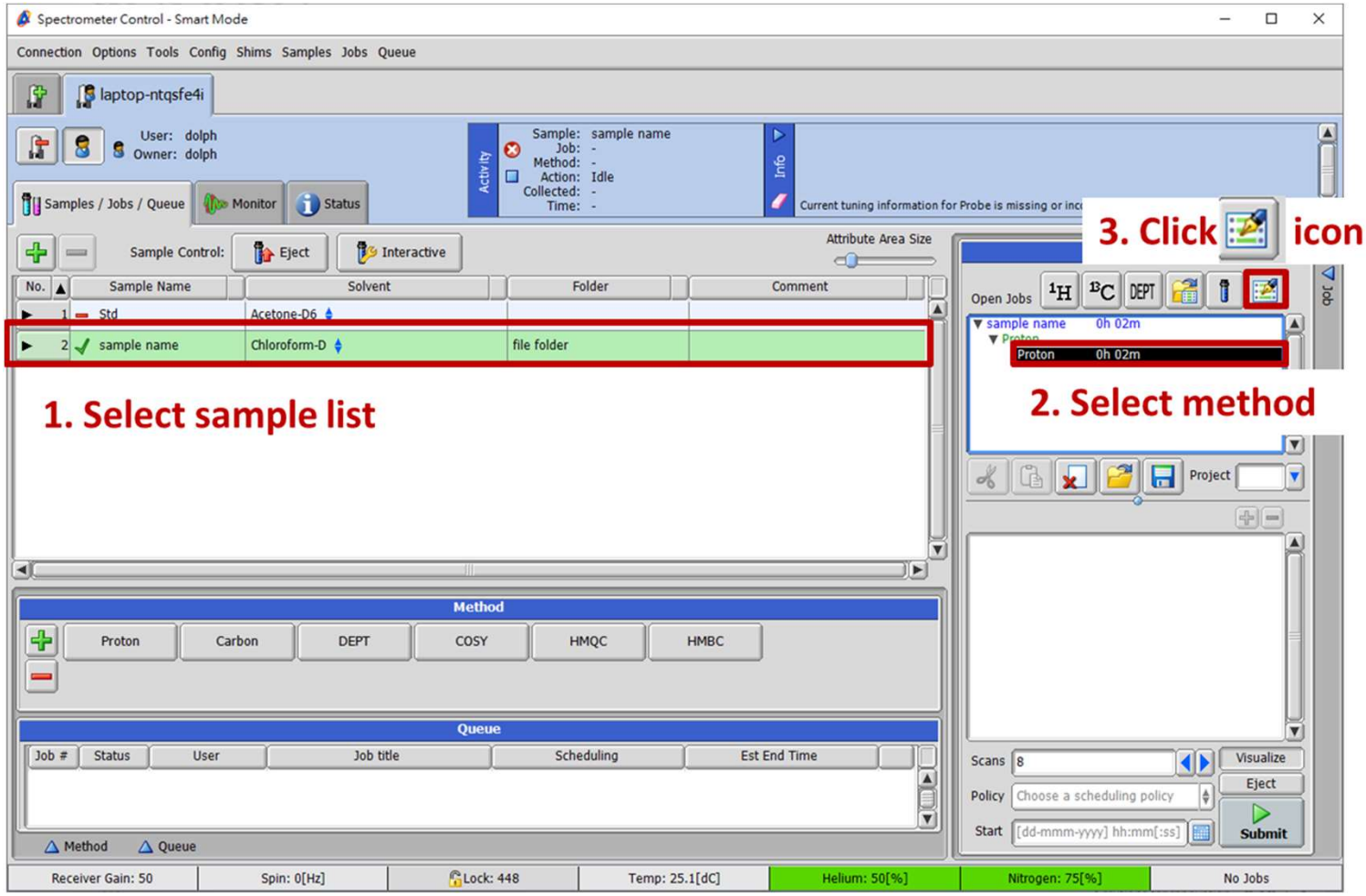
Automation parameters



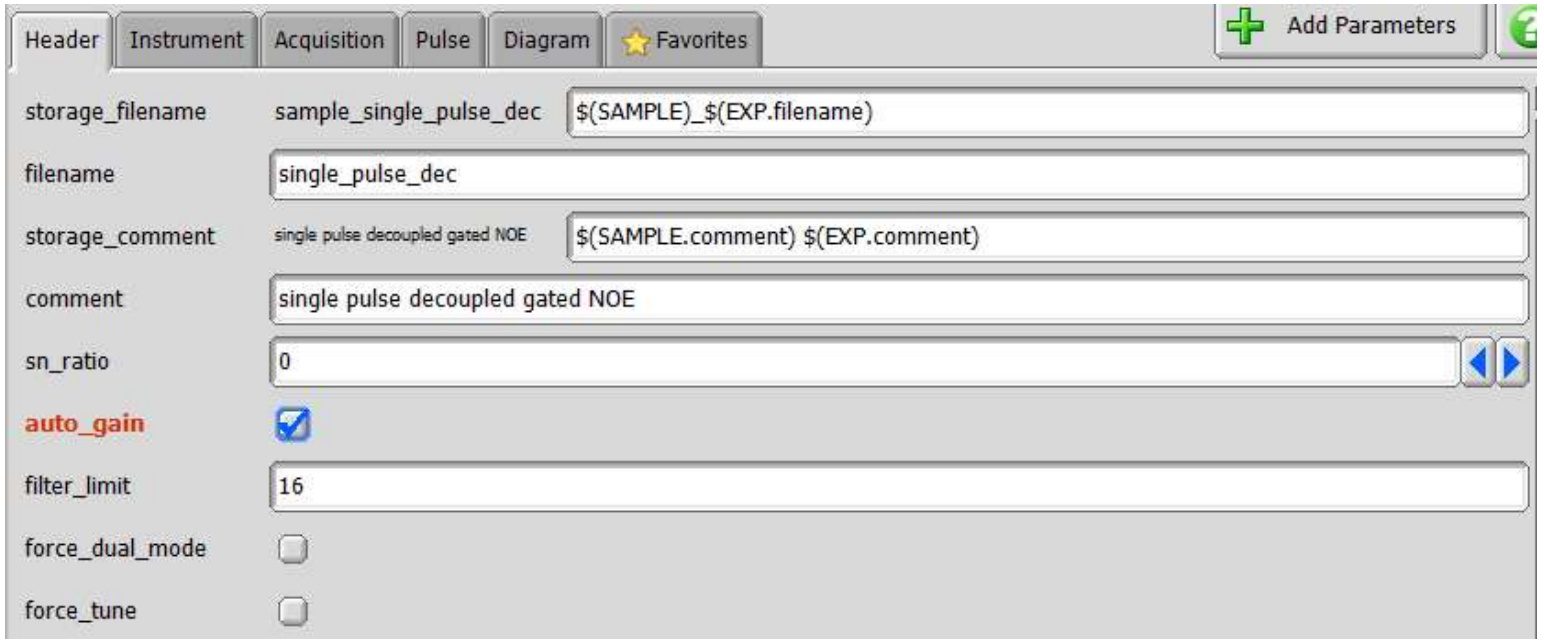
Environment parameters and Normal experiments



Modified parameter for normal experiments

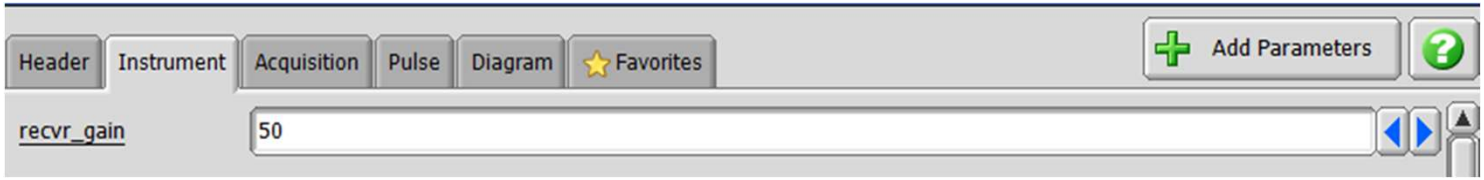


Basic parameters - header

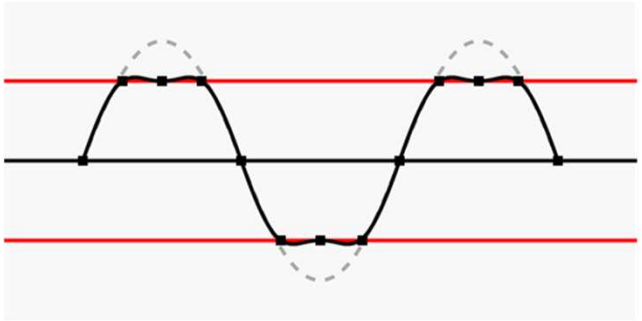


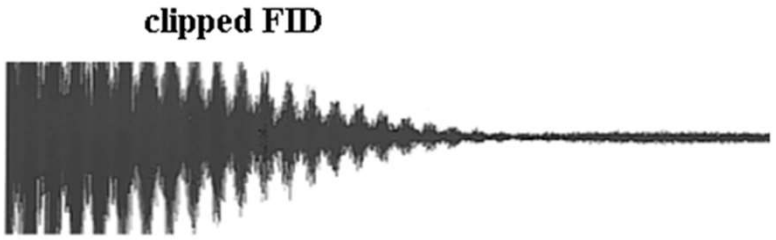
- Storage_filename：存檔檔名
- Comment：檔案備註
- auto_gain：自動調整rcv增益倍率避免訊號過小或過大
- force_tune：實驗前強制執行Tuning

Basic parameters - Instrument



- recvr_gain：receiver增益放大倍率
  - recvr_gain太低，FID訊號微弱造成圖譜訊號微弱
  - recvr_gain太高，FID訊號過強造成圖譜失真





FID clipped

- In log window, “Clipped data in scan xx”

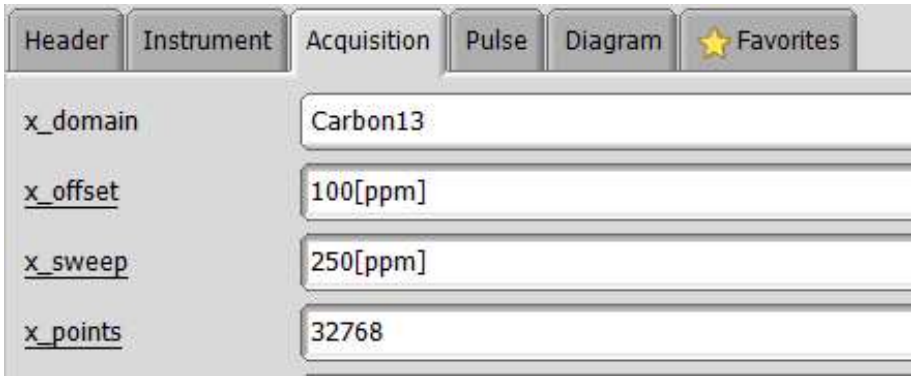
  Example:

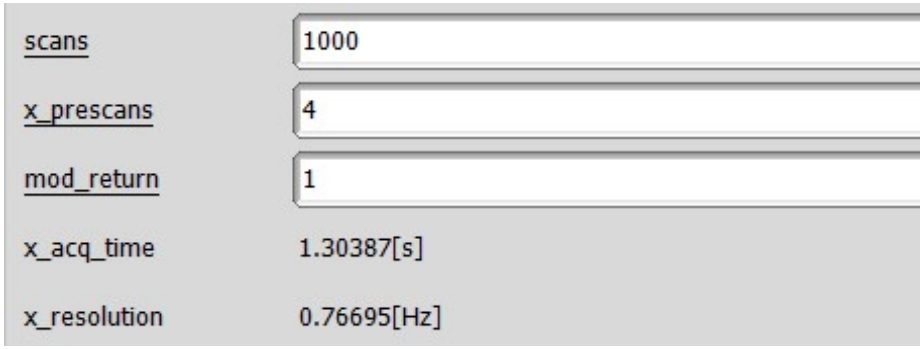


- If this error shows with every scan, please decrease recvr_gain.

**2D and array experiments can’t use auto gain function in normal experiments.

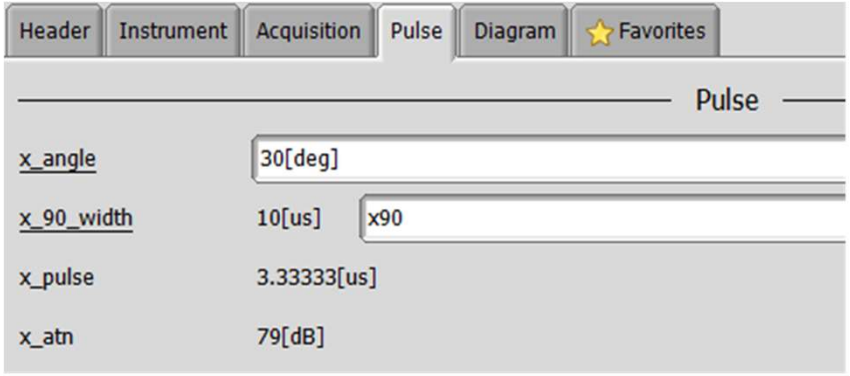
Basic parameters - Acquisition



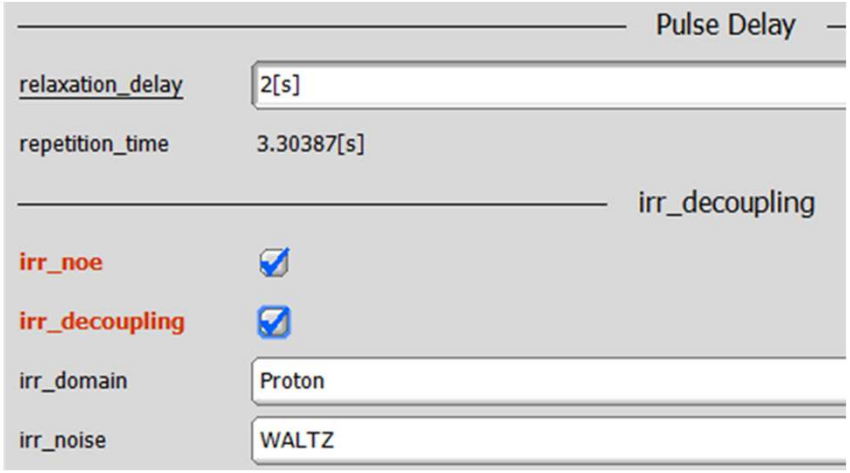


- x_domain (tn) ：nuclei
- x_offset (tof)：offset of spectrum
- x_sweep (sw)：sweep of spectrum
- x_points (np)：FID points (related with acquisition time)
- Scans (nt)：scan number (S/N≅ $\sqrt{scan\ time}$)
- x_prescans (ss)：pre-scan number.
- mod_return (bs)： Send the accumulated data to the workstation and update the files

Basic parameters - Pulse

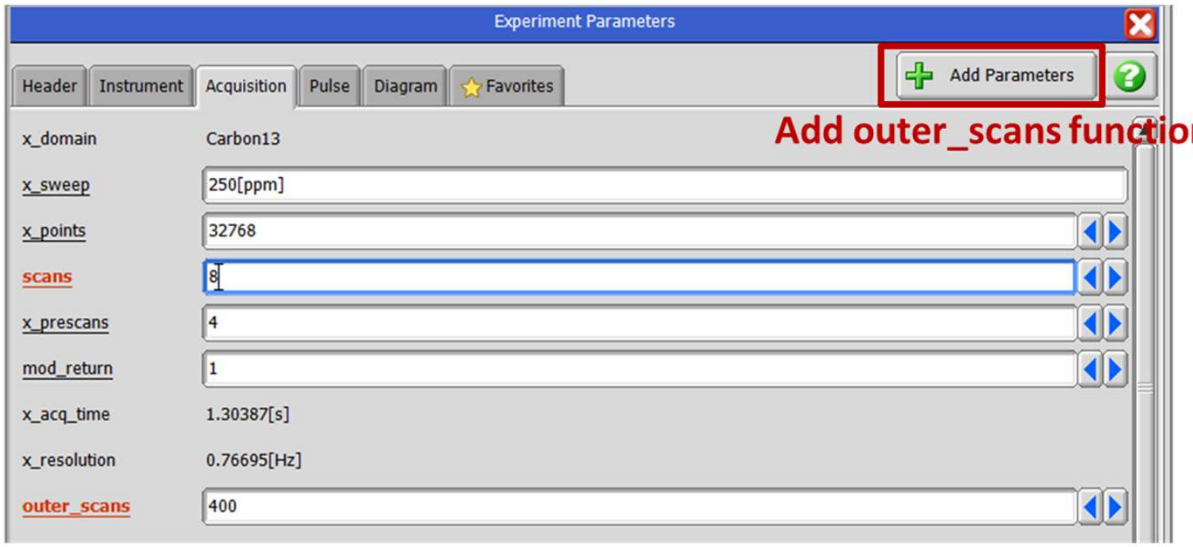


- x_angle：flip angle
- x_90_width (pw90)：90 degree pulse width
- x_pulse (pw)：pulse width



- relaxation_delay (d1)：持豫時間
- irr_noe (dm)：NOE selection
- irr_decoupling (dm)：decoupling selection
- irr_domain (dn)：nuclei of NOE/decoupling

Other function -outer scan



JEOL

- Outer_scans

Varian

Same function with "il"

Normal (scans = 3200)

45[deg] 3200

90[deg] 3200

135[deg] 3200

Outer_scans = 400, Scans = 8 (total = 3200)

8 → 8 → 8 → 8

400 times

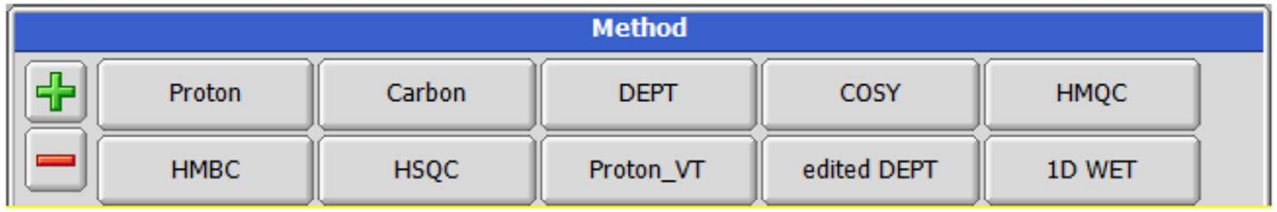
Multinuclear

1. Click  icon. Click Global→Experiments→liquid Advanced → Single_pulse → single_pulse_dec.jxp
2. Select experiment and click  icon to modified parameter.
    1. Under “Header” tab.
        1. Filename
    2. Under “Acquistion” tab.
        1. x_domain: select your nuclei
        2. x_offset
        3. x_sweep
        4. scans
    3. Under “Pulse” tab.
        1. irr_noe: please turn it off if you need integral the data.

☆*you may get negative peak if your NOE effect is negative and you turn NOE on.*

Onserved nucleus	^{11}B	^{13}C	^{15}N	^{29}Sl	^{57}Fe	^{103}Rh	^{109}Ag	^{119}Sn	^{183}W
NOE	2.56	2.99	−3.94	−1.52	16.48	−16.89	−9.75	−0.41	13.0.2
INEPT	3.12	3.98	9.87	5.03	30.95	31.77	21.50	2.81	24.04
DEPT									

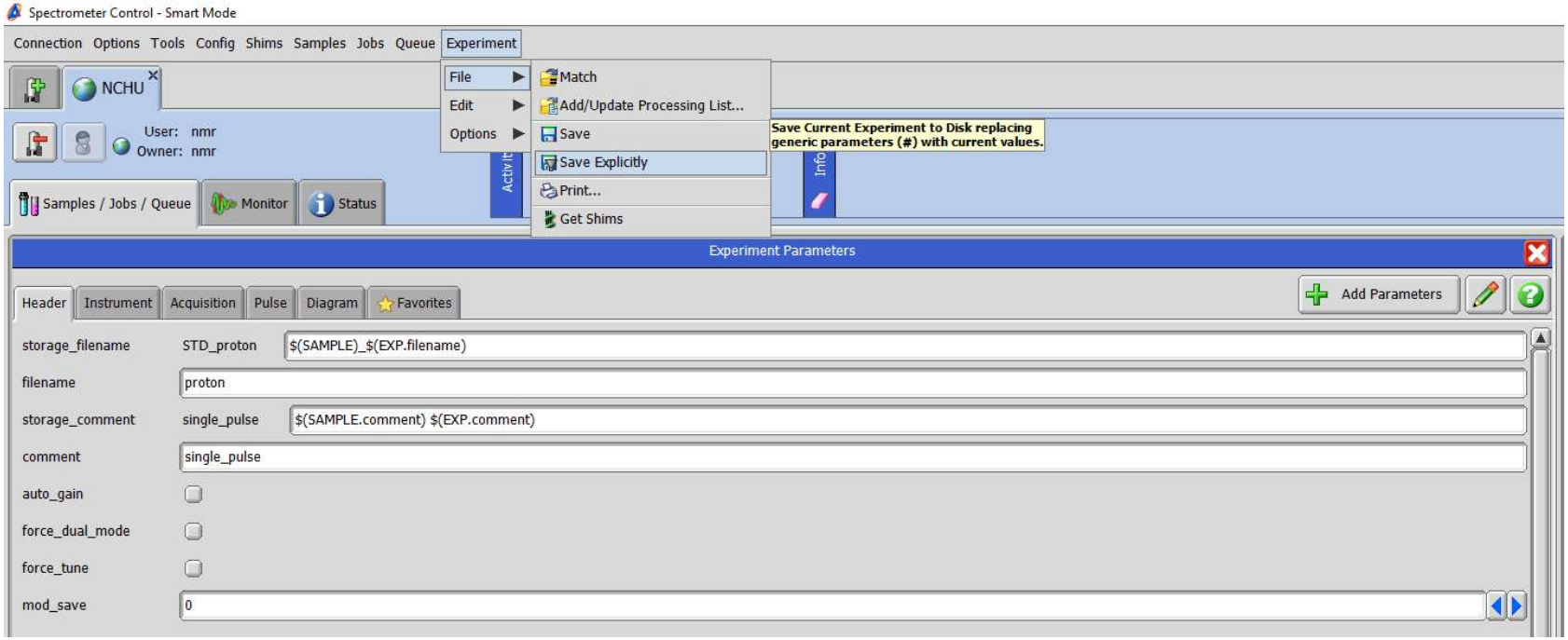
Editing the Method Panel



Click button to add an automation experiments.

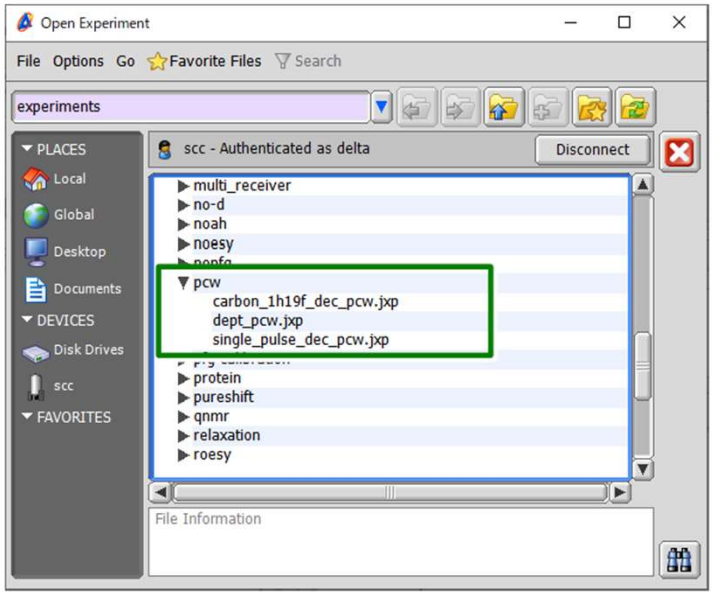
Click + Alt key can add normal experiments to method panel.

Save your experiments



PCW

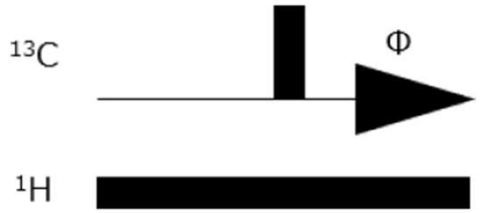
Solution Sequence
Liquid_advanced - pcw



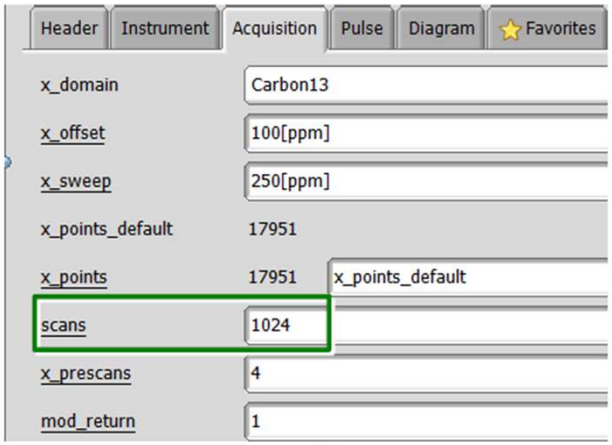
A typical ^{13}C measurement sequence



PCW method ^{13}C measurement sequence



Carbon.jxp



single_pulse_dec_pcw.jxp

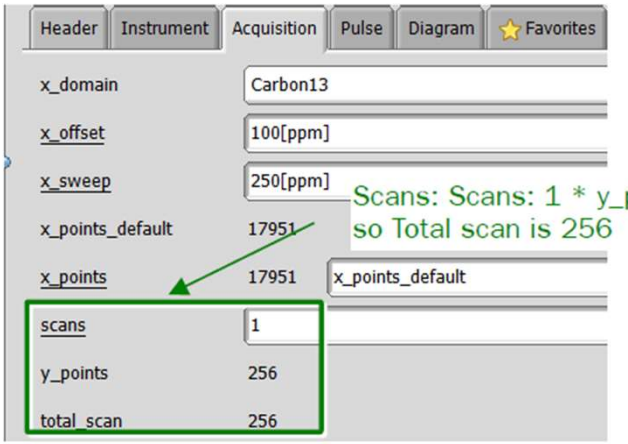
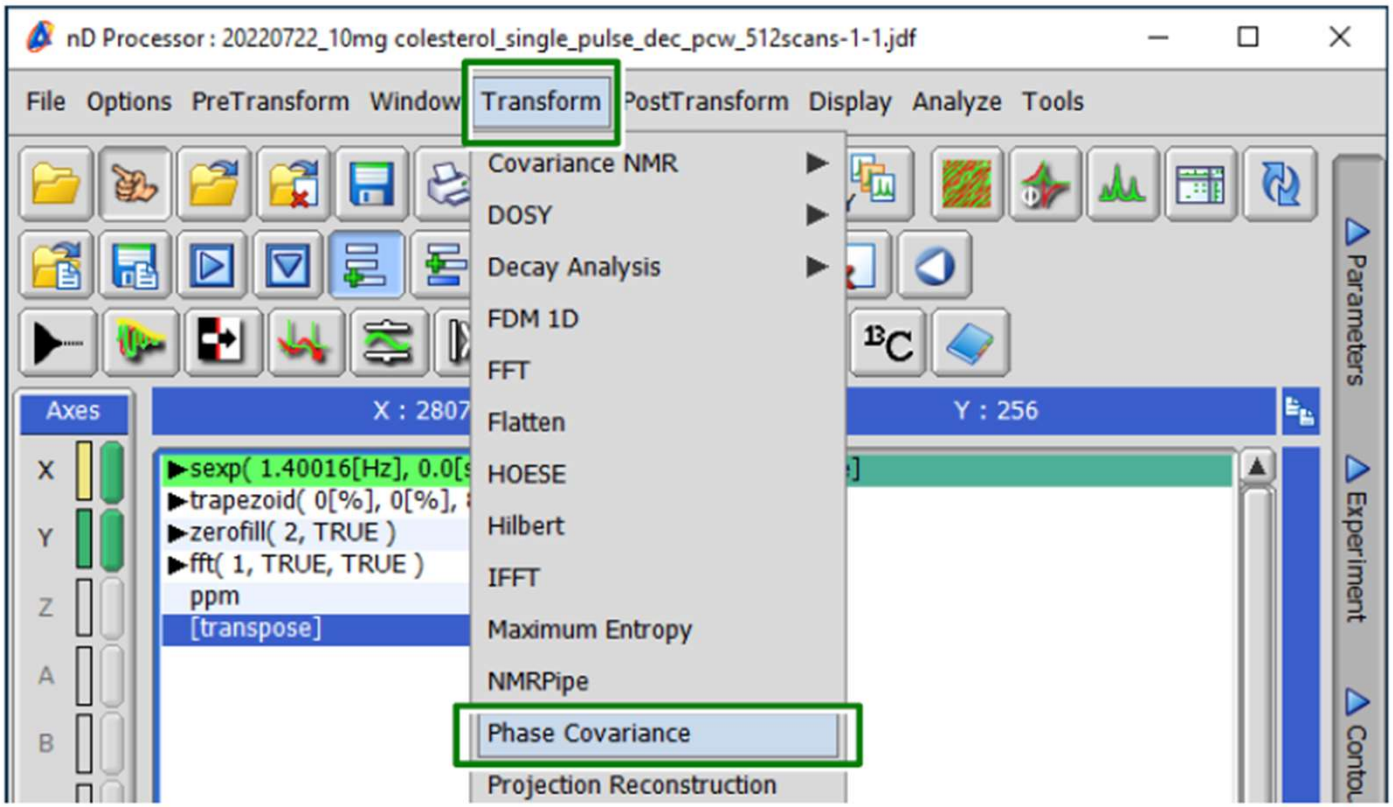


Figure 10.6 Comparison of measurement conditions

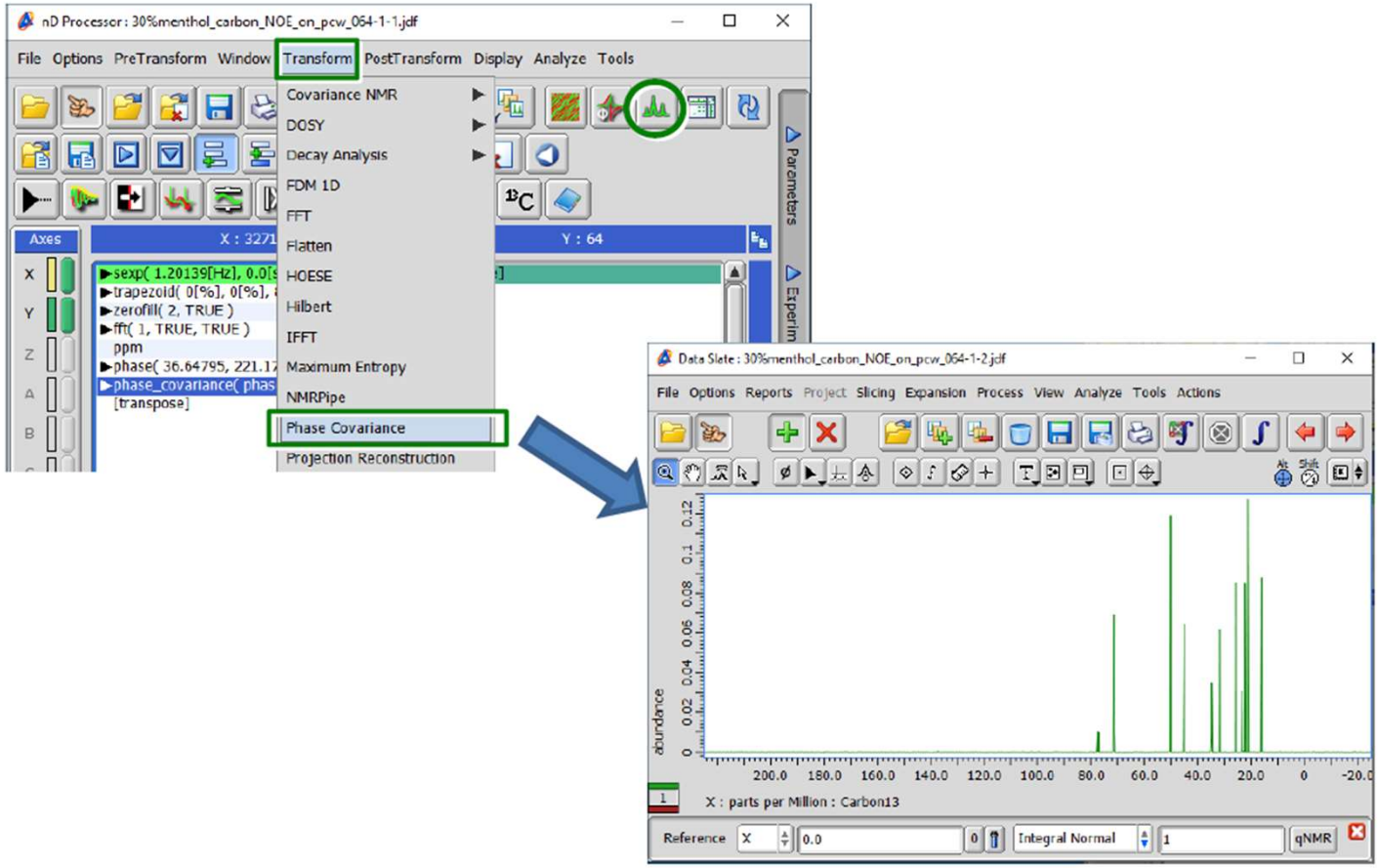
Process of PCW

1. If the spectrum is such that signal cannot be observed in 1scan, add **Transform – Phase Covariance.**



Process of PCW

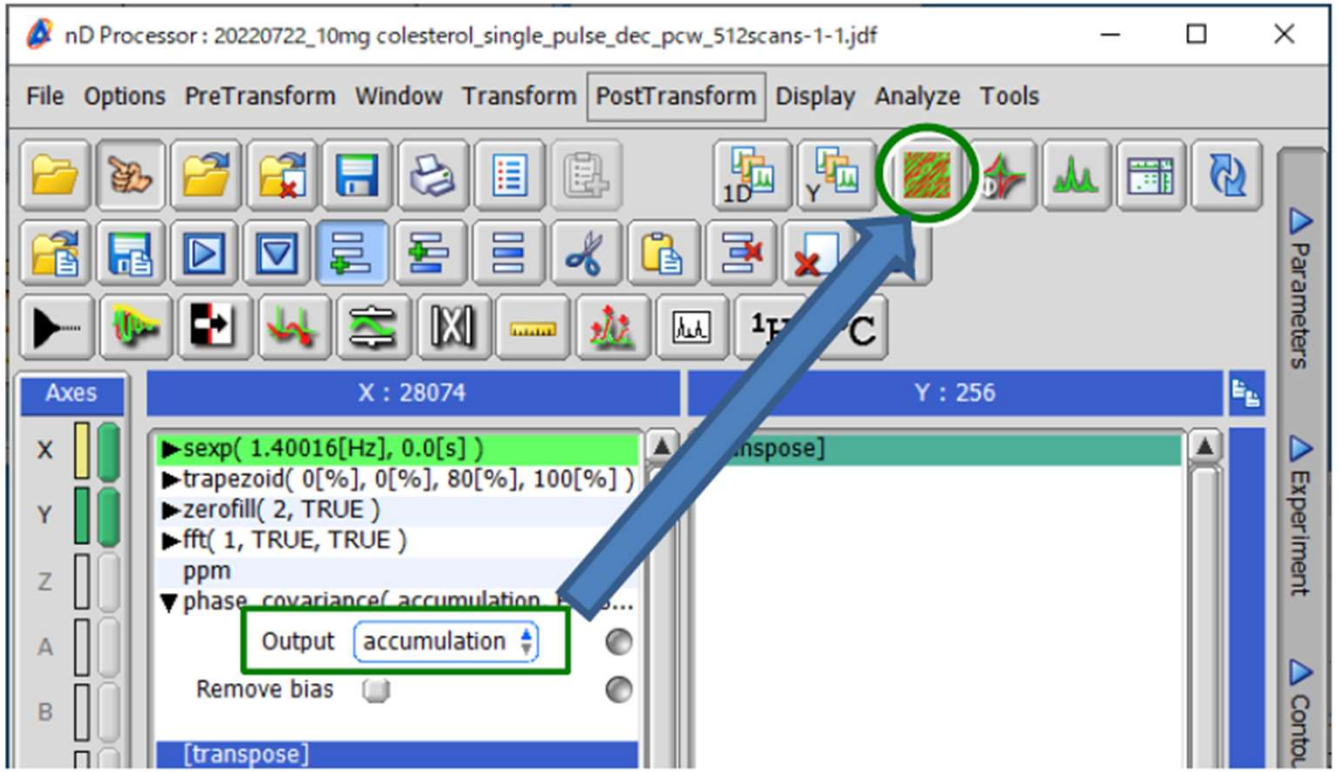
2. Add **Transform – Phase Covariance** after phase processing and open in data slate.



Process of PCW

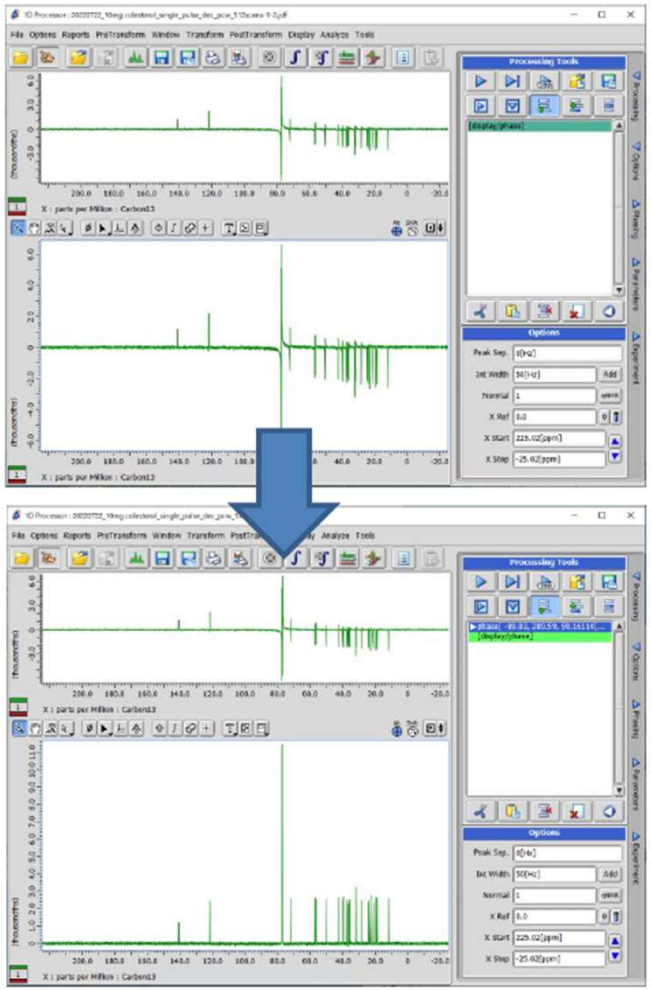
2. After changing the Output parameter of phase covariance to **accumulation**, click the  icon to perform phase processing.

If y_points is large, it will take a long time to process.



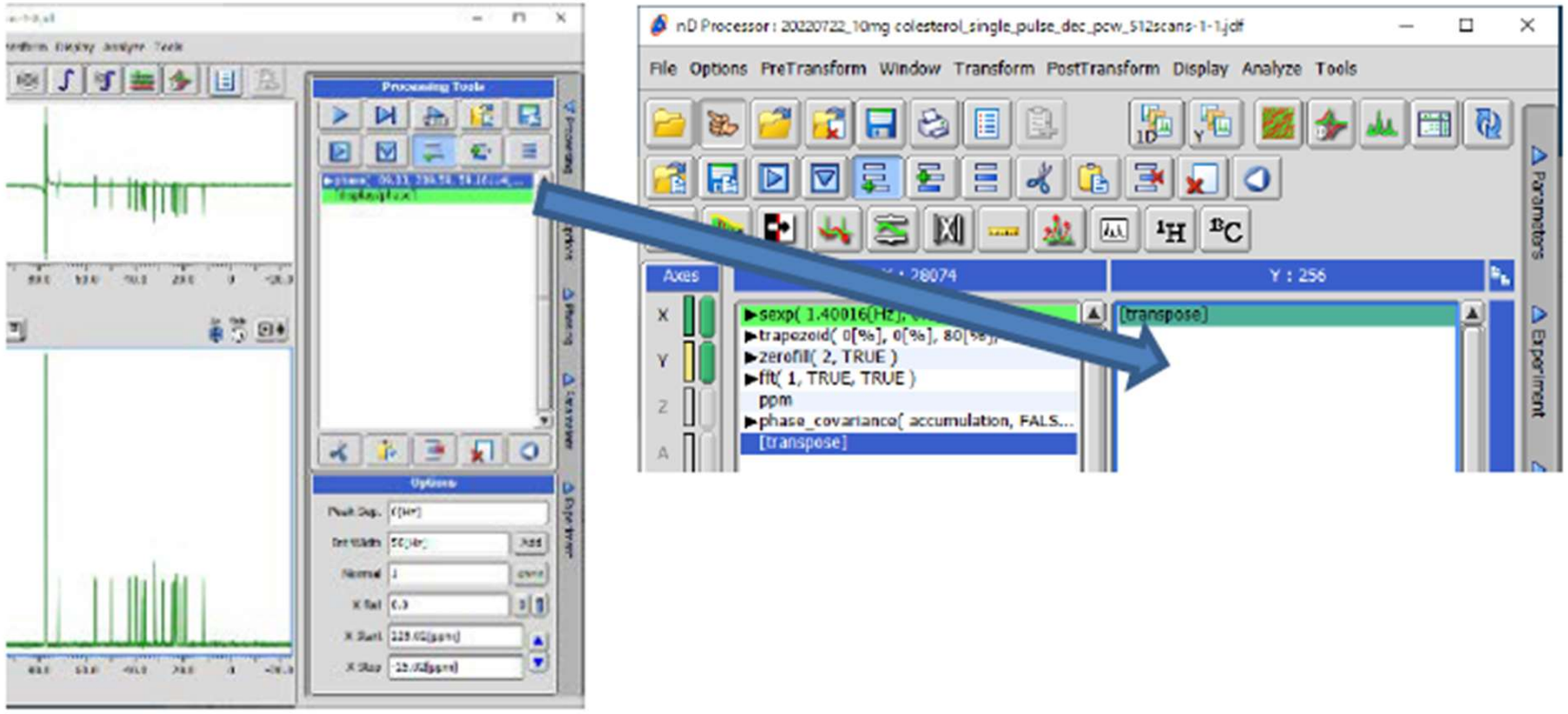
Process of PCW

3. Perform phase matching with a 1D processor.



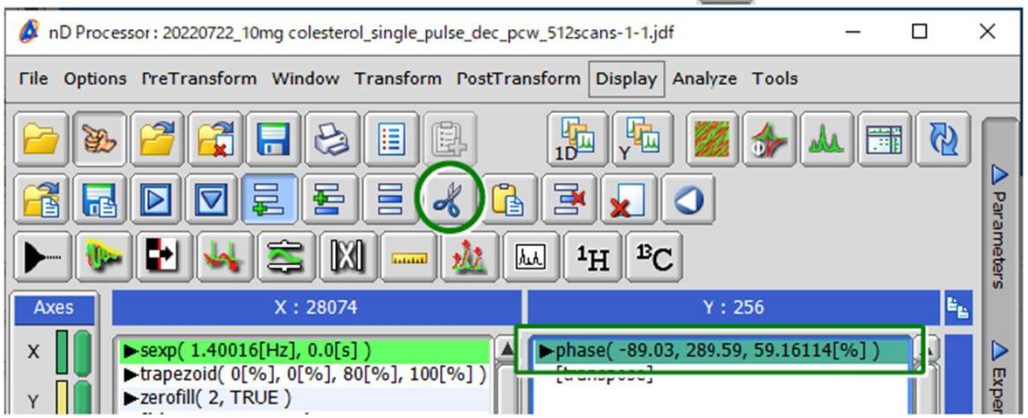
Process of PCW

4. Right-click and drag and drop the phase processing in the 1D processor to the Y axis of the nD processor to paste.

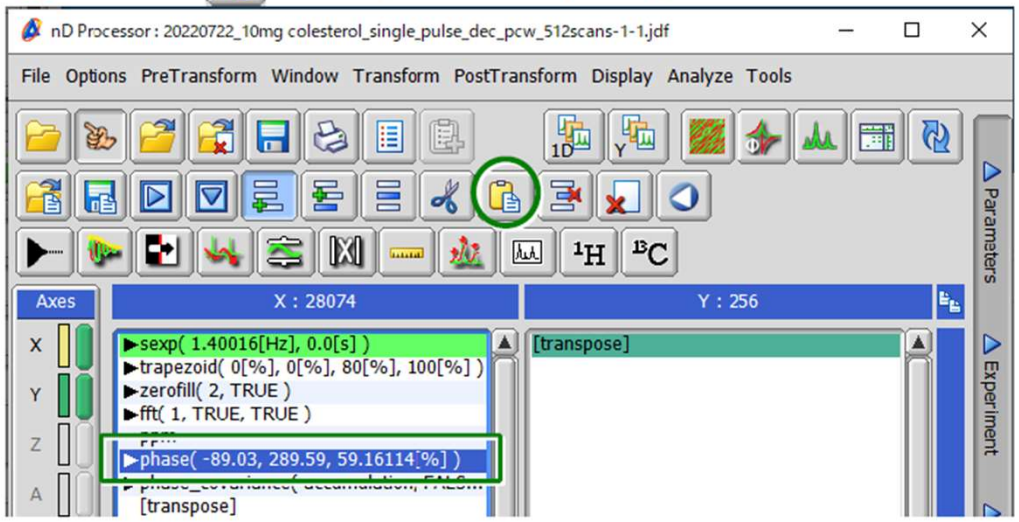


Process of PCW

5. Select Y-axis phase processing and click the icon to cut.

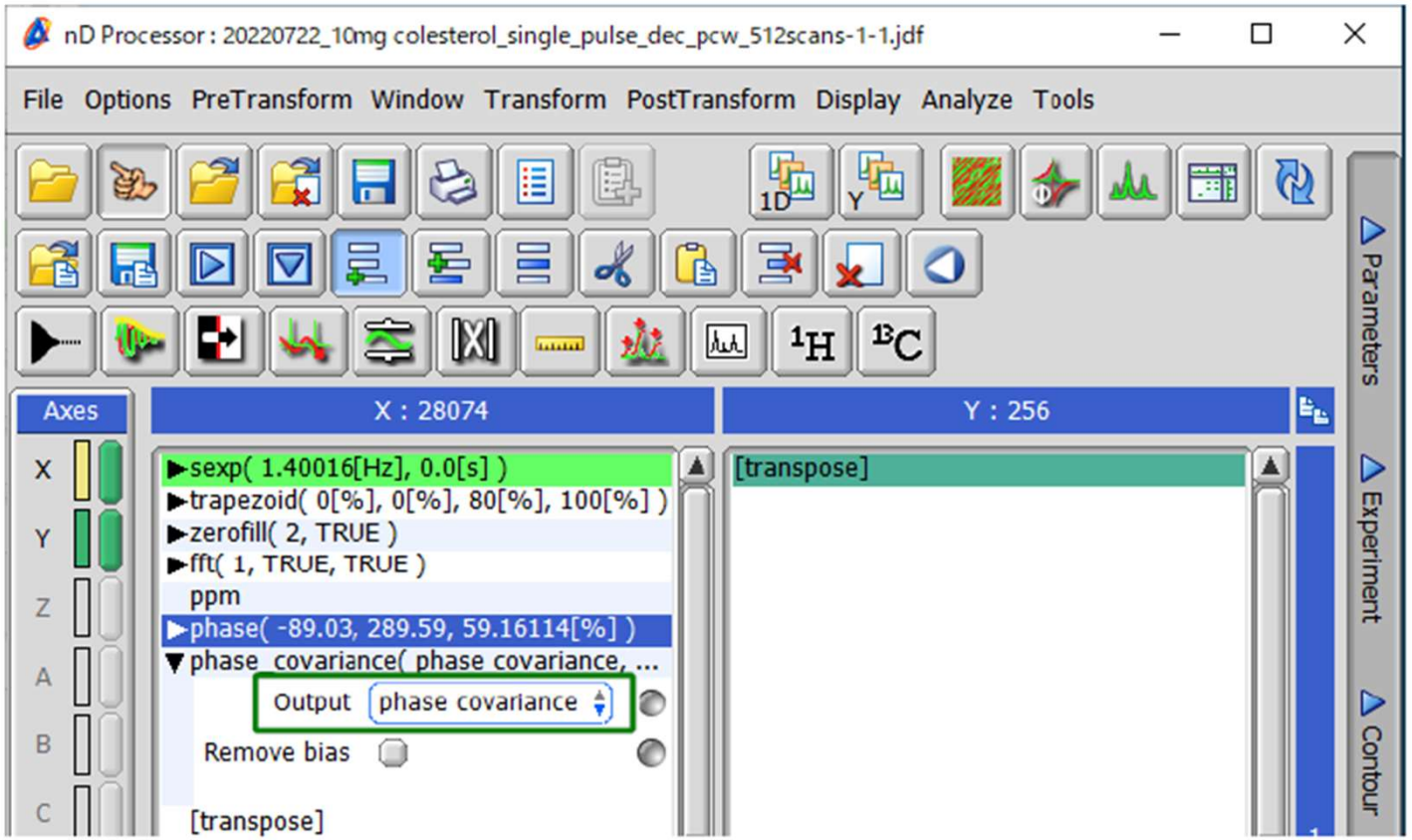


6. Click the icon to paste on the phase_covariance of the X-axis.



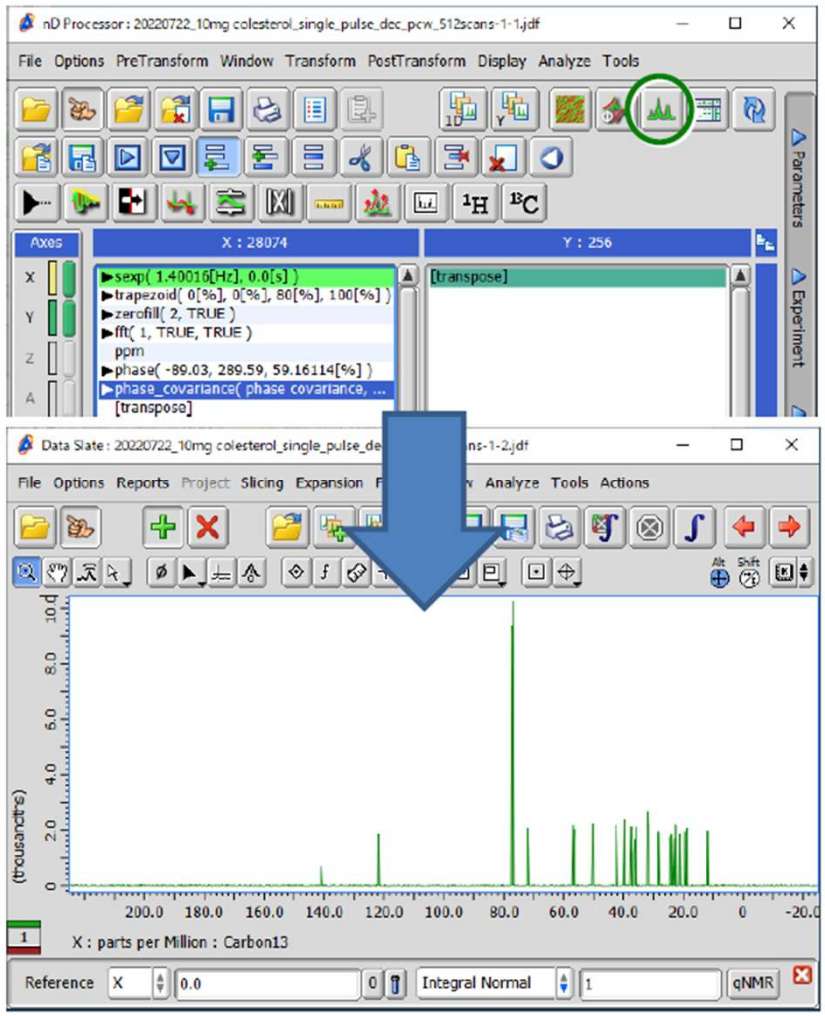
Process of PCW

7. Change the Output parameter of phase covariance to **phase covariance**.

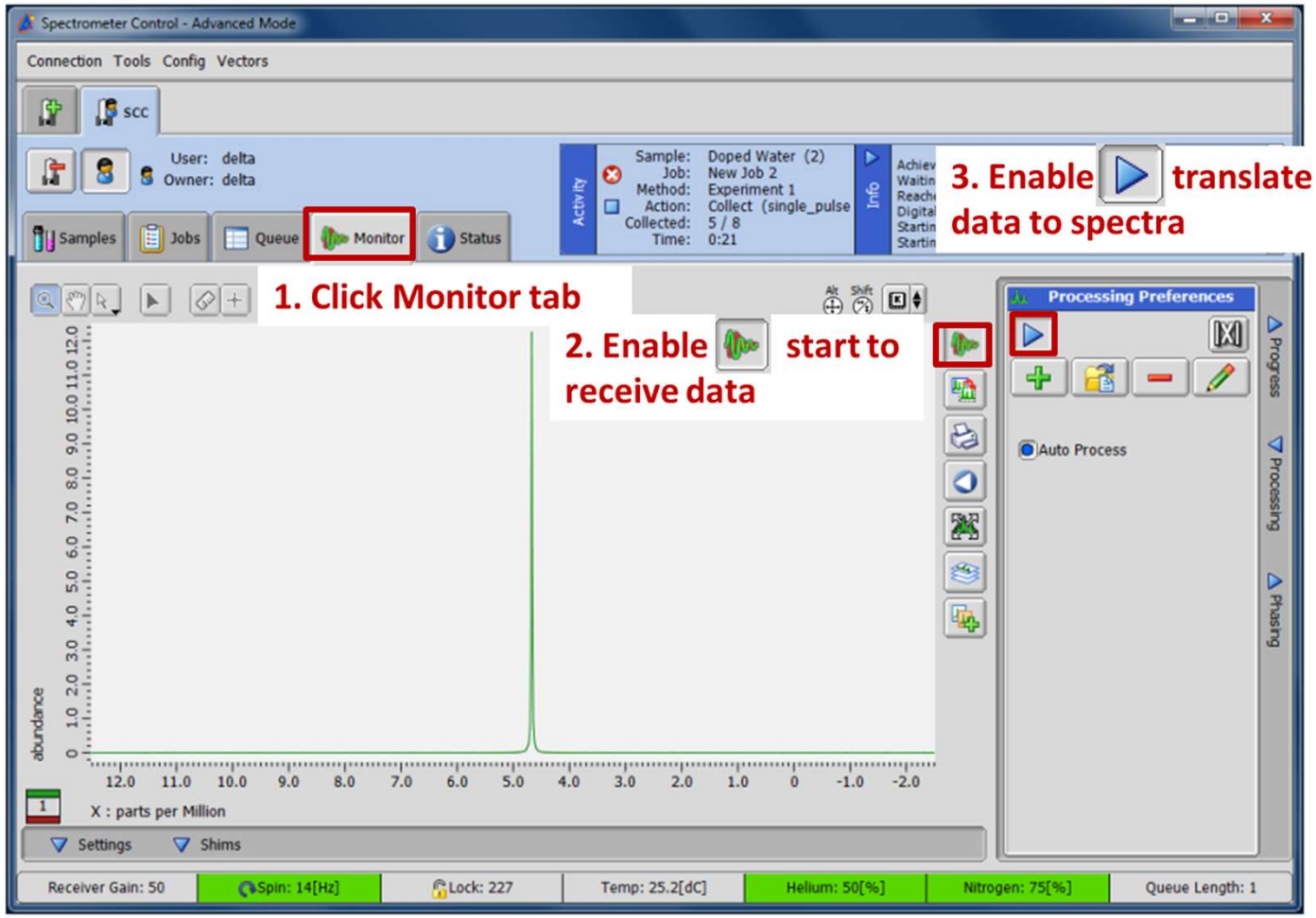


Process of PCW

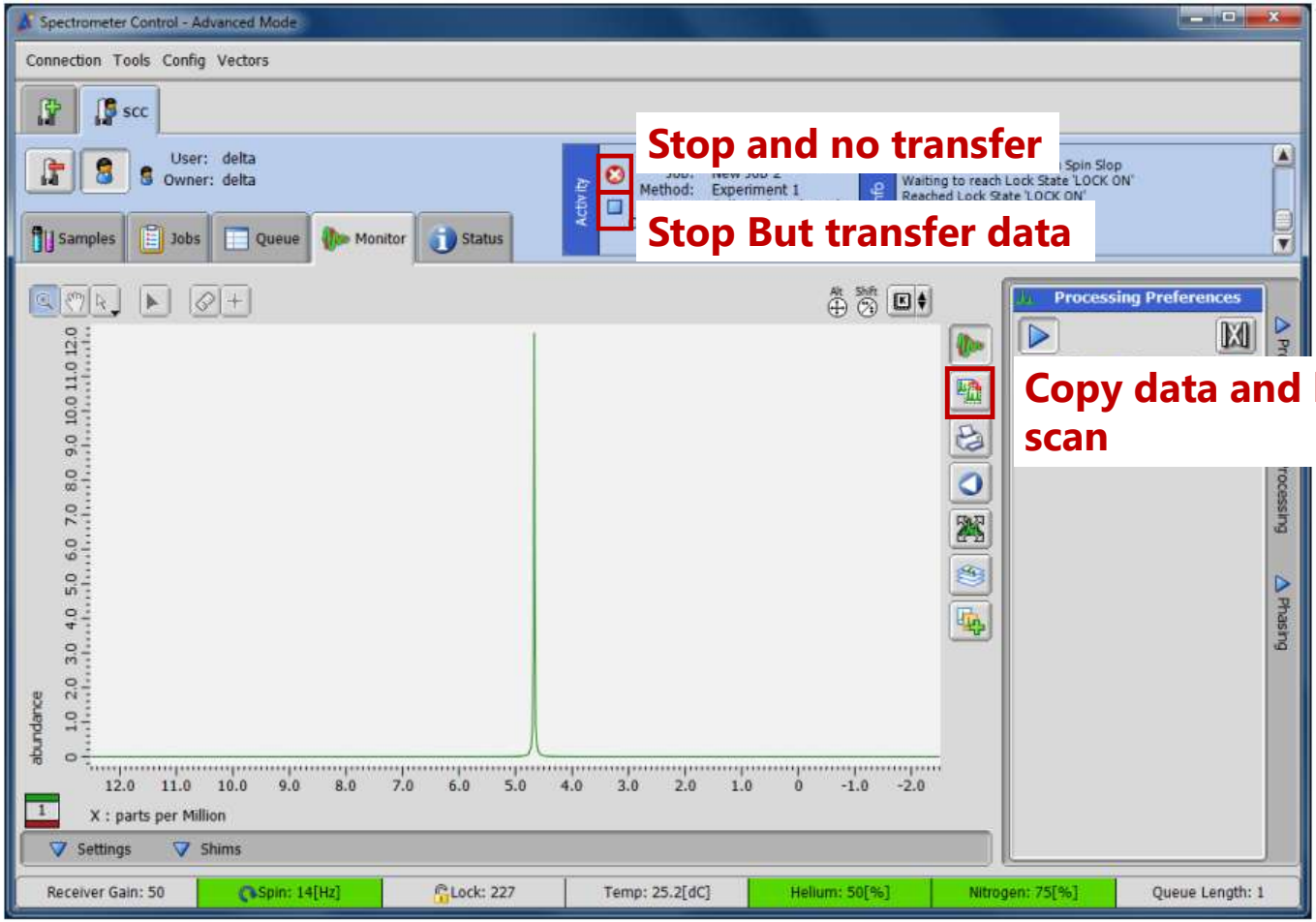
8. Open the processing result in the data slate.



Data Monitor

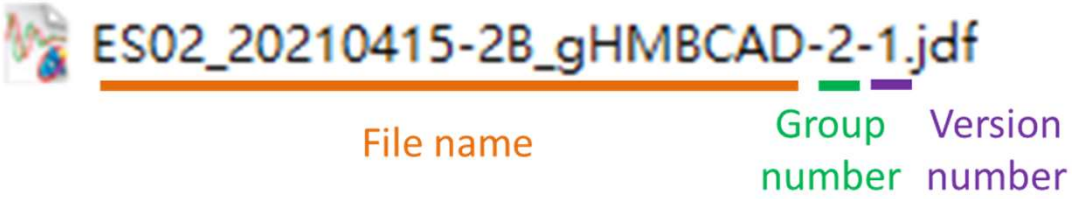


Stop Experiments



Data

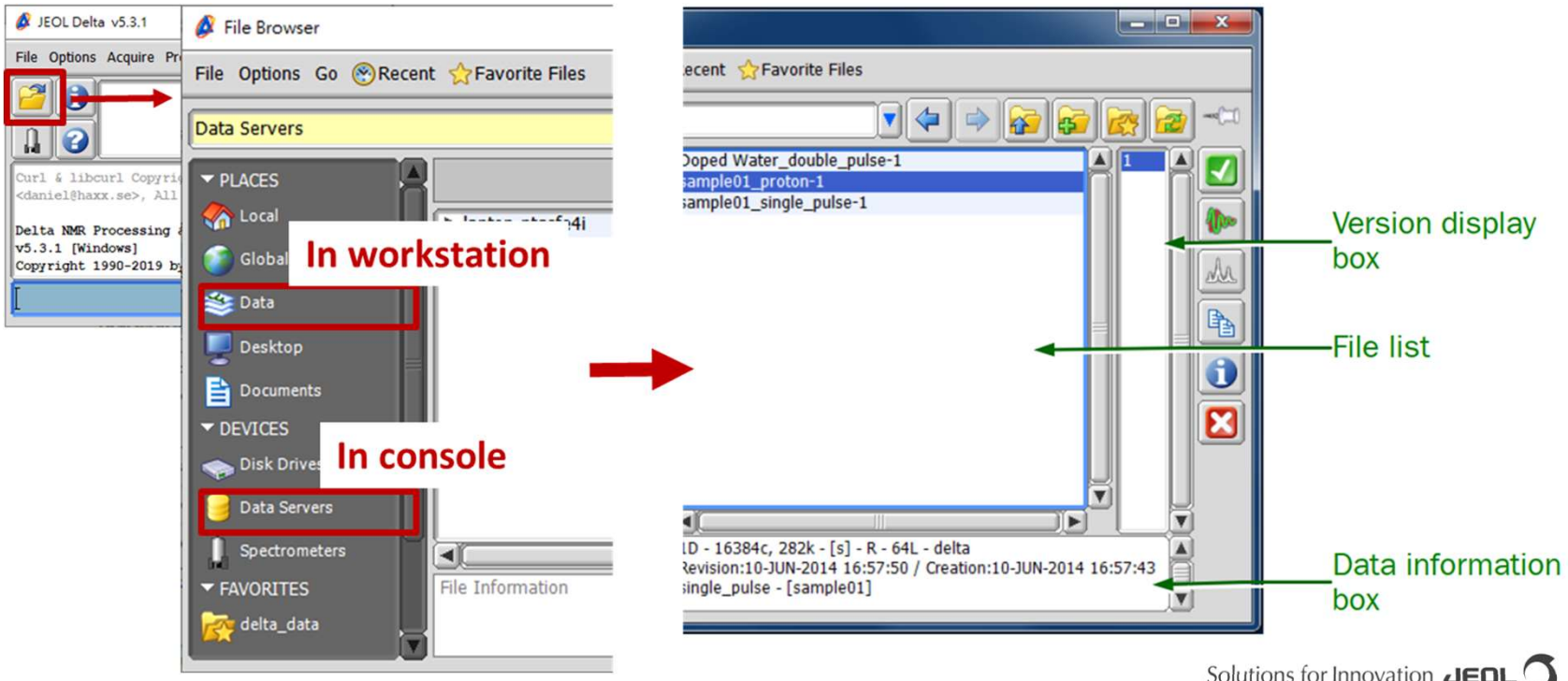
- Pathway:
  - In console data server
  - C:\Users\username\Documents\JEOL\data
- File name:



  - File Name: From sample name and experiment
  - Group Number: This number increase when same file name existing.
  - Version Number: "1" is original FID file. When you save processed file, this number increase.

Browser

- Pathway:
  - In console data server (FID only)
  - C:\Users\username\Documents\JEOL\data

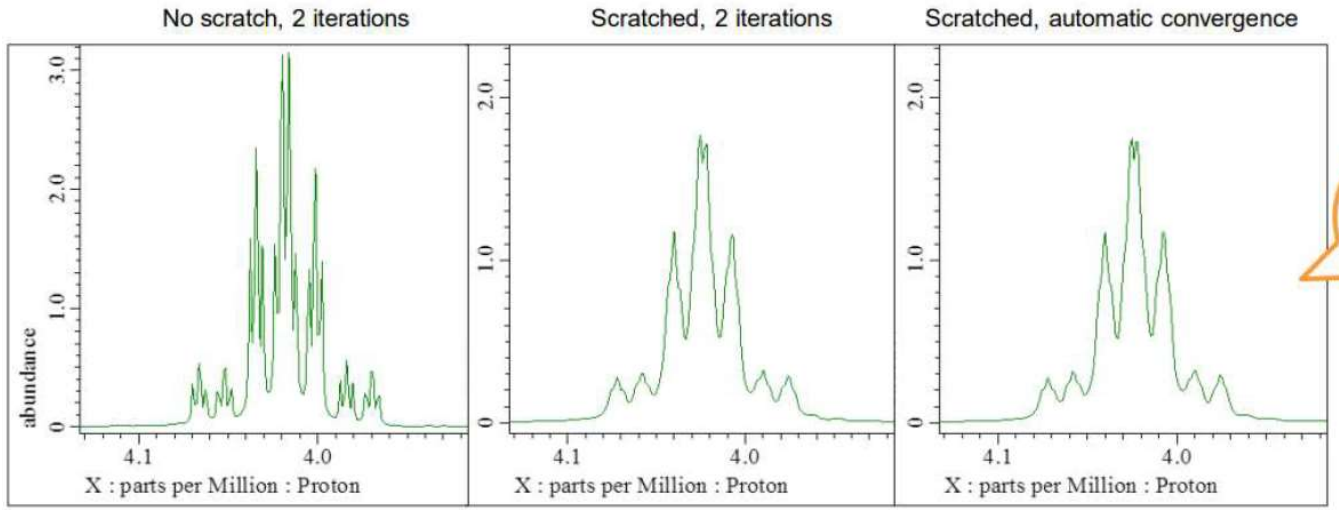


常見問題與錯誤訊息

- Message box
  - Clipped data in scan xx
    - ADC overflow. Please decrease gain.

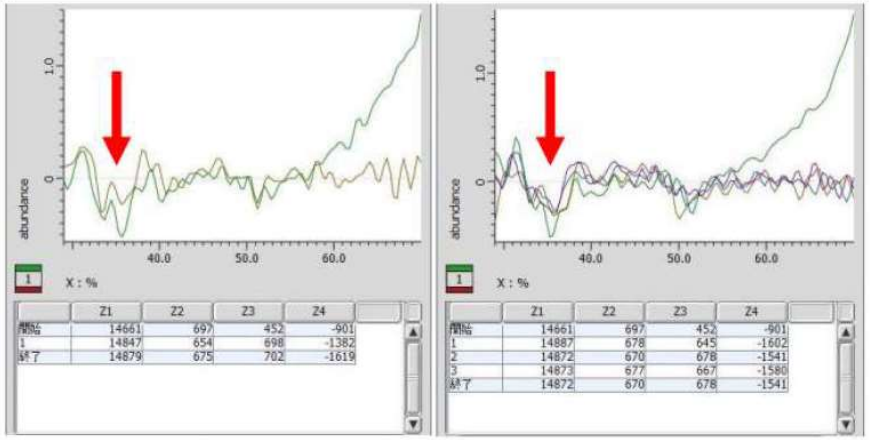
    (In parameter→Instrument tab)
  - Shim z5, xx.xxxxx[Hz] exceeds the lower limit, -60[Hz]
    - Z5 or z6 exceeds the limit. Please check Z5 or Z6 off by manual before start experiment. Usually, the sample or tube may bad.
- Bed shimming (Peak shape is not good)
  - Please check your sample height is enough.
  - Please check your sample solution is clear.
  - Please check your sample is not paramagnetic.
  - Please check the message with exceed shim limit or not.

Tube quality affects



Increasing the number of iterations did not improve the resolution.

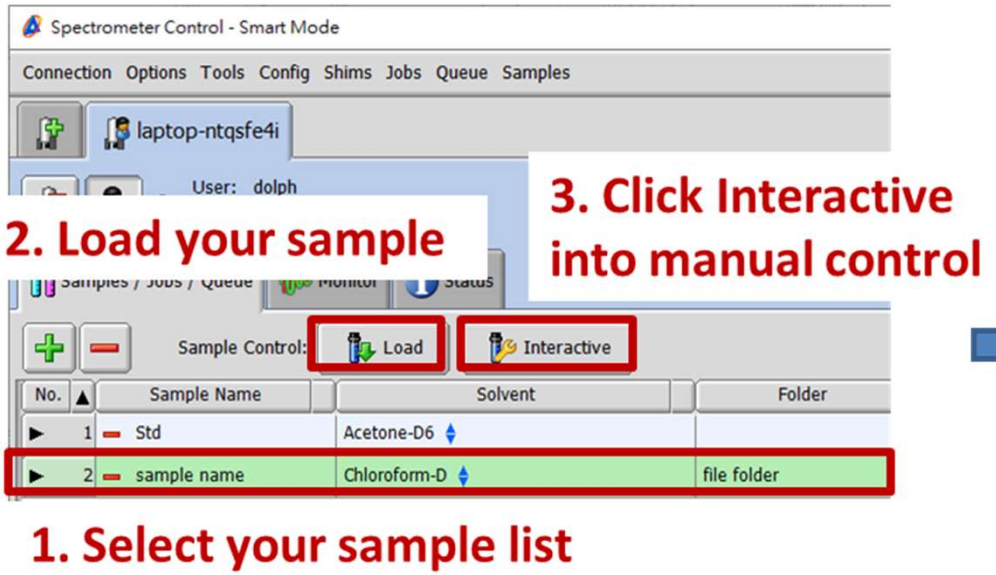
Final variation should be smaller then ±0.1

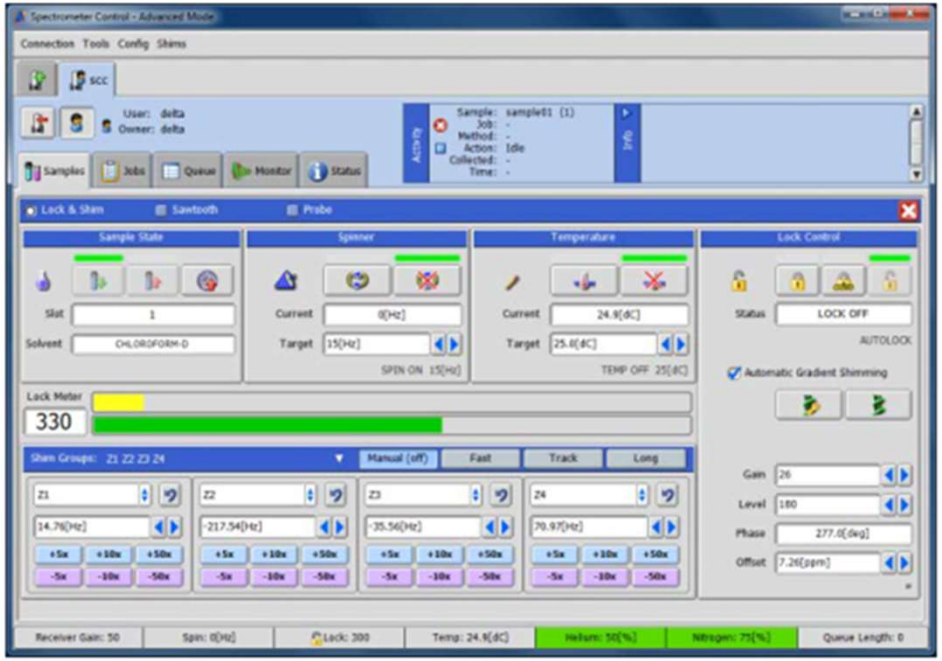


Where there is a scratch, the magnetic field map is distorted.

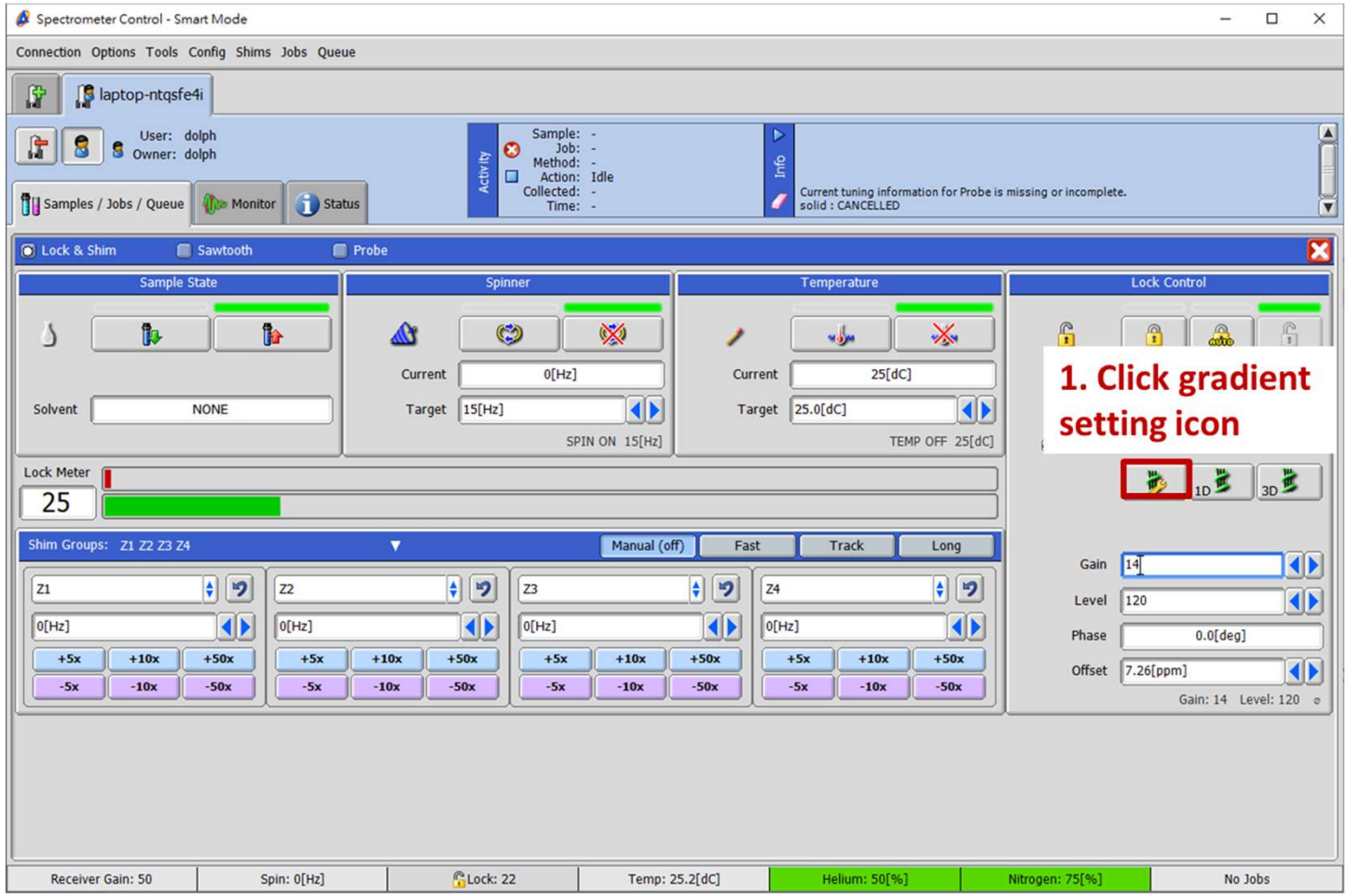
Effect of scratches on resolution

Manual control (Shimming)

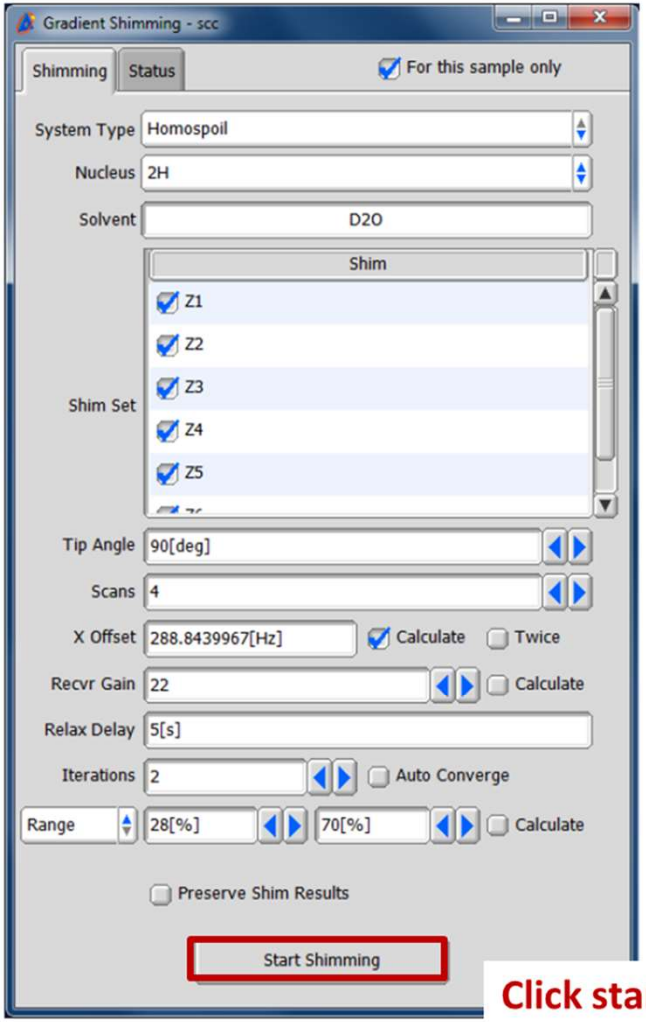




手動控制 (Shimming)



手動控制 (Shimming)

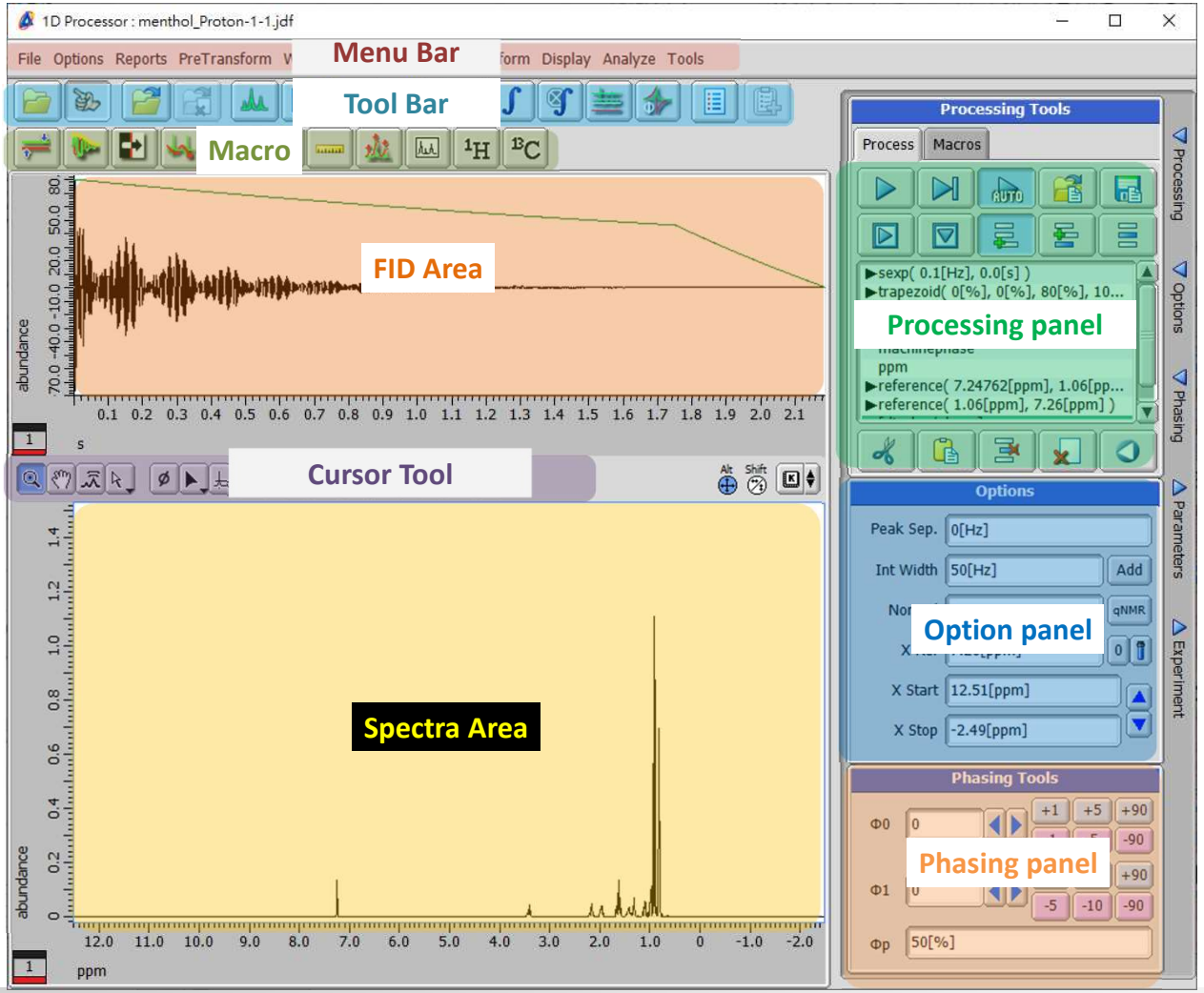


- System type
  - Homospoil_selective
    - Solvent has more then two 2H signal or use mix solvent
  - Homospoil
    - Solvent has only one 2H signal
- Nucleus
  - 2H
    - Deuterium solvent sample
  - 1H
    - No Deuterium solvent sample
- Shim set
  - If message box has z5, z6 exceed error, please check off z5 & z6 here.
  - If you use shigemi tube, please check z6 off.
- Range
  - If your sample is shorter, please try to change this value. Or you can check “calculate” on.

Click start shimming

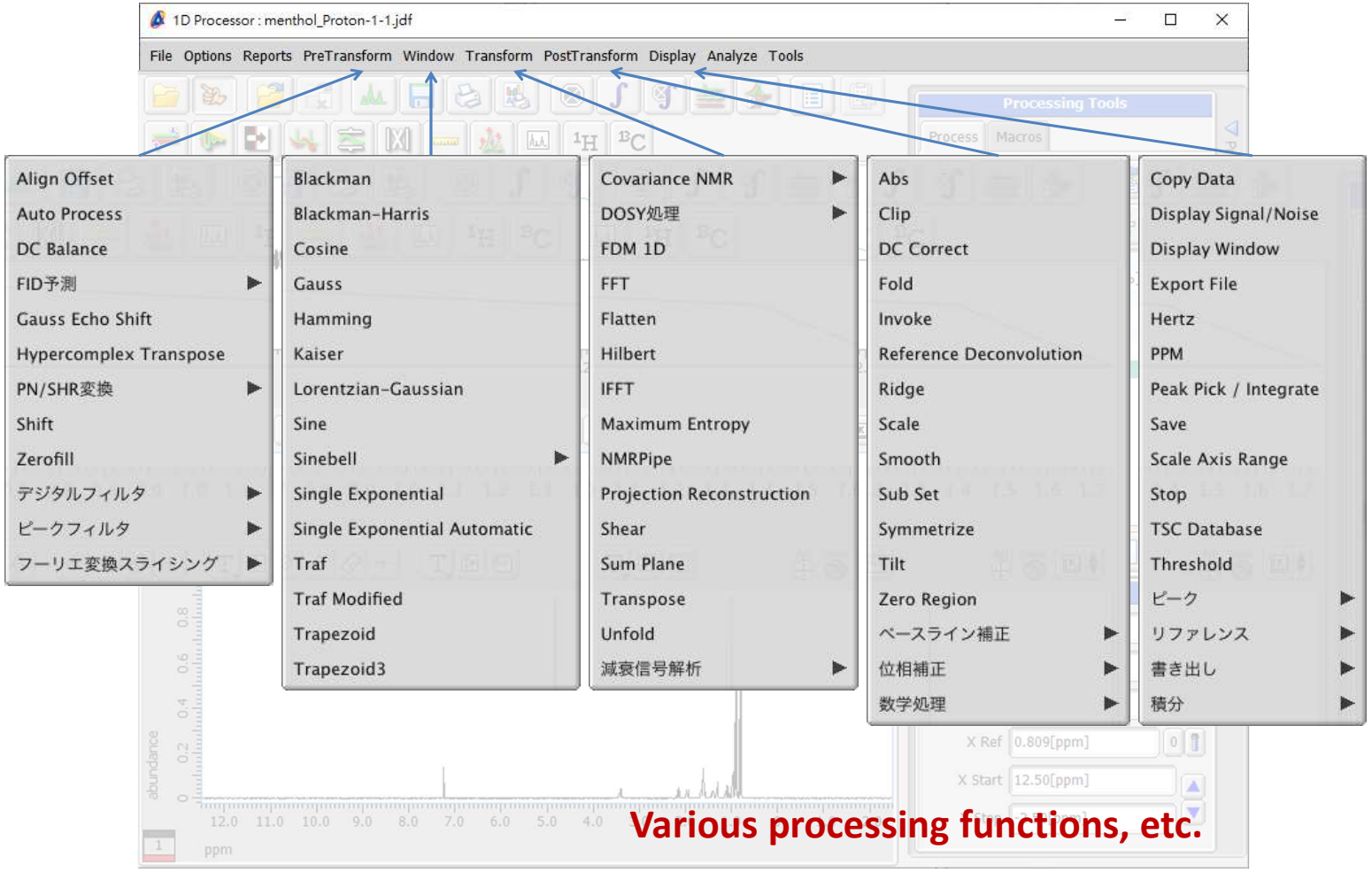
1D Processor

Window



1D Processor

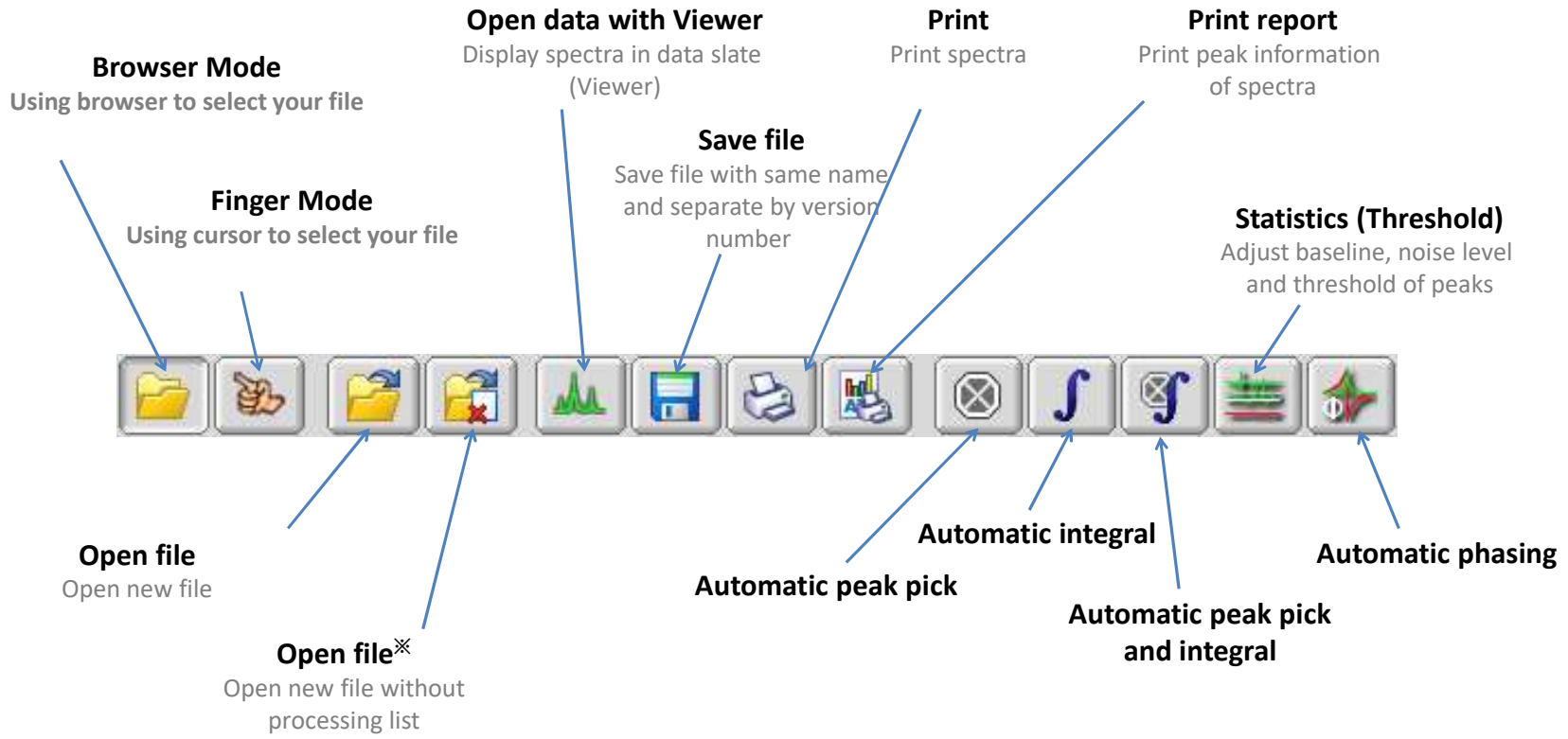
Menu Bar



Various processing functions, etc.

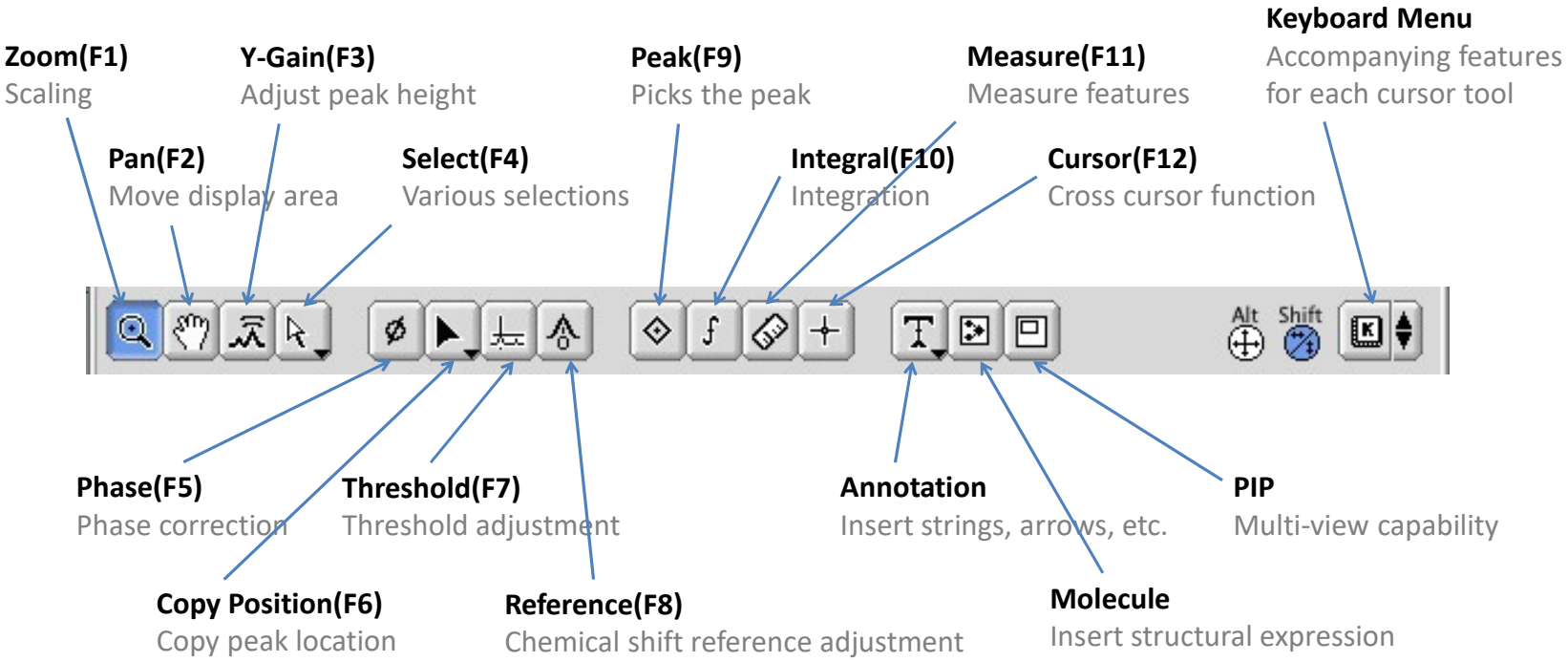
1D Processor

Tool Bar



1D Processor

Cursor Bar



Solutions for Innovation JEOL

Frequently used shortcuts

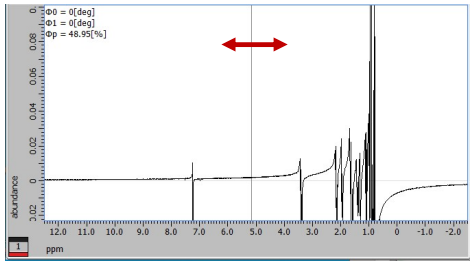
Space	Zoom (enters Zoom mode only while pressing the Space bar)
Home	Reset expansion (full spectra display)
—	Expansion undo (Same with left double click in zoom mode)
End	Enlarged Y-axis
Shift + End	Enlarged reset of X-axis only
ESC	Close window
Alt + F	Show/Hide file names
Alt + Shift + C	Show/Hide comments
Insert	Clear input box (Windows only)
↑	Undo input box values
↓	Clear input box
Alt + G	Show/Hide grid lines
Alt + P	Show/Hide peak marker
Alt + I	Show/Hide integrals
N	Normalize integrals

1H Processing

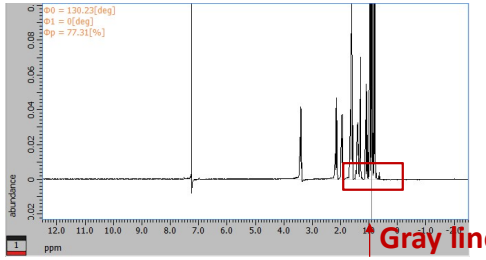
Step1: Phasing

1. Select  phasing tool (shortcut F4)

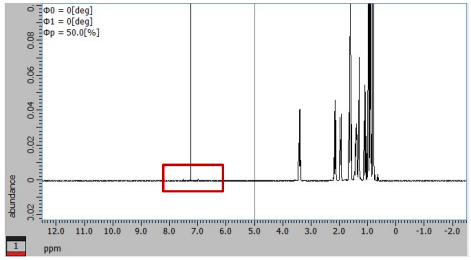
2. Moving gray line to the highest peak.



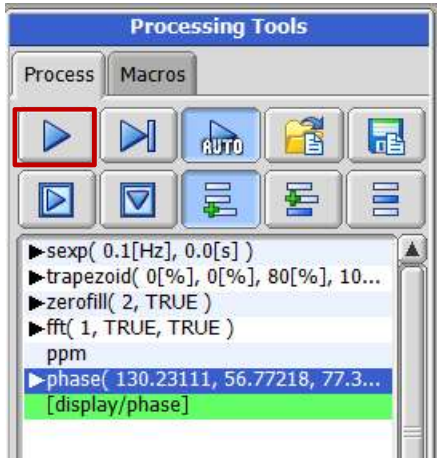
3. Press Left mouse key and move horizontally to adjust the peak which close to gray line.



4. Press middle mouse key (or push ALT key + left key) and move horizontally to adjust the peaks which far from gray line.



5. After adjust the phase, please click apply button.

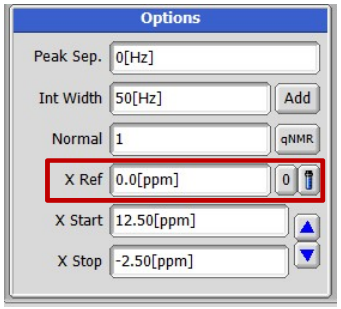


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1H Processing

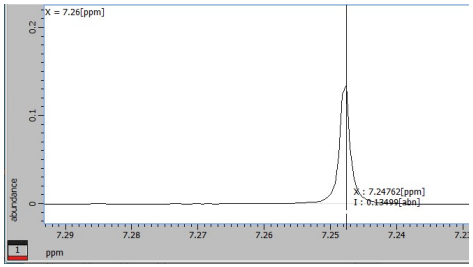
Step2: Reference

1. Click  or input value for reference



2. Select  reference tool (shortcut F8)

3. Click solvent or TMS peak to reference.



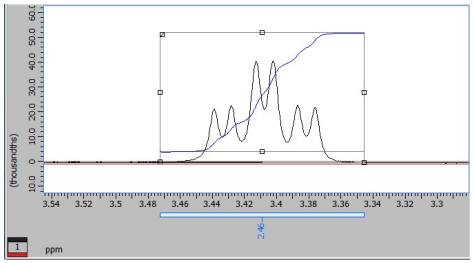
Tips: Please change tool icon after reference otherwise you may mistouch to change the reference.

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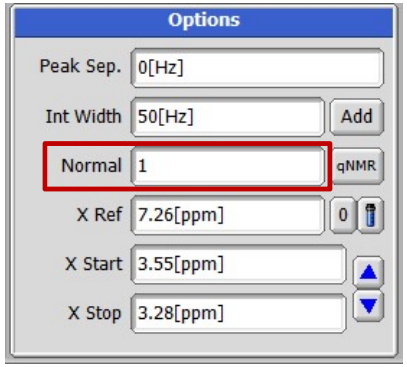
Step3: Integral

1. Select integral icon (shortcut F10).

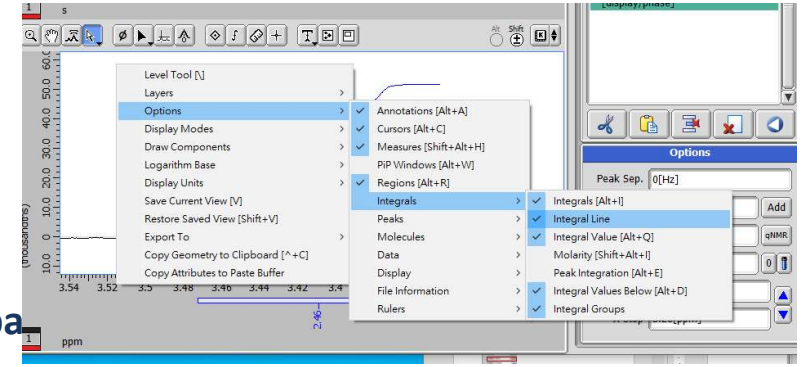
2. Left click and drag the region.

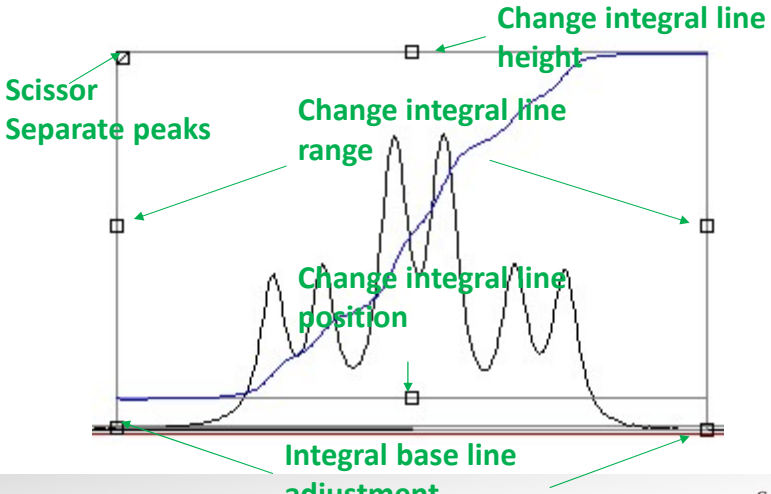


3. Select integral. Input value in option pa
to normalize your integral.



4. Don't show integral line.
Right click mouse,
Options→integrals→integral line





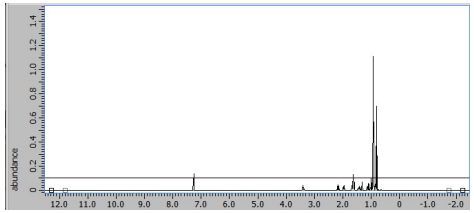
Solutions for Innovation JEOL

1H Processing

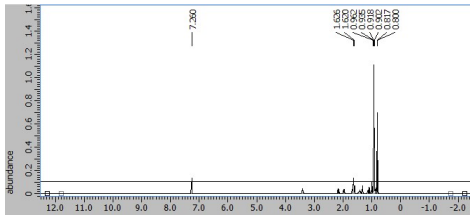
Step4: Peak Pick

1. Click  (shortcut F7).

2. Put your mouse on Y-axis (gray area) and left click (your cursor become ). Then adjust threshold.



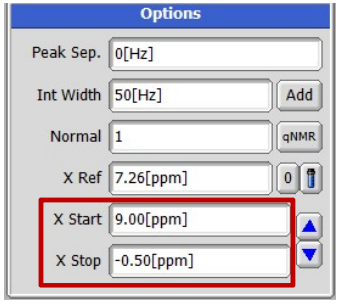
3. Click  on tool bar to pick peaks.



4. Using  (shortcut F9), you can pick peak one by one. (For small peaks, you may need to decrease threshold the first.)

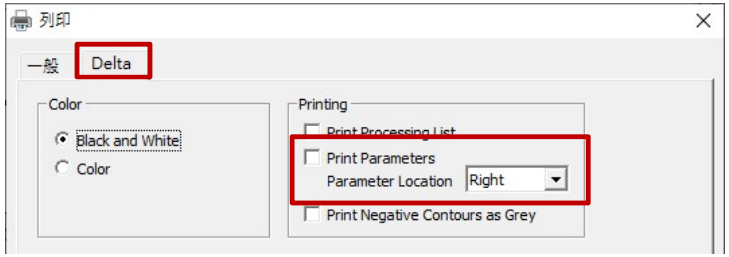
Step5: Set range and lay out

1. Set range on option panel.



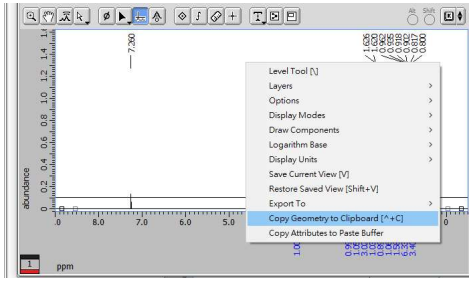
2. After adjust peak height, file name, comment and display setting, click  **to print your spectra out.**

3. In "Delta tab", you can select print parameters or not.



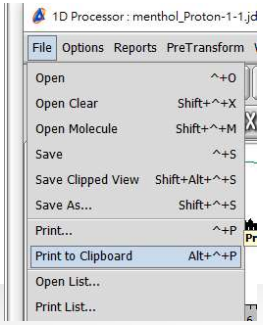
4. Copy your spectra.

Press Ctrl+C you can copy the spectra and past in other software. (The size of specta is depend on window)



5. Copy your spectra in fix size or with parameter.

Select File→Print to clipboard on menu bar. You can get a spectra lay out like print format.

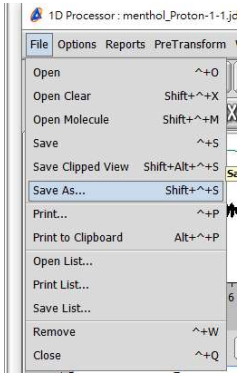


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Step6: Save file

1. Save as new file.

Select File→Save as to save a new spectra file.



2. Save file.

Click  to save your file with same name and just increase version number.

3. Export another format file.

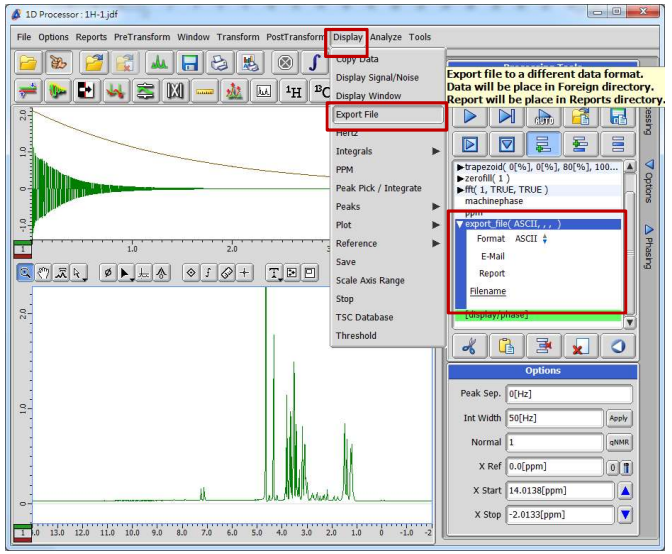
3-1 On menu bar, select Display→Export File.

3-2 Select format to ASCII.

3-3 Select Filename to input path way and file name.

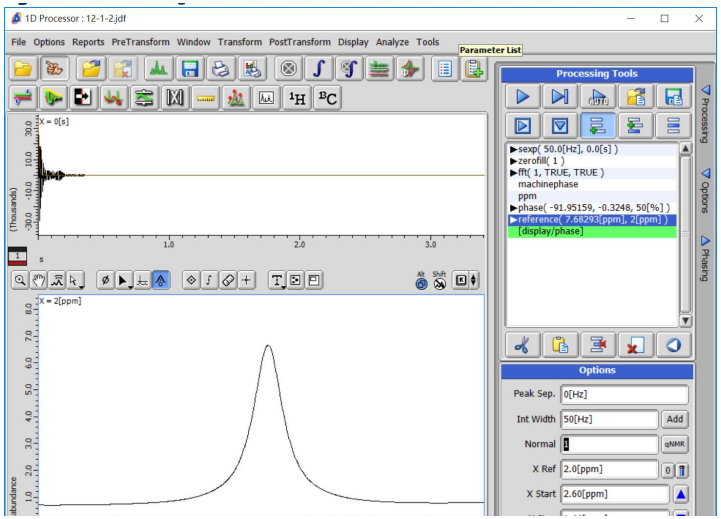
3-4 Click apply button. 

3-5 You can get a file which can open by Excel.



Process 19F、31P

1. Open standard spectrum (you have to
2. Adjust phase and reference.

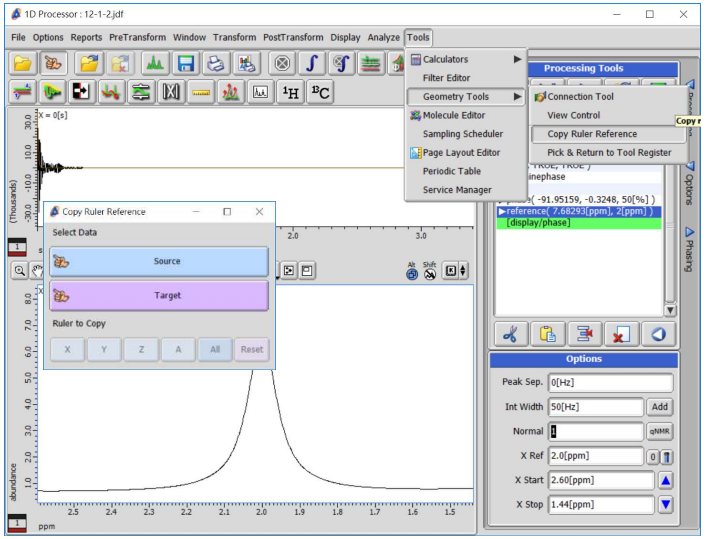


3. Open sample spectrum and adjust phase

Process 19F、31P

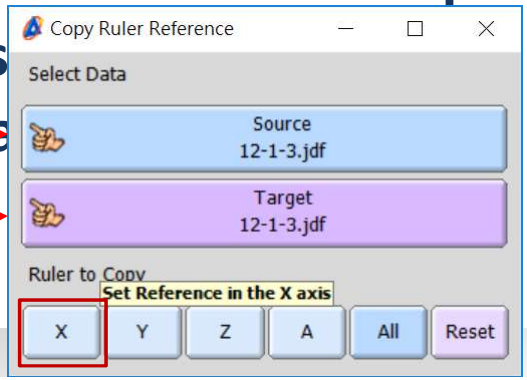
4. Open reference tool (Tools→Geometry Tools→Copy Ruler)

Reference



5. Click Source then select standard spectrum. Click Target then select sample s

Click X to finish ea



Solutions for Innovation JEOL

2D Processing - COSY

Step1: Reference

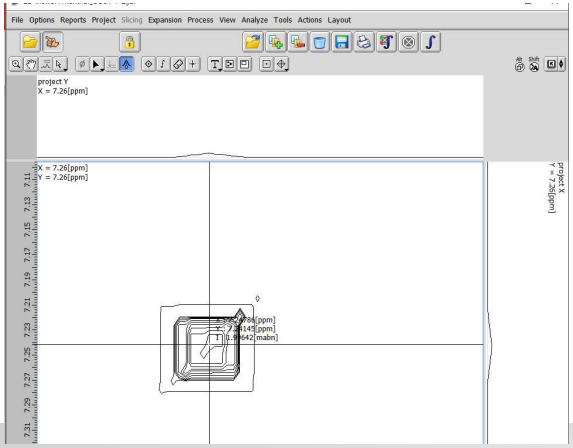
1. Select “X” then Click  to in put default solvent reference or input value by manual on option bar.



2. Select “Y” then Click  to in put default solvent reference or input value by manual on option bar.



3. Select  reference tool (shortcut F8)
4. Click solvent or TMS peak to reference.



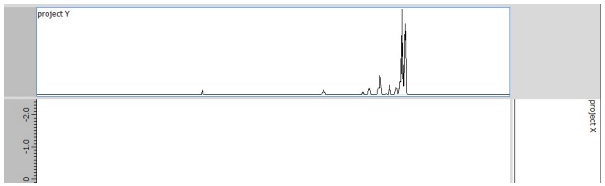
Tips: Please change tool icon after reference otherwise you may mistouch to change the reference.

Solutions for Innovation JEOL

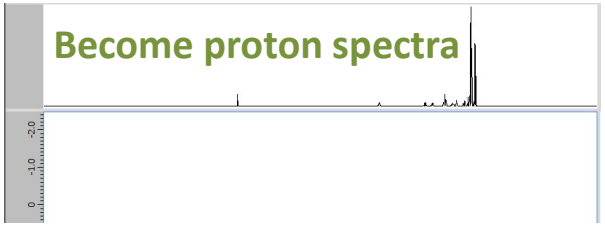
2D Processing - COSY

Step2: Load 1D spectra

1. Select Project Y spectra. (After select, you will see a blue frame on spectra.)



2. Click  to unlock then click . In this time, your cursor become a “hand”. Click your proton spectra then the spectra will be loaded. (Please process your proton spectra the first.)



3. Select Project X spectra. (After select, you will see a blue frame on spectra.)

4. Click  then Click your proton spectra again.

5. If your proton spectra has integral and peak information, you can click  and press “A” then use delete to eliminate.

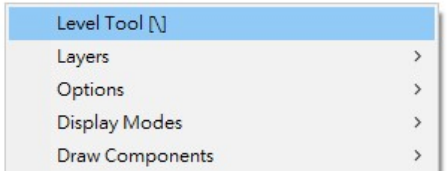
Tips: You can work in three frames. Please make sure you have select the frame which you want to work. (You will see a blue frame on active frame.)

Solutions for Innovation JEOL

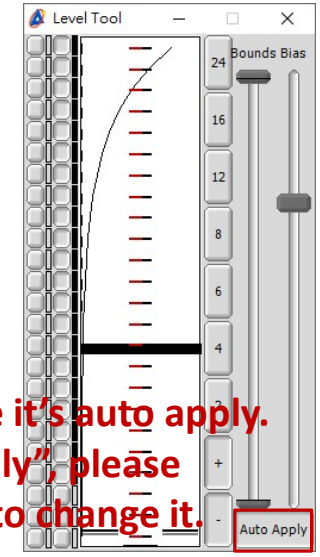
2D Processing - COSY

Step3: Level tool

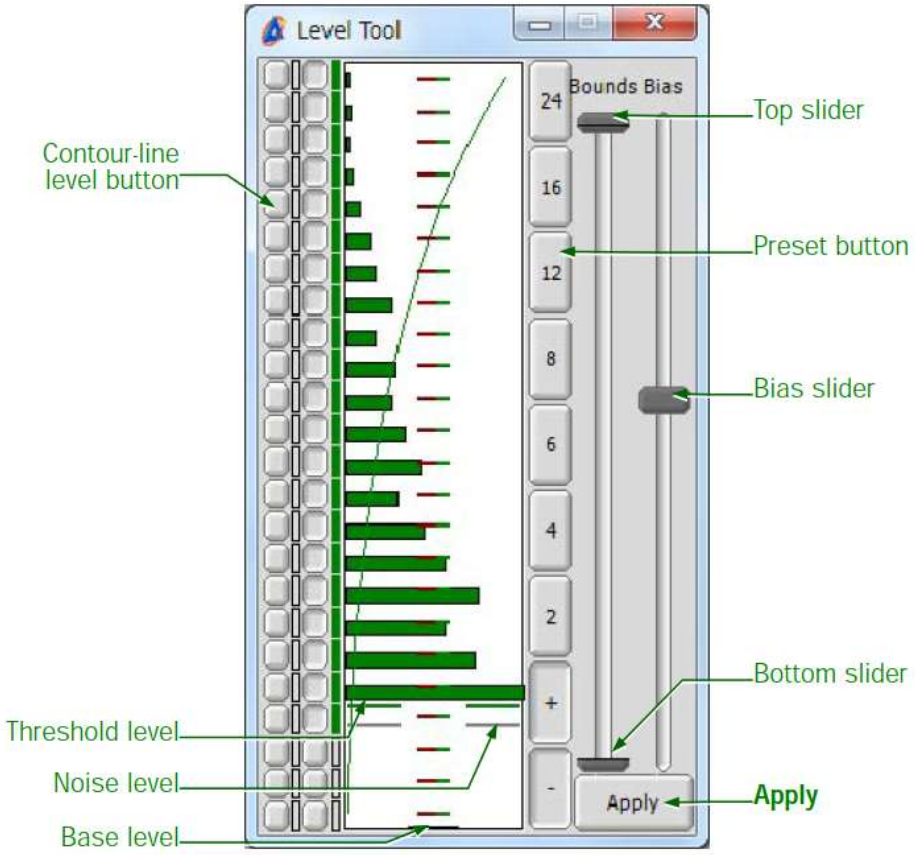
1. Right click, you can call level tool out.
   (shortcut "\")



2. Move "Bias" to change signal level.

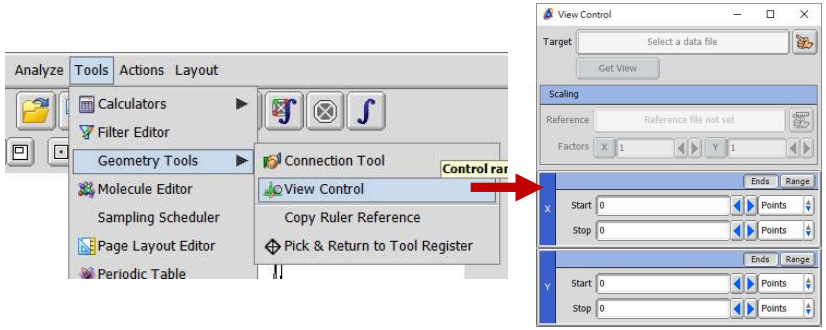


Make sure it's auto apply.
If it's "Apply", please
press "A" to change it.



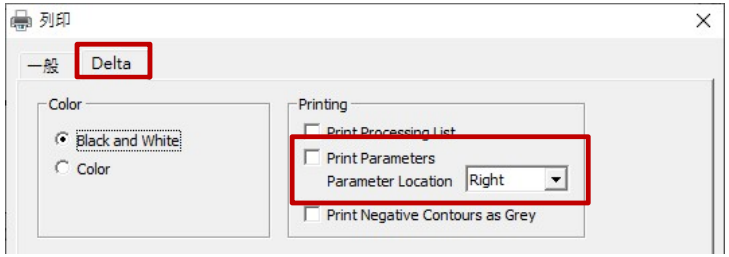
Step4: Set range and lay out

1. You can use View control to set range for 2D spectra.



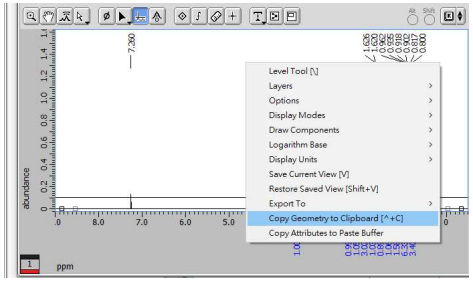
2. After adjust peak height, file name, comment and display setting, click  to print your spectra out.

3. In “Delta tab”, you can select print parameters or not.



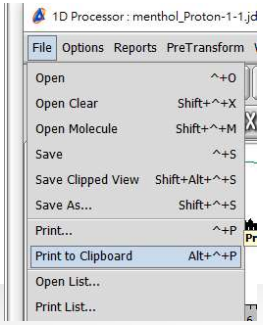
4. Copy your spectra.

Press Ctrl+C you can copy the spectra and past in other software. (The size of specta is depend on window)



5. Copy your spectra in fix size or with parameter.

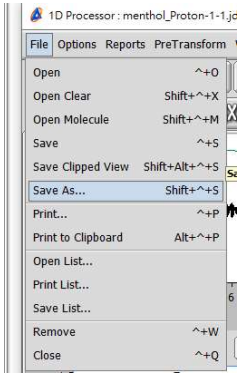
Select File→Print to clipboard on menu bar. You can get a spectra lay out like print format.



Step5: Save file

1. **Save as new file.**

   Select File→Save as to save a new spectra file.



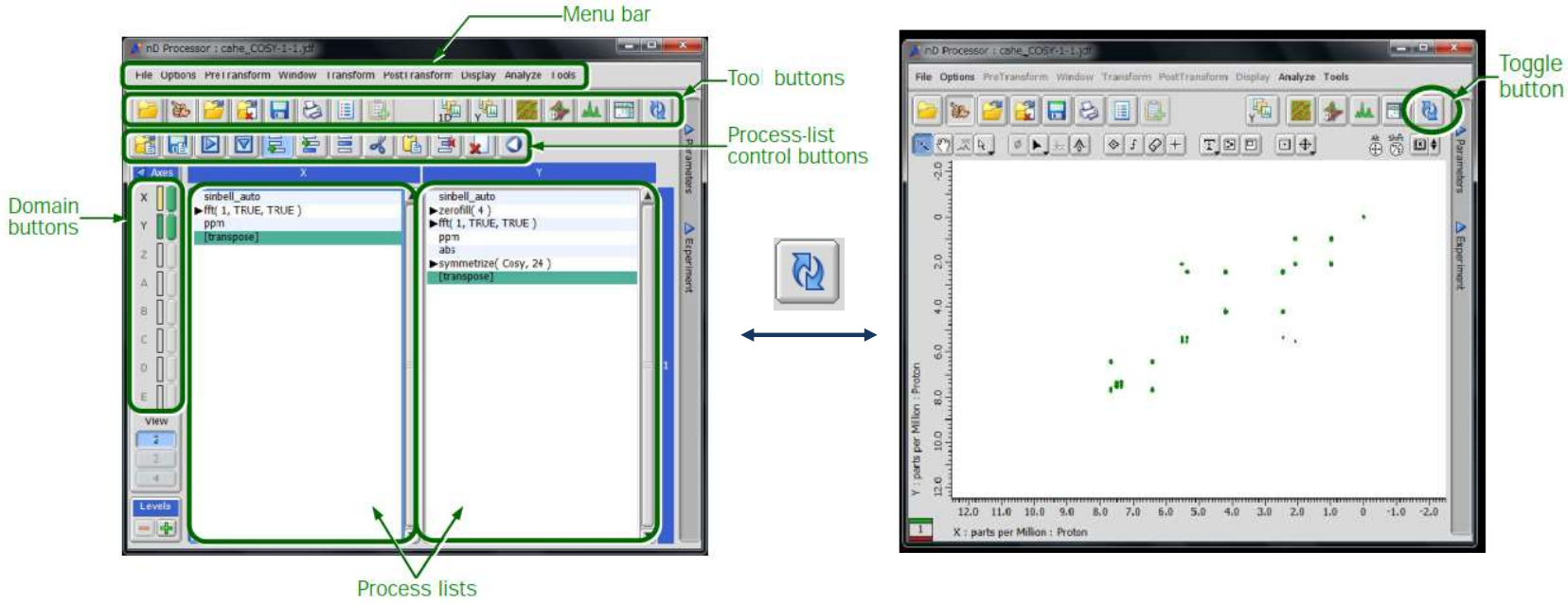
2. **Save file.**

   Click  to save your file with same name and just increase version number.

2D Processing - HMBC

2D Processor

1. Using  toggle button to switch process list and data view.
2. If data is fine then click  to open data in viewer.



Processor Window **After data processing**

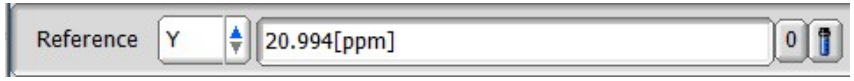
2D Processing - HMBC

Step1: Reference

1. Select “X” then Input a proton signal position as on option bar.

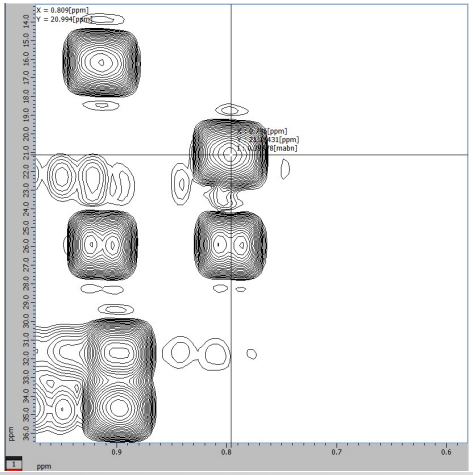


2. Select “X” then Input a proton signal position as on option bar.



3. Select  reference tool (shortcut F8)

4. Click solvent or TMS peak to reference.



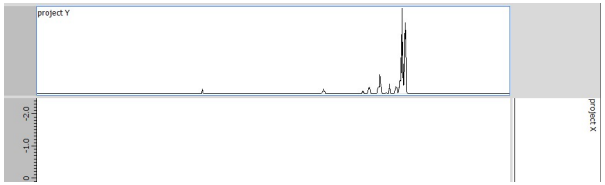
Tips: HMBC can’t use solvent as reference. (HMBC signals are 1H to 13C. Carbon signal of solvent is 2H-13C. It’s a little shift.)

Tips: Please change tool icon after reference otherwise you may mistouch to change the reference.

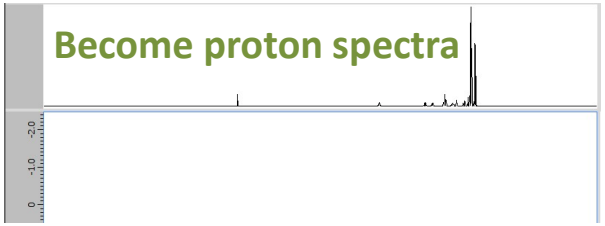
2D Processing - HMBC

Step2: Load 1D spectra

1. Select Project Y spectra. (After select, you will see a blue frame on spectra.)



2. Click  to unlock then click . In this time, your cursor become a “hand”. Click your proton spectra then the spectra will be loaded. (Please process your proton spectra the first.)



3. Select Project X spectra. (After select, you will see a blue frame on spectra.)

4. Click  then Click your carbon spectra. (Please process your carbon spectra the first)

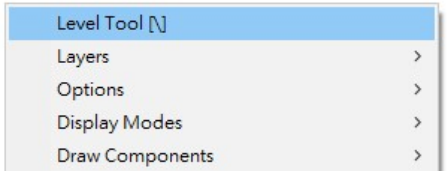
5. If your spectrum has integral and peak information, you can click  and press “A” then use delete to eliminate.

Tips: You can work in three frames. Please make sure you have select the frame which you want to work. (You will see a blue frame on active frame.)

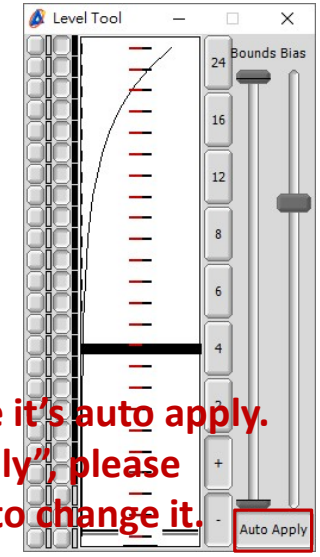
2D Processing - HMBC

Step3: Level tool

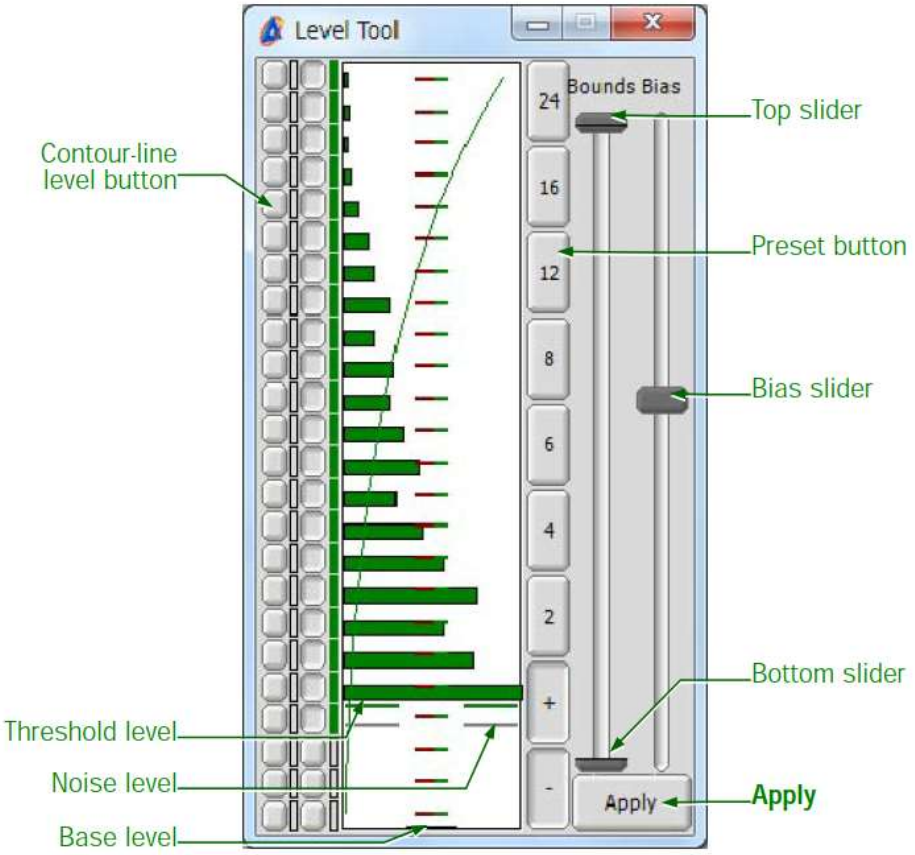
1. Right click, you can call level tool out.
   (shortcut "\")



2. Move "Bias" to change signal level.



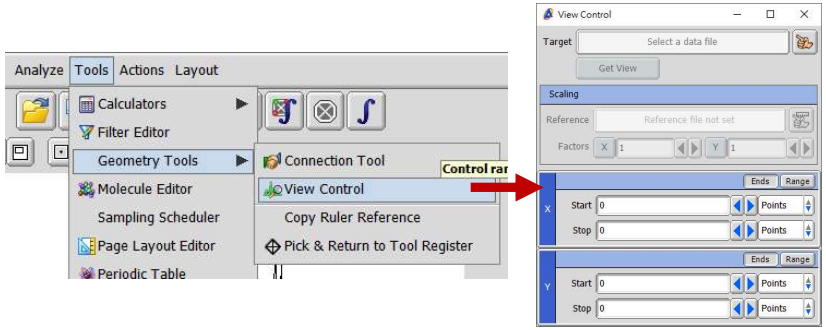
Make sure it's auto apply.
If it's "Apply", please press "A" to change it.



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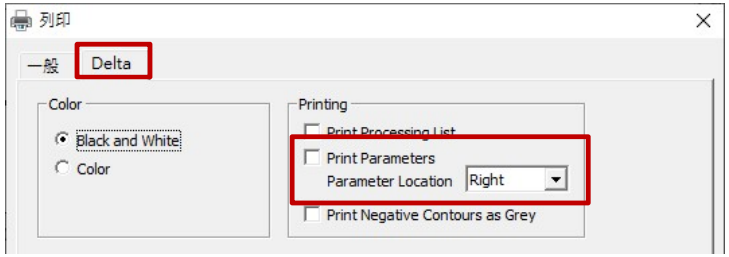
Step4: Set range and lay out

1. You can use View control to set range for 2D spectra.



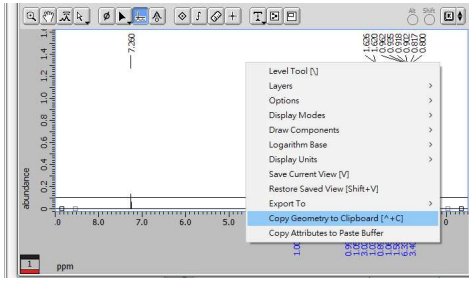
2. After adjust peak height, file name, comment and display setting, click  to print your spectra out.

3. In “Delta tab”, you can select print parameters or not.



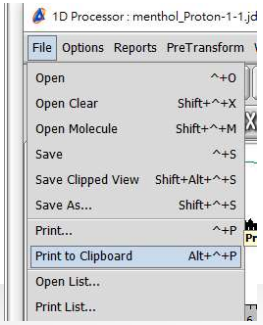
4. Copy your spectra.

Press Ctrl+C you can copy the spectra and past in other software. (The size of specta is depend on window)



5. Copy your spectra in fix size or with parameter.

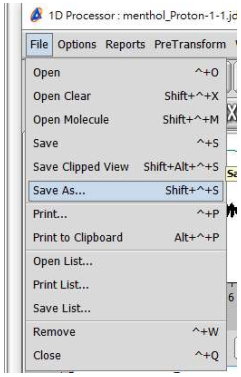
Select File→Print to clipboard on menu bar. You can get a spectra lay out like print format.



Step5: Save file

1. Save as new file.

Select File→Save as to save a new spectra file.



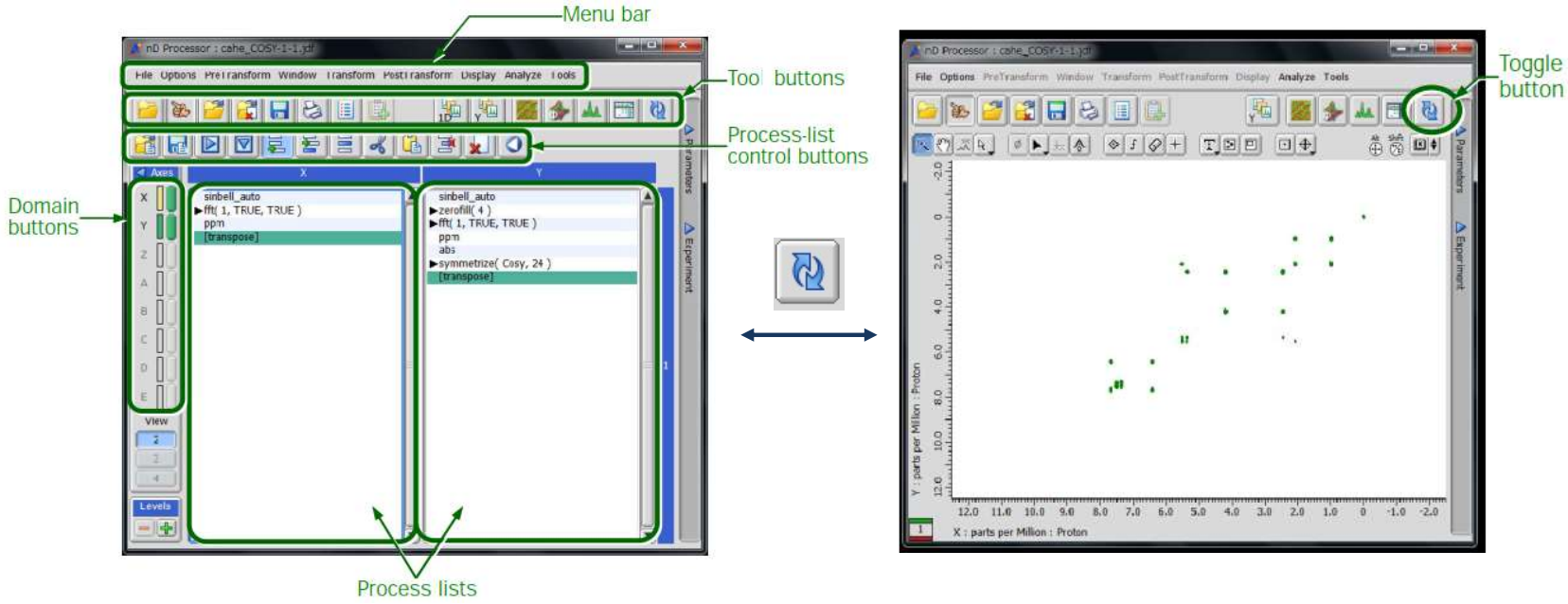
2. Save file.

Click  to save your file with same name and just increase version number.

2D Processing – HSQC (phase 2D)

2D Processor

1. Using  toggle button to switch process list and data view.
2. If data is fine then click  to open data in viewer.

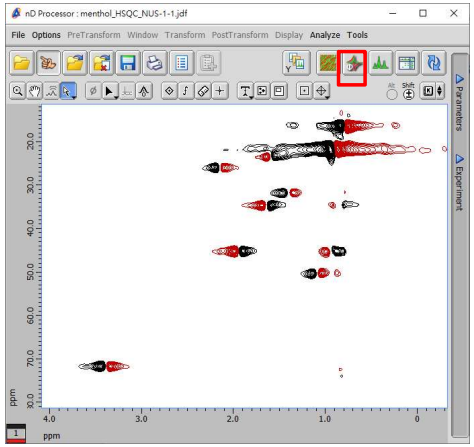


Processor Window **After data processing**

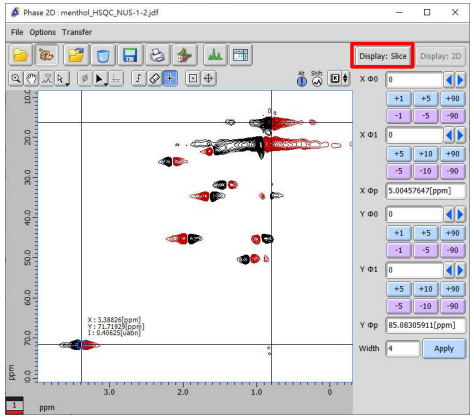
2D Processing – HSQC (phase 2D)

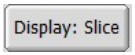
Step1: phasing

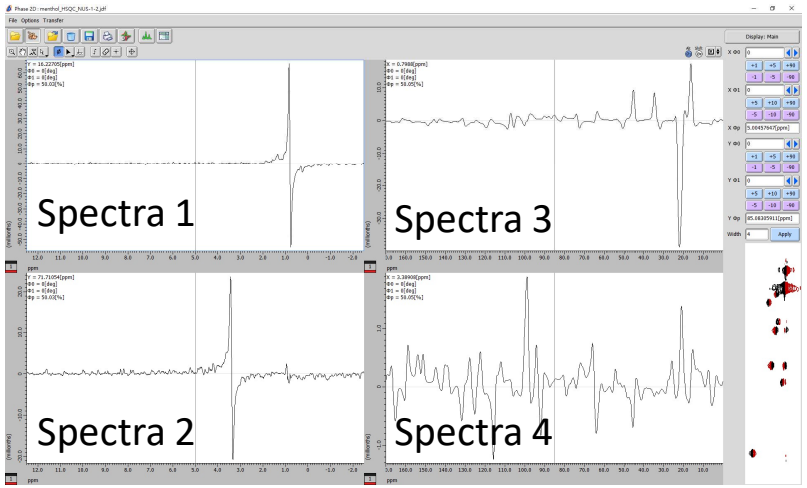
1. Click  switch to phasing tool.



2. Click  to mark two in window.



3. Click  start to adjust phase.

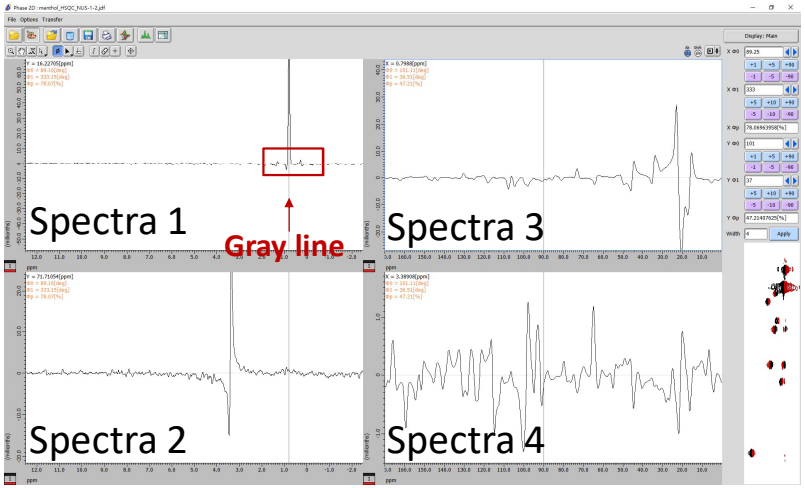


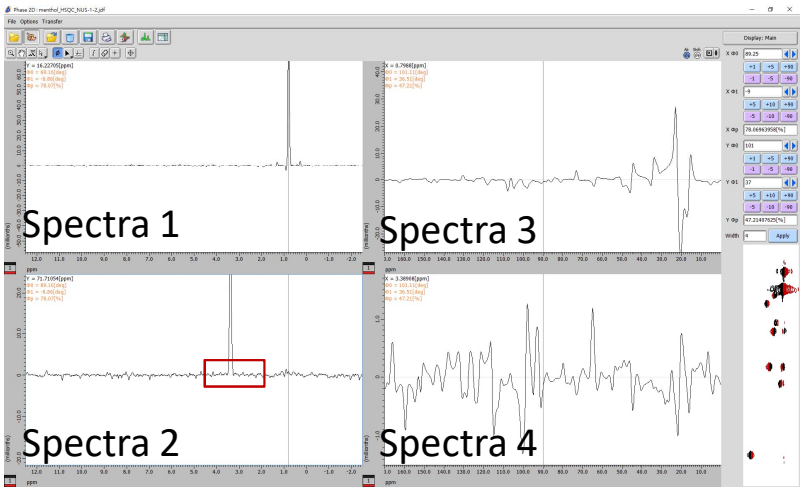
Solutions for Innovation JEOL

2D Processing – HSQC (phase 2D)

Step1: phasing

1. Select  phasing tool (shortcut F5)
2. Moving gray line to the peak in spectra 1.
3. Press Left mouse key and move horizontally to adjust the peak in spectra 1.
4. Press middle mouse key (or push ALT key + left key) and move horizontally to adjust the peak in spectra 2.





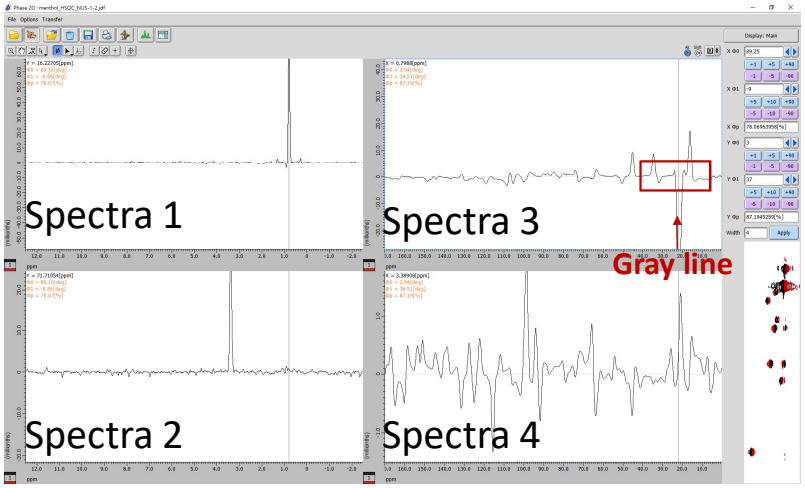
Solutions for Innovation JEOL

2D Processing – HSQC (phase 2D)

Step1: phasing

5. Moving gray line to the peak in spectra 3.

6. Press Left mouse key and move horizontally to adjust the peak in spectra 3.



7. Press middle mouse key (or push ALT key + left key) and move horizontally to adjust the peak in spectra 4.

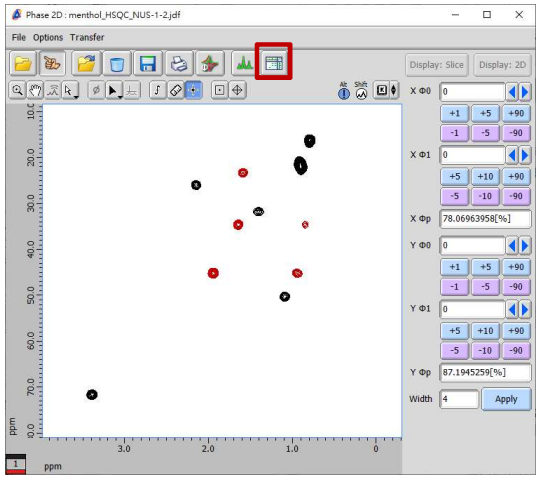


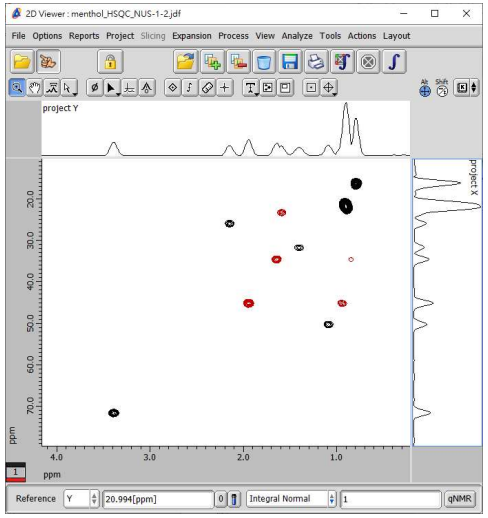
5. Click  to finish phasing.

2D Processing – HSQC (phase 2D)

Step1: phasing

8. If phase is fine, click  to open data with viewer.





Tips: In edit-HSQC, CH2 is negative signal and CH, H3 are positive signals.

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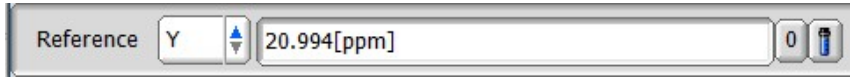
2D Processing - HSQC

Step2: Reference

1. Select “X” then Input a proton signal position as on option bar.

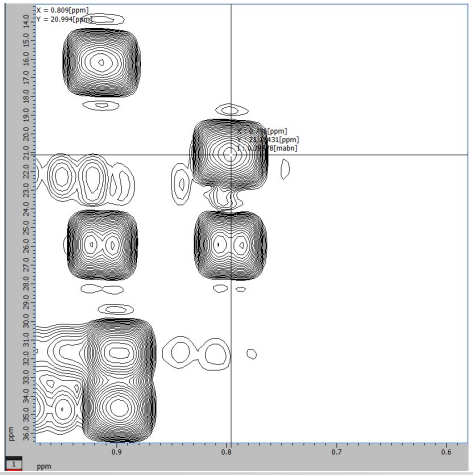


2. Select “X” then Input a proton signal position as on option bar.



3. Select  reference tool (shortcut F8)

4. Click solvent or TMS peak to reference.



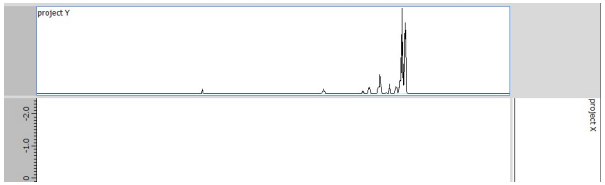
Tips: HSQC can’t use solvent as reference. (HSQC signals are 1H to 13C. Carbon signal of solvent is 2H-13C. It’s a little shift.)

Tips: Please change tool icon after reference otherwise you may mistouch to change the reference.

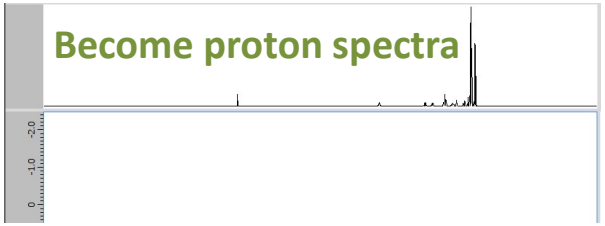
2D Processing - HSQC

Step3: Load 1D spectra

1. Select Project Y spectra. (After select, you will see a blue frame on spectra.)



2. Click  to unlock then click . In this time, your cursor become a “hand”. Click your proton spectra then the spectra will be loaded. (Please process your proton spectra the first.)



3. Select Project X spectra. (After select, you will see a blue frame on spectra.)

4. Click  then Click your carbon spectra. (Please process your carbon spectra the first)

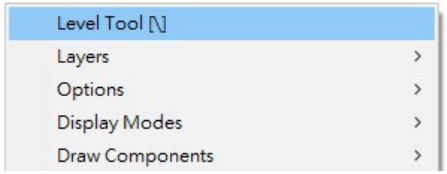
5. If your spectrum has integral and peak information, you can click  and press “A” then use delete to eliminate.

Tips: You can work in three frames. Please make sure you have select the frame which you want to work. (You will see a blue frame on active frame.)

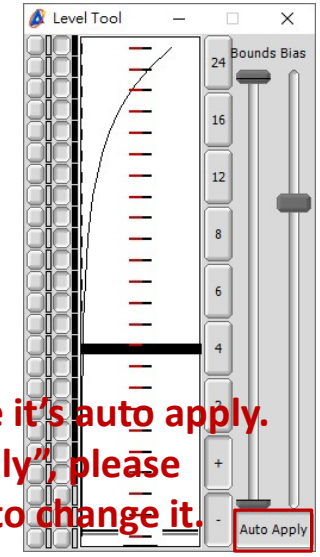
2D Processing - HSQC

Step4: Level tool

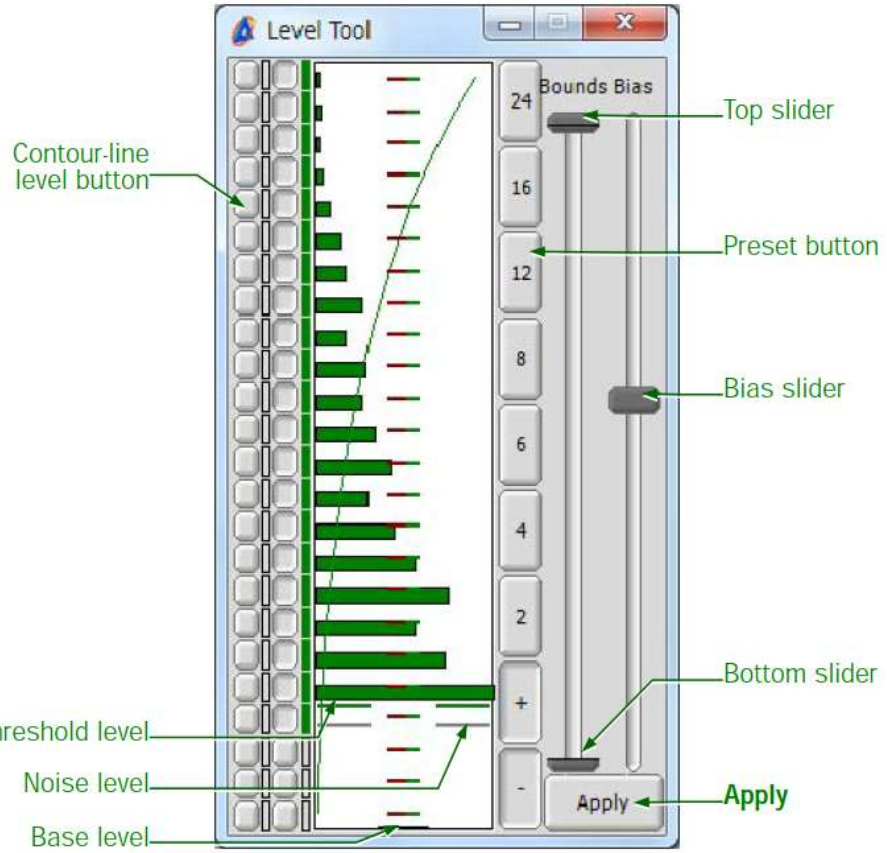
1. Right click, you can call level tool out.
   (shortcut "\")



2. Move "Bias" to change signal level.



Make sure it's auto apply.
If it's "Apply", please
press "A" to change it.

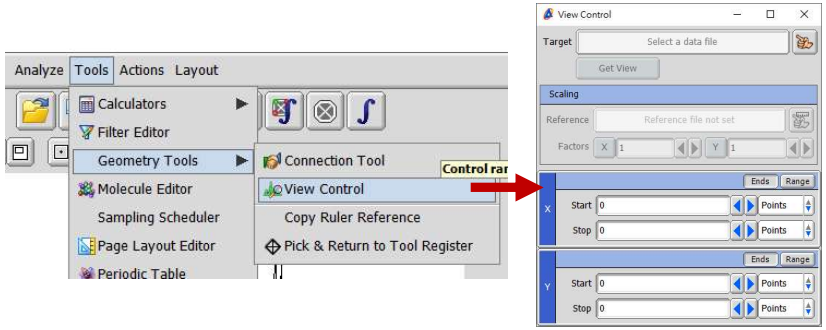


Tips: You can use contour-line level button to control negative and positive signals separately.

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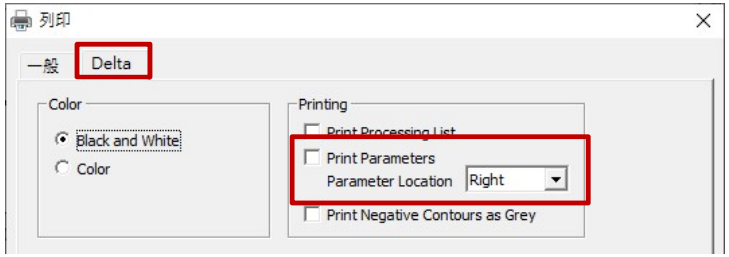
Step5: Set range and lay out

1. You can use View control to set range for 2D spectra.



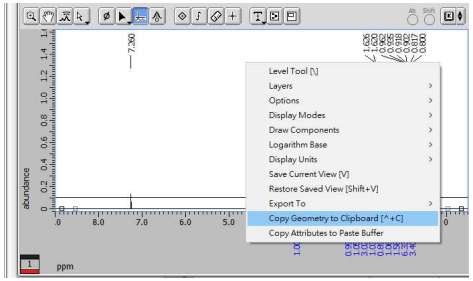
2. After adjust peak height, file name, comment and display setting, click  to print your spectra out.

3. In “Delta tab”, you can select print parameters or not.



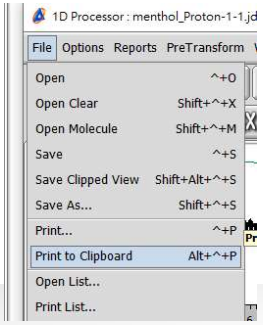
4. Copy your spectra.

Press Ctrl+C you can copy the spectra and past in other software. (The size of specta is depend on window)



5. Copy your spectra in fix size or with parameter.

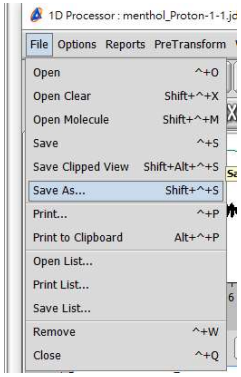
Select File→Print to clipboard on menu bar. You can get a spectra lay out like print format.



Step6: Save file

1. Save as new file.

Select File→Save as to save a new spectra file.



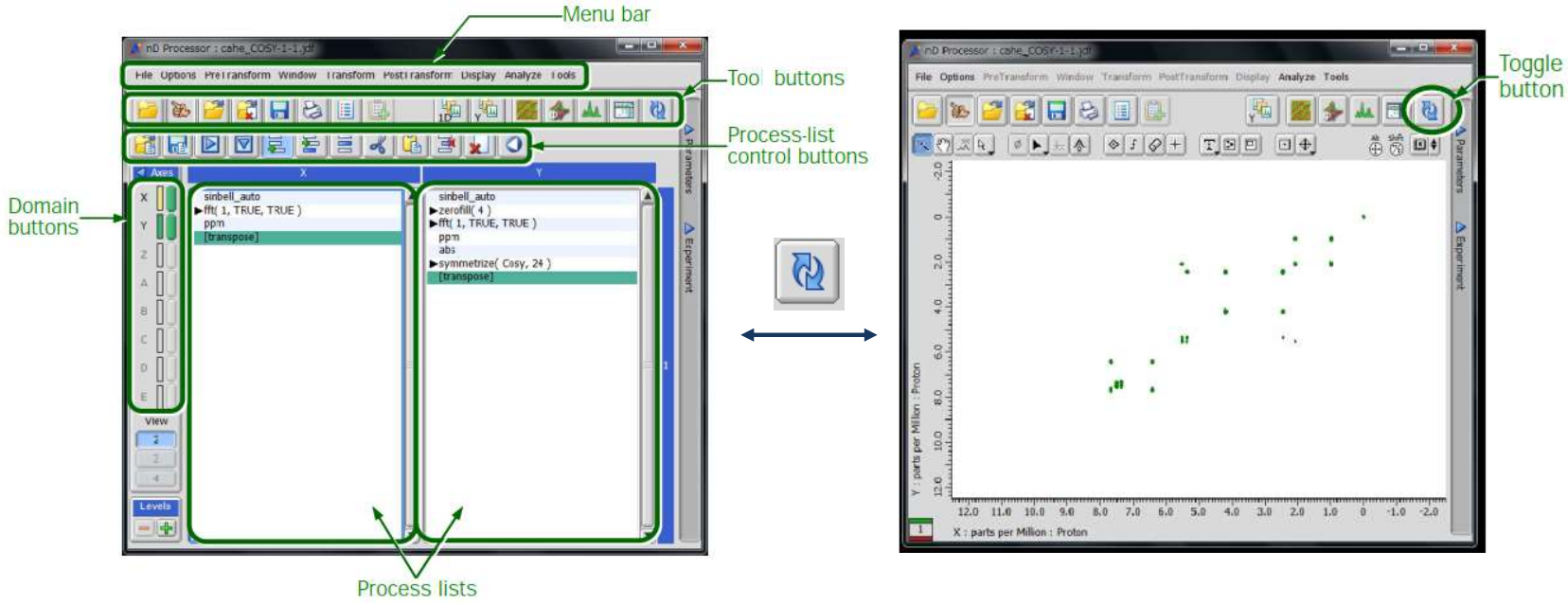
2. Save file.

Click  to save your file with same name and just increase version number.

2D Processing – NOESY (phase 2D)

2D Processor

1. Using  toggle button to switch process list and data view.
2. If data is fine then click  to open data in viewer.

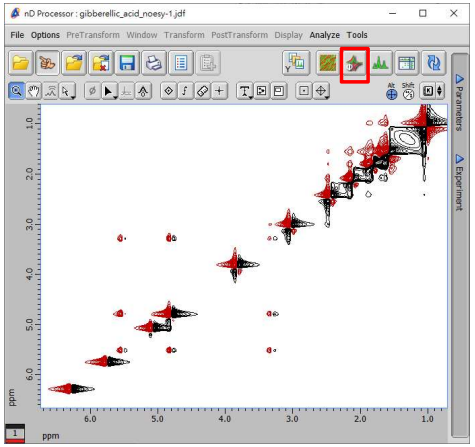


Processor Window **After data processing**

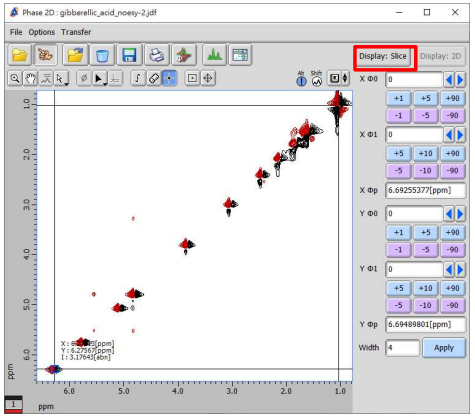
2D Processing – NOESY (phase 2D)

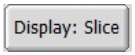
Step1: phasing

1. Click  switch to phasing tool.

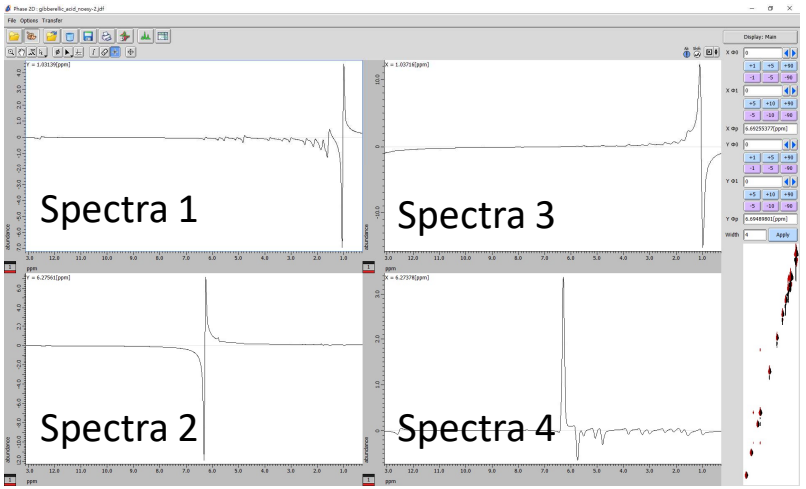


2. Click  to mark two in window.



3. Click 

start to adjust phase.



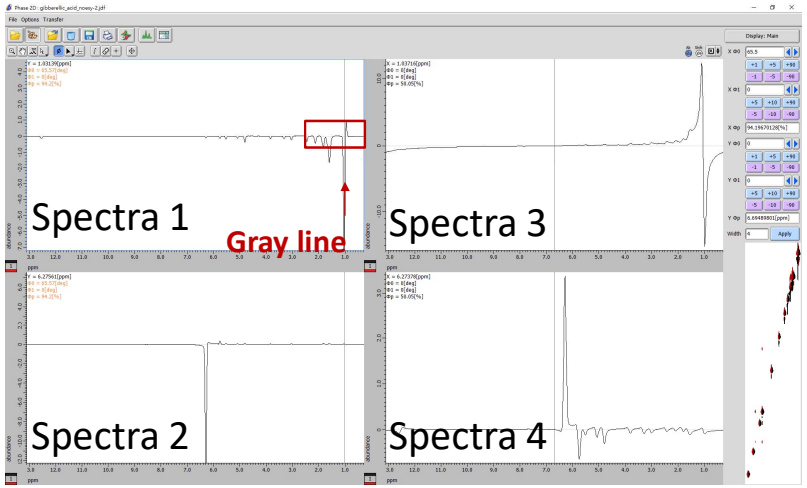
Tips: In NOESY, diagonal signals are negative.

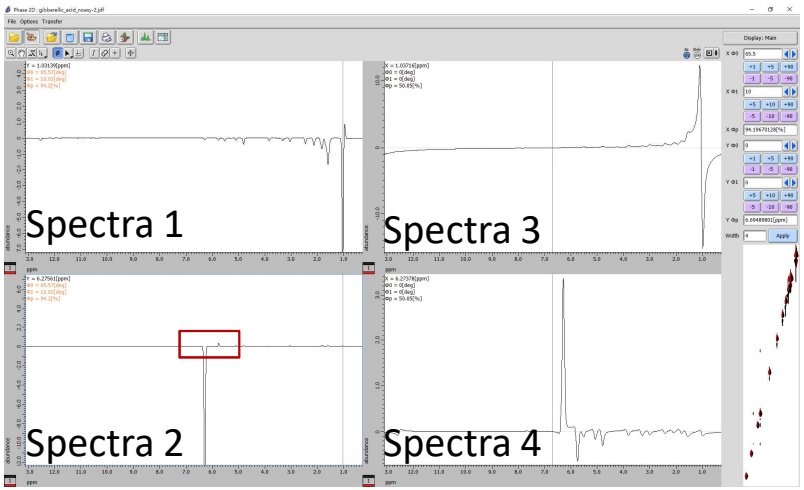
Solutions for Innovation JEOL

2D Processing – NOESY (phase 2D)

Step1: phasing

1. Select  phasing tool (shortcut F5)
2. Moving gray line to the peak in spectra 1.
3. Press Left mouse key and move horizontally to adjust the peak in spectra 1.
4. Press middle mouse key (or push ALT key + left key) and move horizontally to adjust the peak in spectra 2.



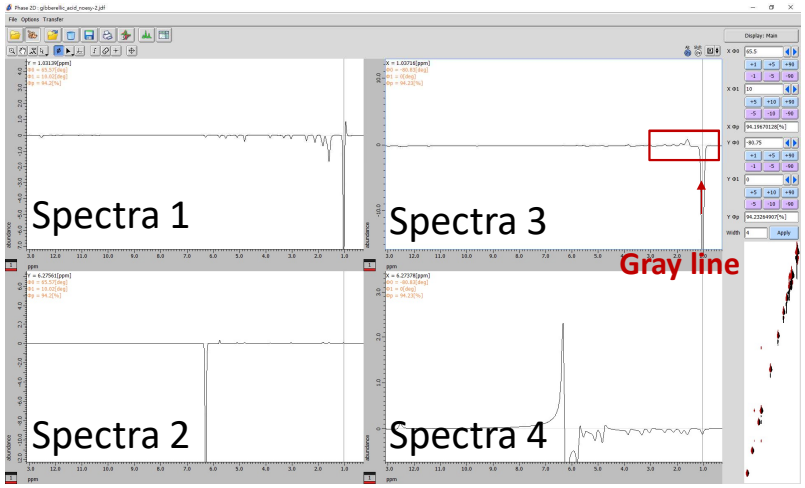


2D Processing – NOESY (phase 2D)

Step1: phasing

5. Moving gray line to the peak in spectra 3.

6. Press Left mouse key and move horizontally to adjust the peak in spectra 3.



7. Press middle mouse key (or push ALT key + left key) and move horizontally to adjust the peak in spectra 4.

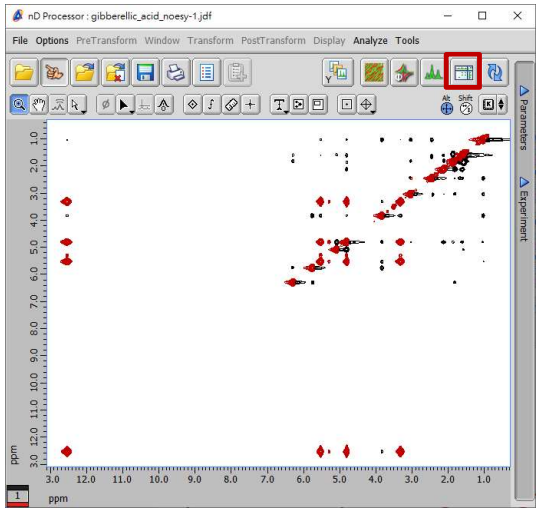


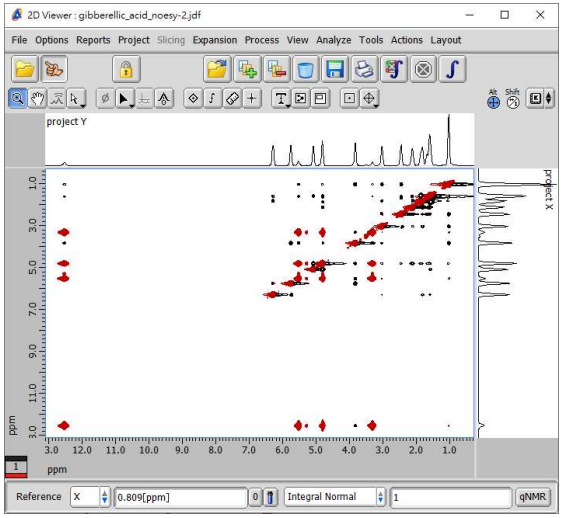
5. Click  to finish phasing.

2D Processing – NOESY (phase 2D)

Step1: phasing

8. If phase is fine, click  to open data with viewer.





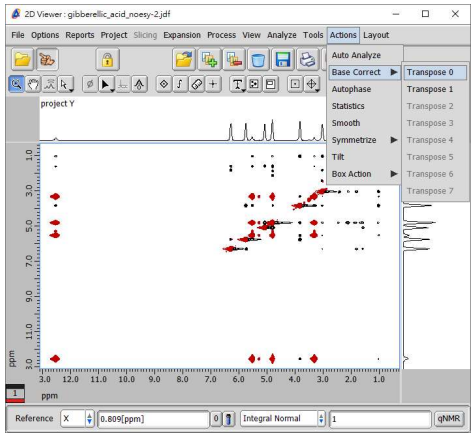
Tips: In NOESY, diagonal signals are negative.

Solutions for Innovation JEOL

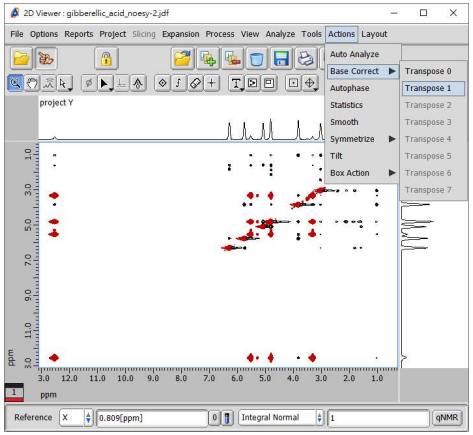
2D Processing – NOESY (phase 2D)

Step2: baseline correction

1. **In menu bar, click Actions→Base Correct→Transpose 0.**



2. **In menu bar, click Actions→Base Correct→Transpose 1.**



Solutions for Innovation JEOL

2D Processing – NOESY (phase 2D)

Step3: Reference

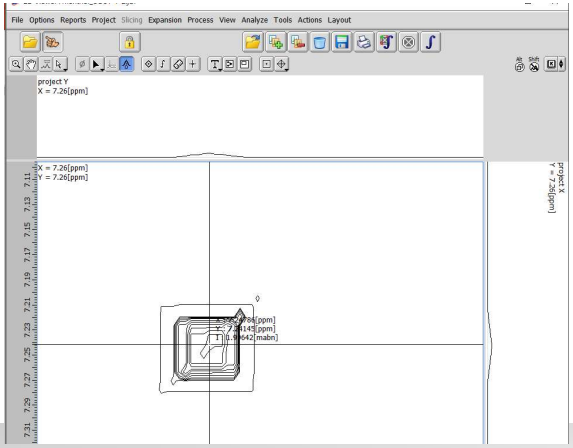
1. Select “X” then Click  to in put default solvent reference or input value by manual on option bar.



2. Select “Y” then Click  to in put default solvent reference or input value by manual on option bar.



3. Select  reference tool (shortcut F8)
4. Click solvent or TMS peak to reference.

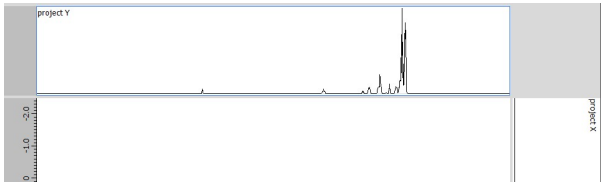


Tips: Please change tool icon after reference otherwise you may mistouch to change the reference.

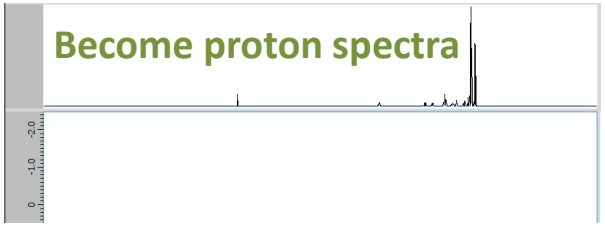
2D Processing – NOESY (phase 2D)

Step4: Load 1D spectra

1. Select Project Y spectra. (After select, you will see a blue frame on spectra.)



2. Click  to unlock then click . In this time, your cursor become a “hand”. Click your proton spectra then the spectra will be loaded. (Please process your proton spectra the first.)



3. Select Project X spectra. (After select, you will see a blue frame on spectra.)

4. Click  then Click your proton spectra again.

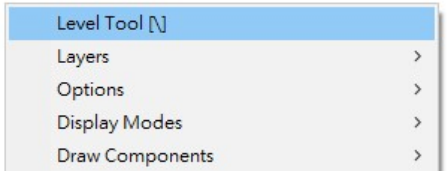
5. If your proton spectra has integral and peak information, you can click  and press “A” then use delete to eliminate.

Tips: You can work in three frames. Please make sure you have select the frame which you want to work. (You will see a blue frame on active frame.)

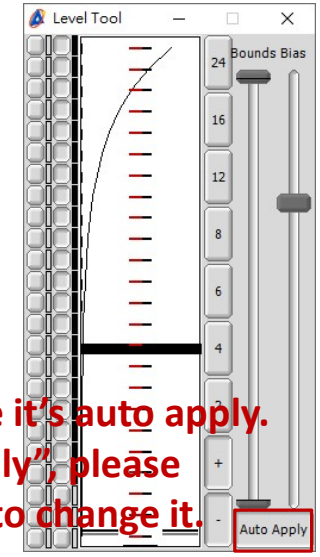
2D Processing - NOESY

Step5: Level tool

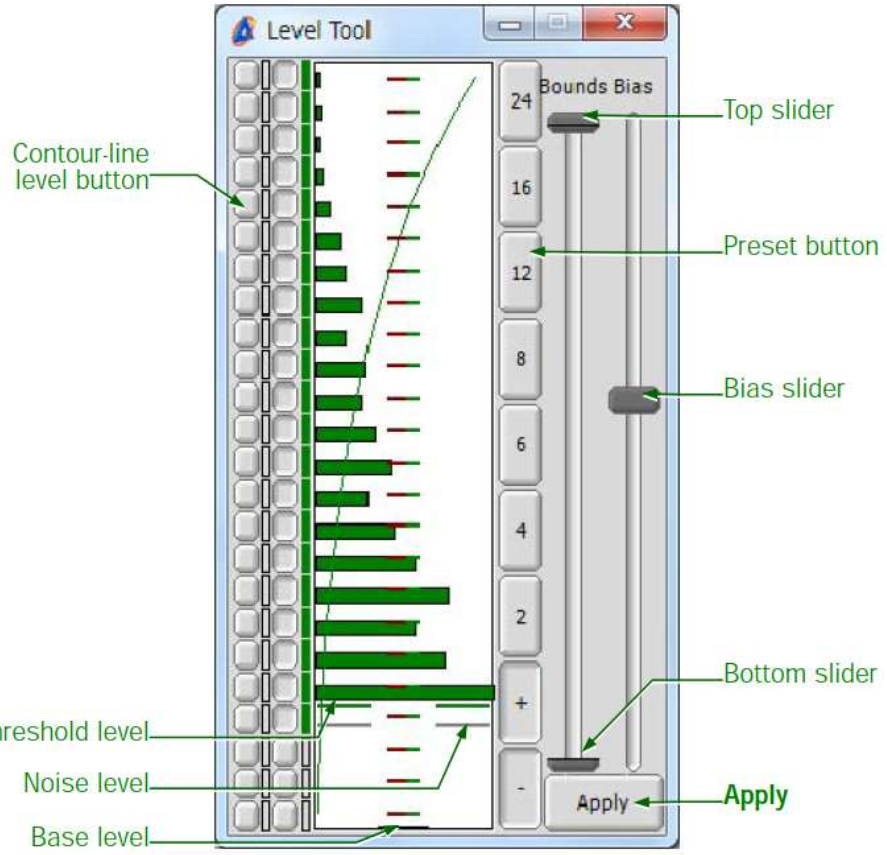
1. Right click, you can call level tool out.
   (shortcut "\")



2. Move "Bias" to change signal level.



Make sure it's auto apply.
If it's "Apply", please
press "A" to change it.

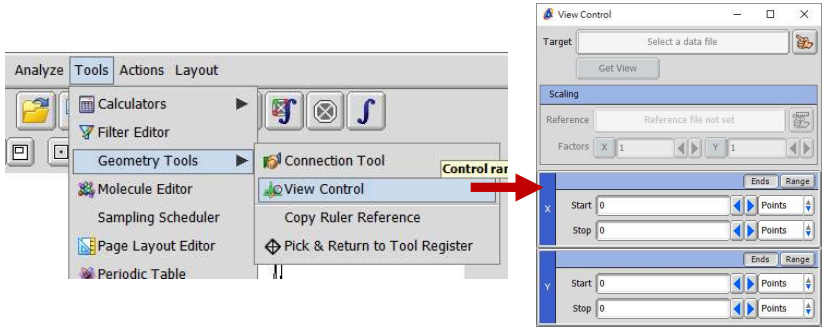


Tips: You can use contour-line level button to control negative and positive signals separately.

Solutions for Innovation JEOL

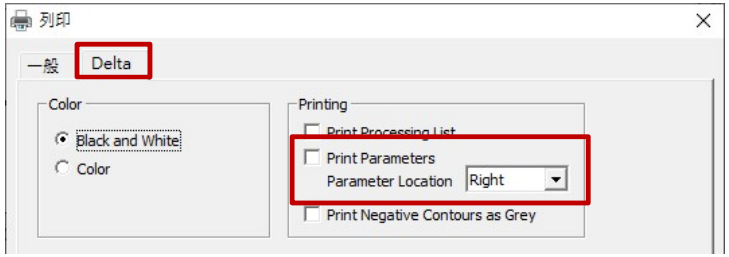
Step6: Set range and lay out

1. You can use View control to set range for 2D spectra.



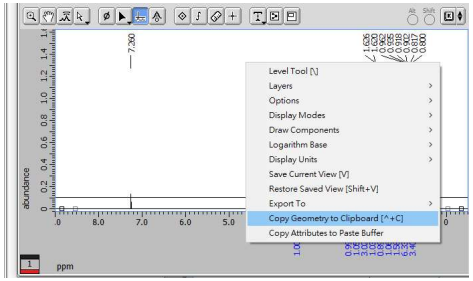
2. After adjust peak height, file name, comment and display setting, click  to print your spectra out.

3. In “Delta tab”, you can select print parameters or not.



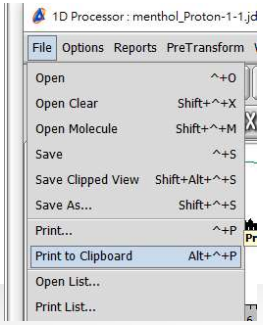
4. Copy your spectra.

Press Ctrl+C you can copy the spectra and past in other software. (The size of specta is depend on window)



5. Copy your spectra in fix size or with parameter.

Select File→Print to clipboard on menu bar. You can get a spectra lay out like print format.

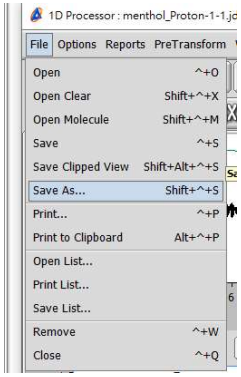


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Step7: Save file

1. **Save as new file.**

   Select File→Save as to save a new spectra file.



2. **Save file.**

   Click  to save your file with same name and just increase version number.