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TOPSPIN

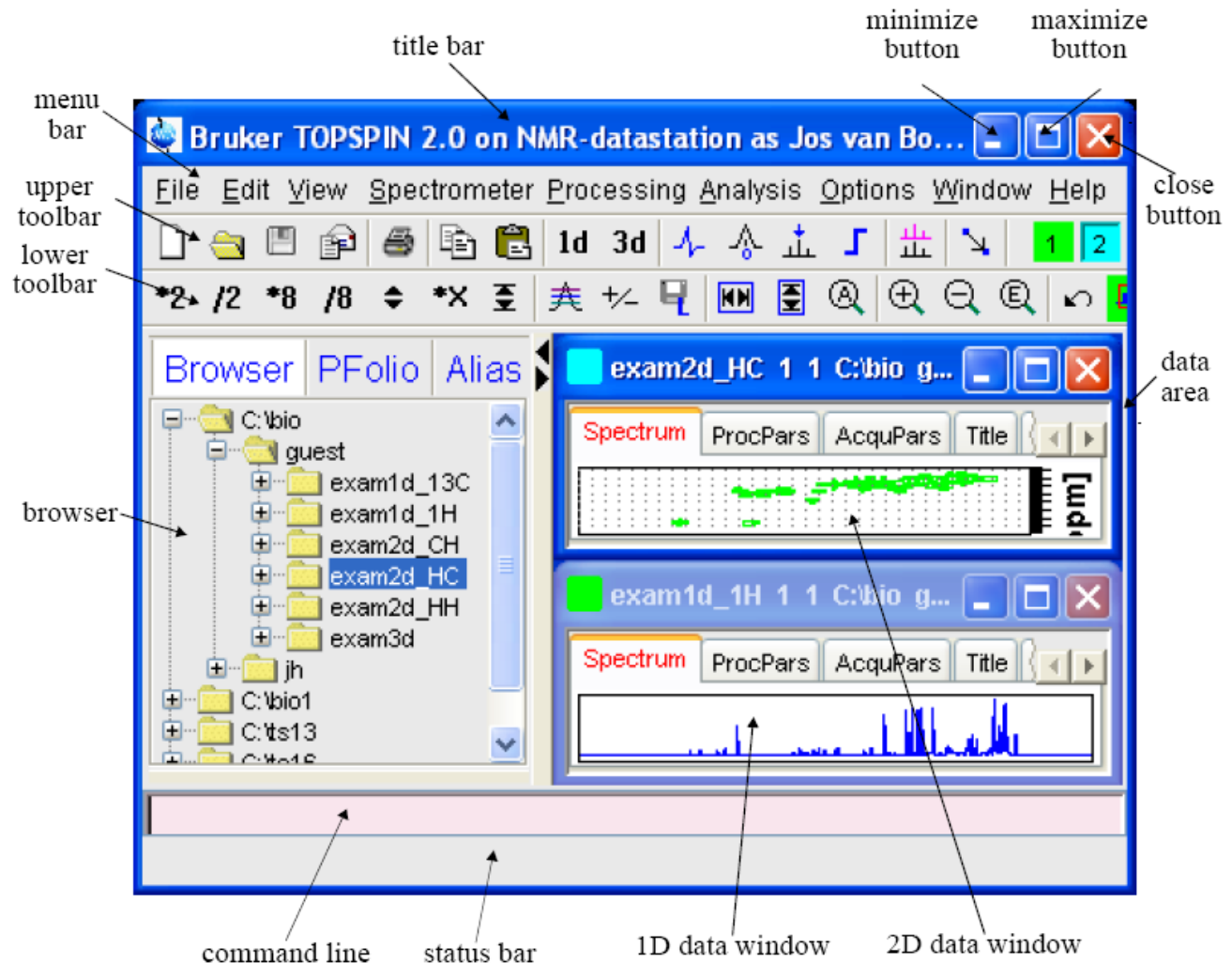
Bruker files are directory tree: required directory in bold, user input: between <>.

<dir>**data**\<user>**nmr**\<dataname>\<expno>**pdata**\<procno>


<mydata>\<name>\<expno>\pdata\<procno>

Open File can be done with multitude of ways:

- Open data from menu (or tool bar), choose browser file.
- In Window explorer, go to your file and drag it in the graphic window




Expand Spectral Region

Drag with the left mouse around the region you want to expand. Or click on  on the lower tool bar.

To Display integral or peaks on spectra:

Move mouse on data window, right click and choose *Display Properties...* in the popup menu. Check the desired item.


To Display projection or 1D Spectra on a 2D:

If there are no projections, click on  in the upper tool bar. In the projection area, right click and choose one of the option.

External Projection ... : an existing 1D spectrum can be read.

Internal projection : a projection can be calculated and displayed.

To Superimpose spectra in multiple display mode

Click on  in the upper tool bar. When you open a new data set (or drag from browser), it will be superimpose on current spectrum. You can scale and shift each spectra individually. Multiple display is available for 1D as well as 2D data sets.

How to print the data:

To print the content of the data window: <Ctrl>p or use **File → Print** [select print active window]

You can also copy data to the clipboard and paste it in windows application.

How to process data

Use Topspin processing guide. In automatic mode it execute processing commands with default parameters.

How to archive the data

File → Save → data set in Zip.

How to fit peaks and deconvolve overlapping peaks

Analysis → deconvolution

Data can be open in multiple window

Click in the browser on another data set : right click and select **Display in a new window**

In the Window menu you can select different arrangement like display in stack, display side-by-side etc...

The mouse cursor in the data window is consistent with all data sets.

One of the window is active. (highlighted title bar) : it has mouse focus, menu and toolbar.

The Upper Tool Bar:

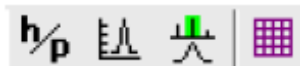


Most useful buttons are : open file, print, Copy, Paste, Switch to last 2d dataset.



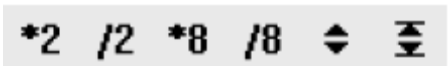
: manipulation button.

Adjust Phase,
Calibrate,
Correct Baseline,
Enter Peak picking mode,
Enter integrate mode,
Switch to multiple display,
Distance measurement mode.



Toggle Hz \leftrightarrow PPM
Y-Axis display : Abs, Rel, off
Overview : on/off
Grid toggle

The Lower Tool Bar:

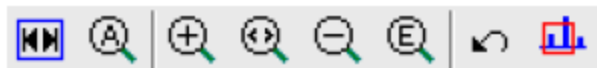


: Intensity scaling

Double arrow: Mouse drag of intensity
Double arrow with limits: Reset Scale.

Intensity can also be changed with mouse wheel.

Intensity can also be changed with Keyboard : <Alt><PageUp>, <Alt><PageDown>, <Alt><Enter>



: Horizontal scaling

Reset Full spectra window
Reset Full spectra window as well as the scale
Increase Zoom
Drag zoom with Left mouse
Decrease zoom
Enter Zoom with Dialogue box
Go to previous zoom
Retain Vertical and Horizontal zoom to display another data set

You can also zoom using left mouse drag in the data set.



: shift spectra

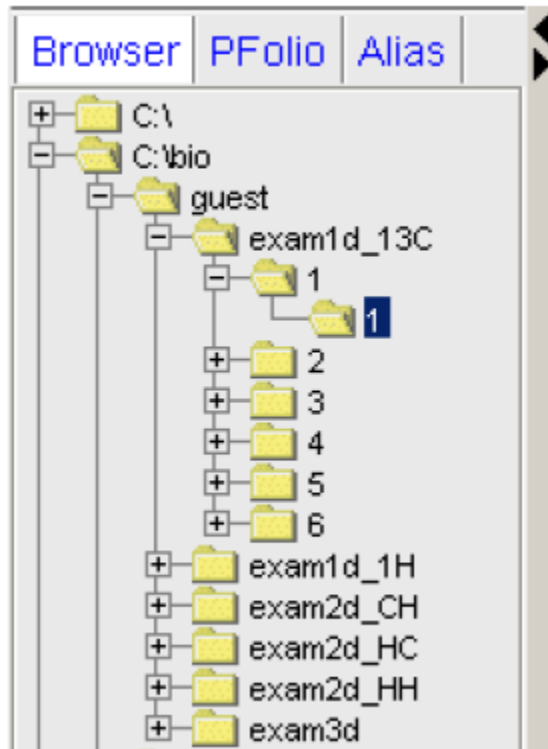
Shift Left, with mouse Drag or Shift right. The last to move to the end of the window,



: Vertical shift

Reset baseline in the center, Mouse drag the baseline, Reset baseline at the bottom.

File Handling



The Browser:



The Portfolio :

displays last used datasets

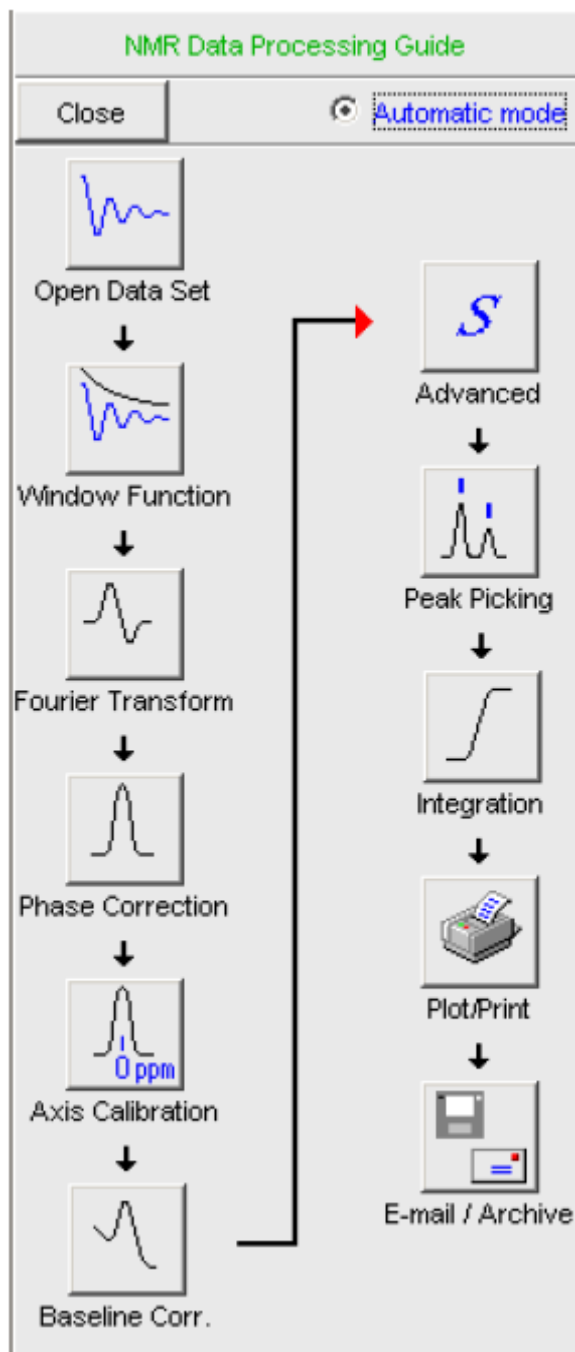
If the browser is not visible : **View** → **Browser panel On/Off**

Working with Portfolio:

To save a portfolio: right click inside a portfolio and choose **Open portfolio...**, specify folder and filename (with .prop extension) and click **save**.

To open a portfolio: right click inside a portfolio and choose **Save portfolio...**, Navigate to the folder and filename (with .prop extension) and click **Open**.

To remove data set from portfolio: right a dataset and choose **Remove from portfolio...**, click **OK**



Data processing

Semi-Automatic processing

Click **Processing** → **Processing guide**

Click on “*Automatic mode*”

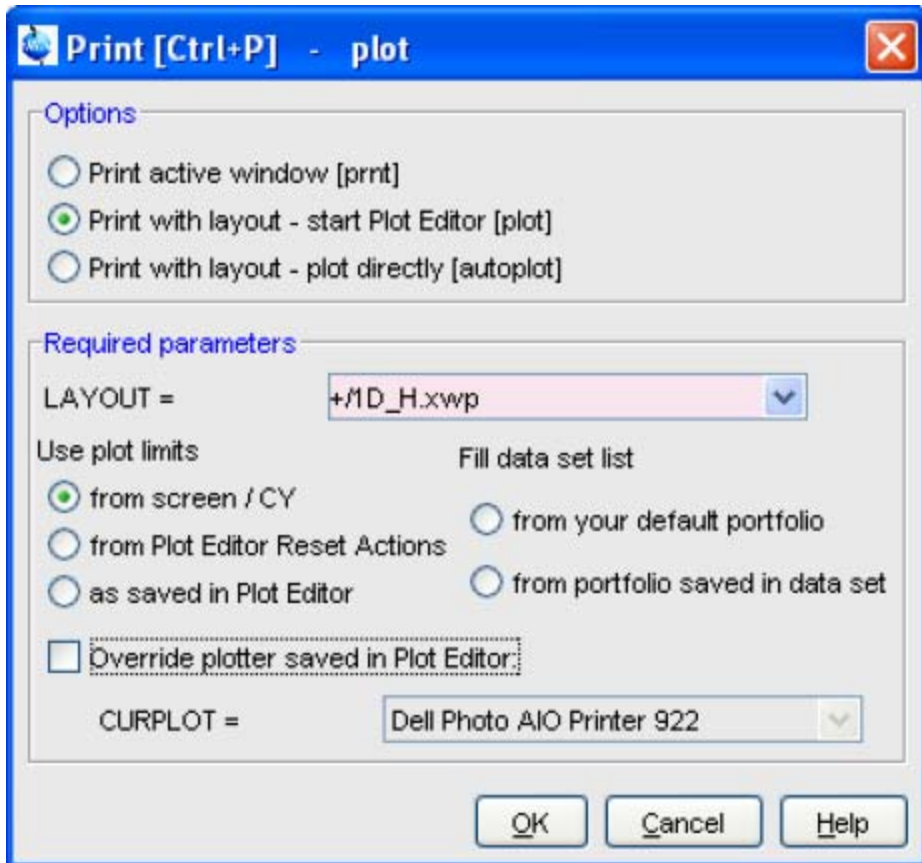
Open a data set, click on “*Window Function*” → “*Fourier Transform*” → “*Phase Correction*” etc... All the steps will be executed without user interaction.

If “*Automatic mode*” is not selected, when you click on a button, optional parameters are presented to you.

To Print / Plot, click on printer icon in upper tool bar or in processing guide, or type <Ctrl>p, or select **File** → **Print**.

The print dialogue will appear.

Print Dialogue :



The “*Print active window*” will print the way data are displayed.

‘*Print with Layout - start Plot Editor*’ – equivalent to typing ‘plot’

Print Integral and peak list:

Click in “*integrals tab*”, type “print” (or <Ctrl>p)

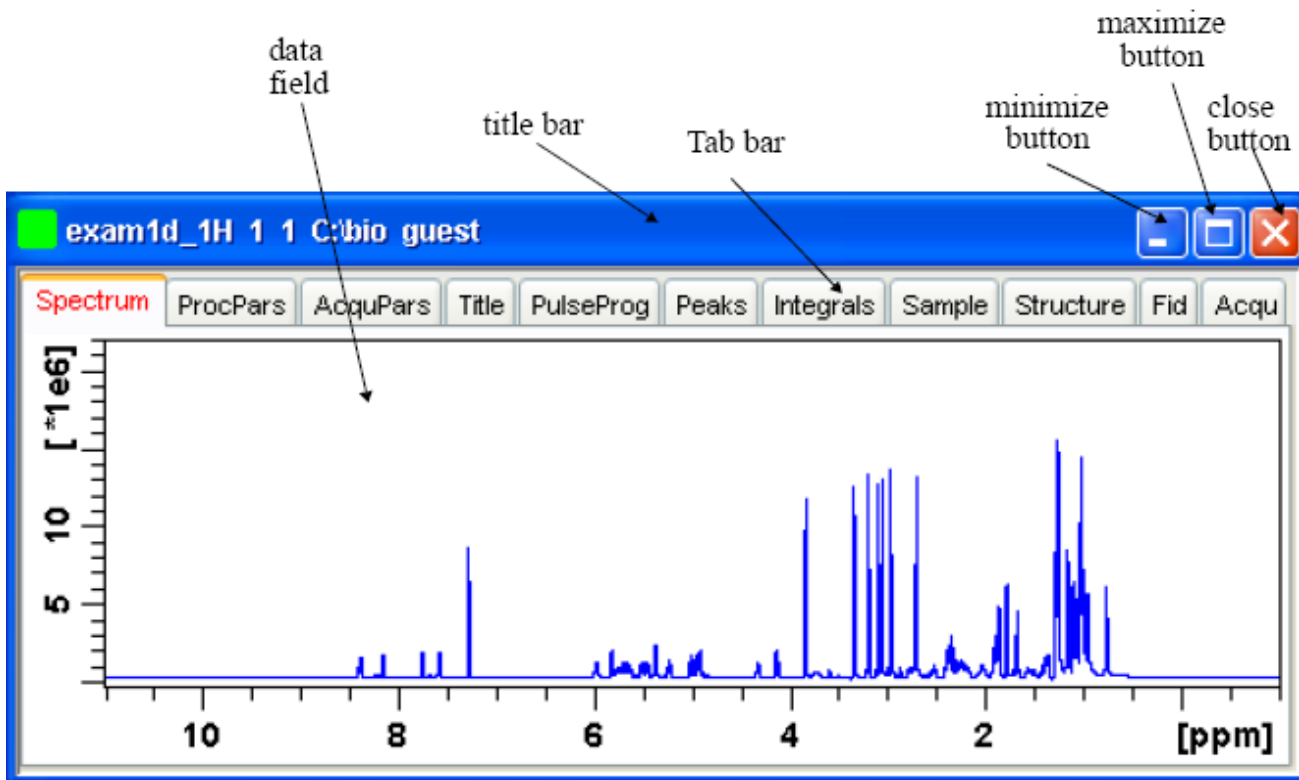
Click in “*Peaks tab*”, type “print” (or <Ctrl>p)

You can use also select data, copy the data and paste it in another application (like plot editor)

To Store data as Graphic File

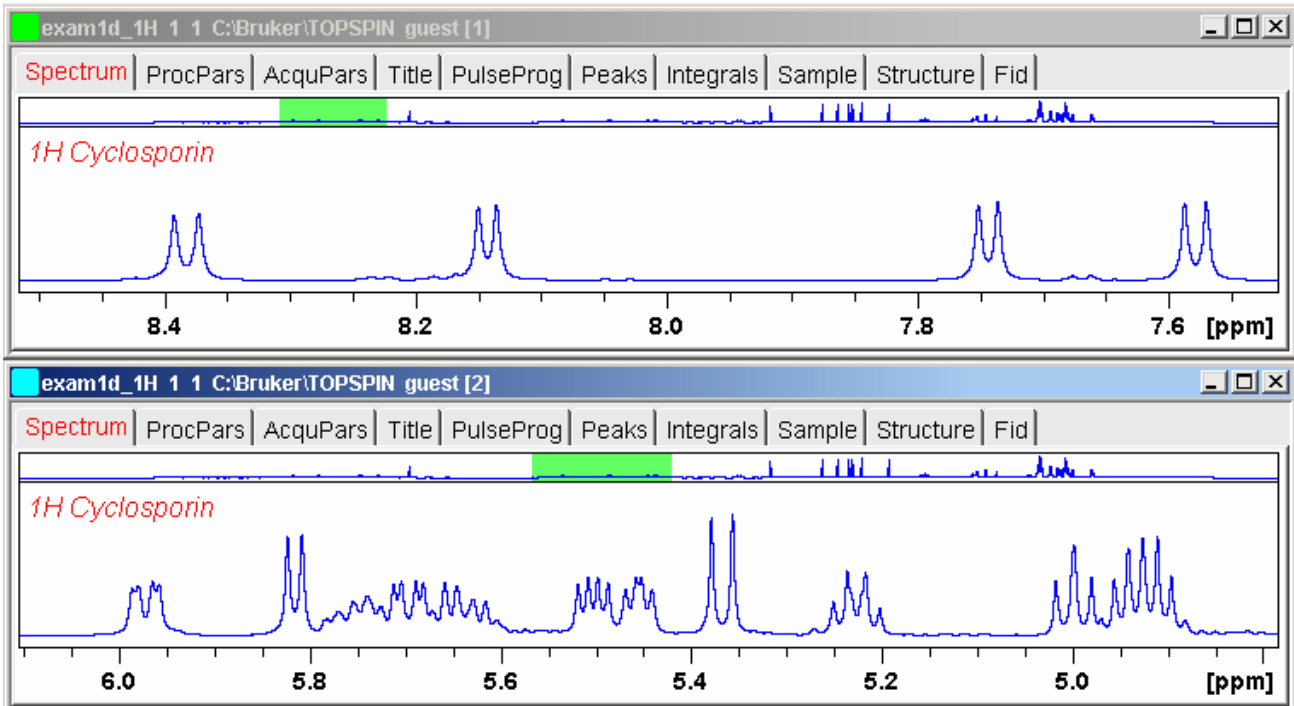
Click on **File** → **Export ...**, navigate to the storage folder, enter file name and extension, Click on “**Export**”

1D-Display



You can display the same dataset in different window (convenient way to view various expansion or various parameters (Spectra, peak picking...))

To reopen the same dataset, select : **File → Reopen**



When you have multiple window, the manipulation button (scale width etc...) work only on the active window.

To affect all the windows : use <Ctrl> + *2 (for example). Or <Ctrl> <Alt> <PageUp>

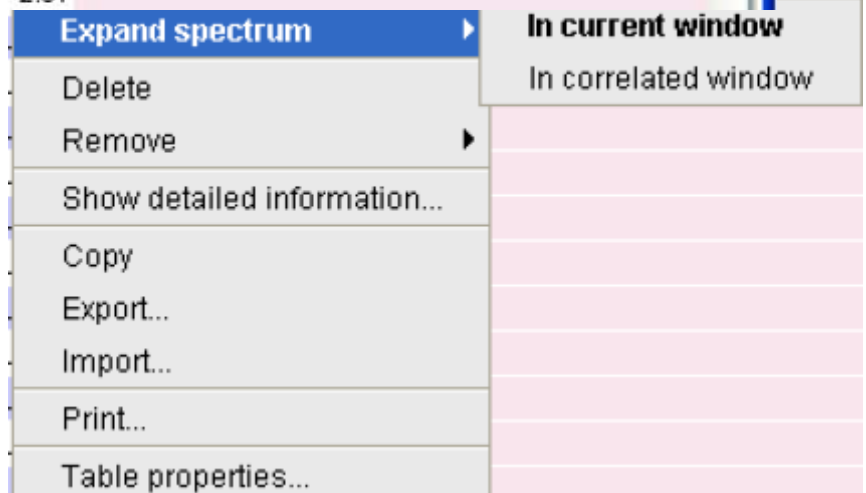
Display Peak list:

Click on Peaks tab:

Peak	v(F1) [ppm]	Intensity
1	8.3923	1.70
2	8.3728	1.74
3	8.1499	1.92
4	8.1354	1.94
5	7.7515	1.98
6	7.7360	2.04
7	7.5871	2.01

By default peak list show Peak number, Chemical shift (ppm) and the intensity. If you want more options (like Hz listing), right mouse click and select the option you want.

To display the spectra around a peak, right click on the peak and select



“**Expand spectrum in current window**” This will change current display to spectrum display, showing region around the peak.

Double clicking on a peak go to that displayed region.

Enter key, automatically display the zoom region containing the peak.

To export a peak list to an excel program, select the peaks (using Ctrl or Shift keys to select several peaks), Right click and in the popup window select **Copy**. This table can then be pasted in Excel.

To delete or remove a peak from the list, Right click and in the popup window select **Delete**.

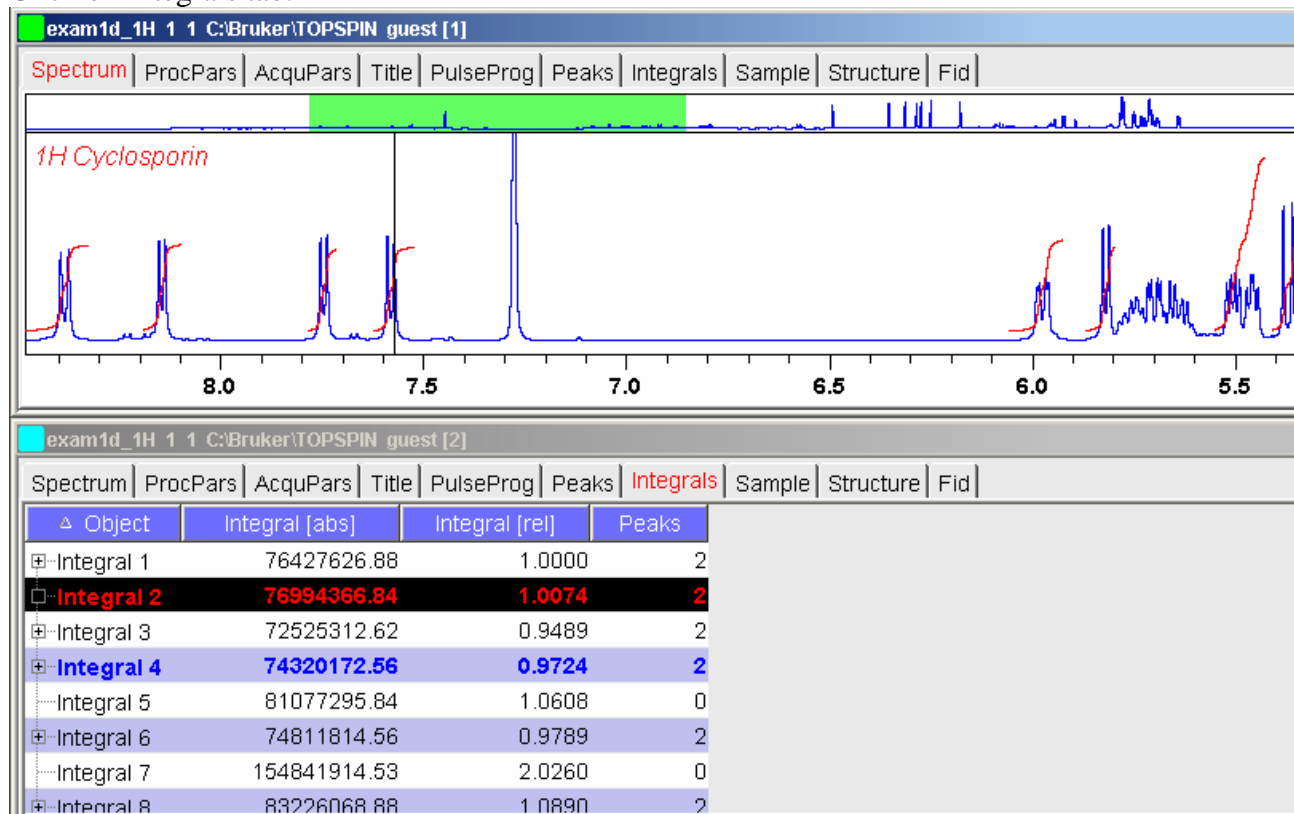
To remove duplicate peaks, choose **Remove → Duplicate peaks**

In the **Table properties...** , in the popup window, we can set columns to be viewed, and by selecting one item, we can select number of decimal to be seen.

When the cursor move in a peak list and there is a correlated spectra displayed, the cursor vertical line will move in the spectra showing the corresponding peak.

Display Integral list:

Click on Integrals tab.



Integral list displays integral number, The absolute value of the integral, The relative value of the integral, the number of peaks in the integral region.

The selected integral is in black: if right clicking, enter or delete key is used, it will affect that integral or set displayed window to that region. For popup menu, refer to description of peak list.

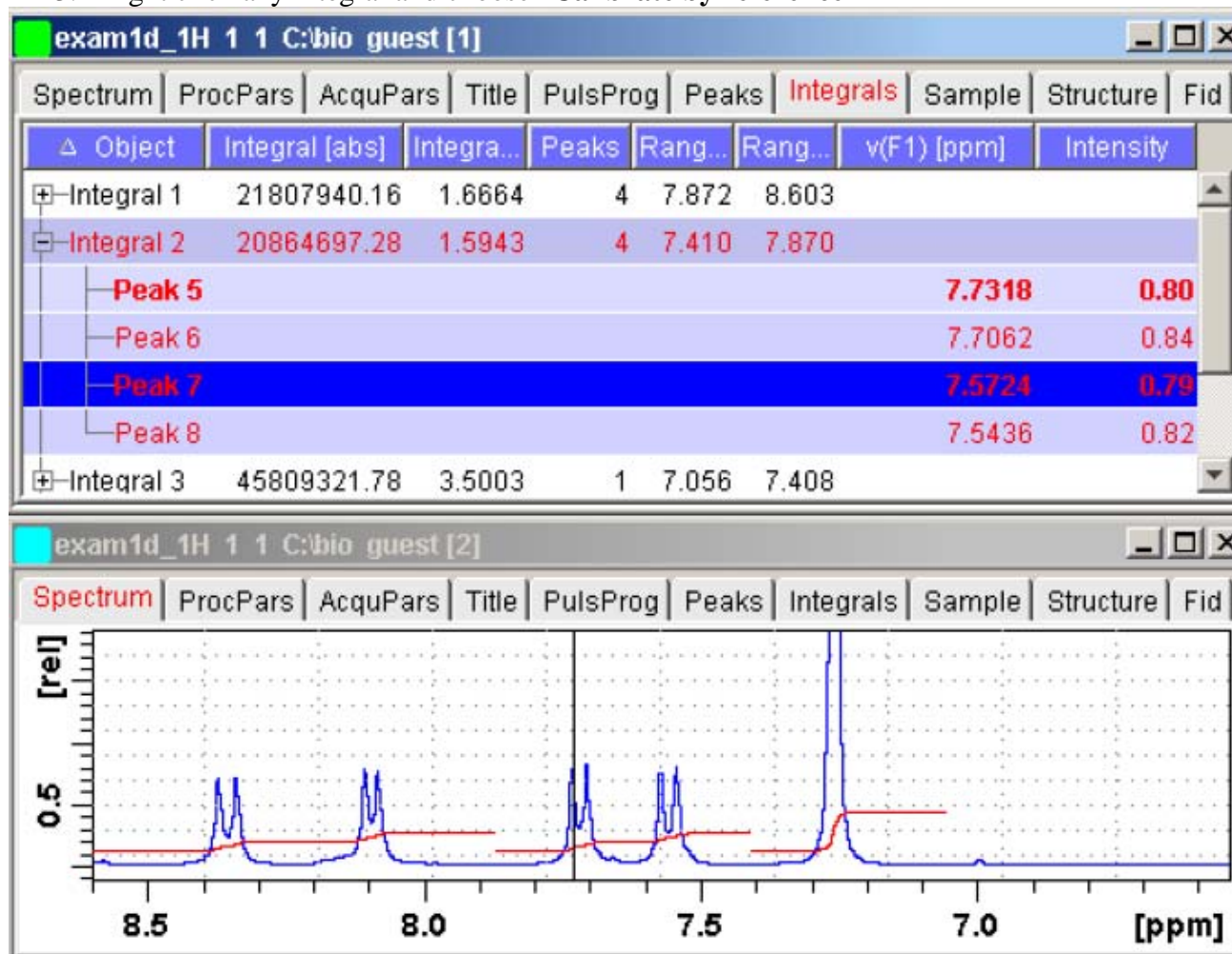
The **active integral is in blue**, the cursor in the data window indicate this integral.

To calibrate integrals to compare spectra

1. Right click the reference integral and choose: **Define as reference** in the popup menu.
2. Right click any integral and choose **Calibrate by reference** : this will divide all integrals by calibration constant, setting reference integral to 1.0.

Now you can read another spectrum and calibrate it's integral with respect to the reference integral:

1. Read the spectrum and define integral ranges.
2. click on **Integrals** tab
3. Right click any integral and choose “**Calibrate by reference**”



If you click on the “+” sign to expand the integral, peak listing within this integral will be displayed.

Display a structure:

Click on “**Structure**” tab, and click on **Jmol** button.

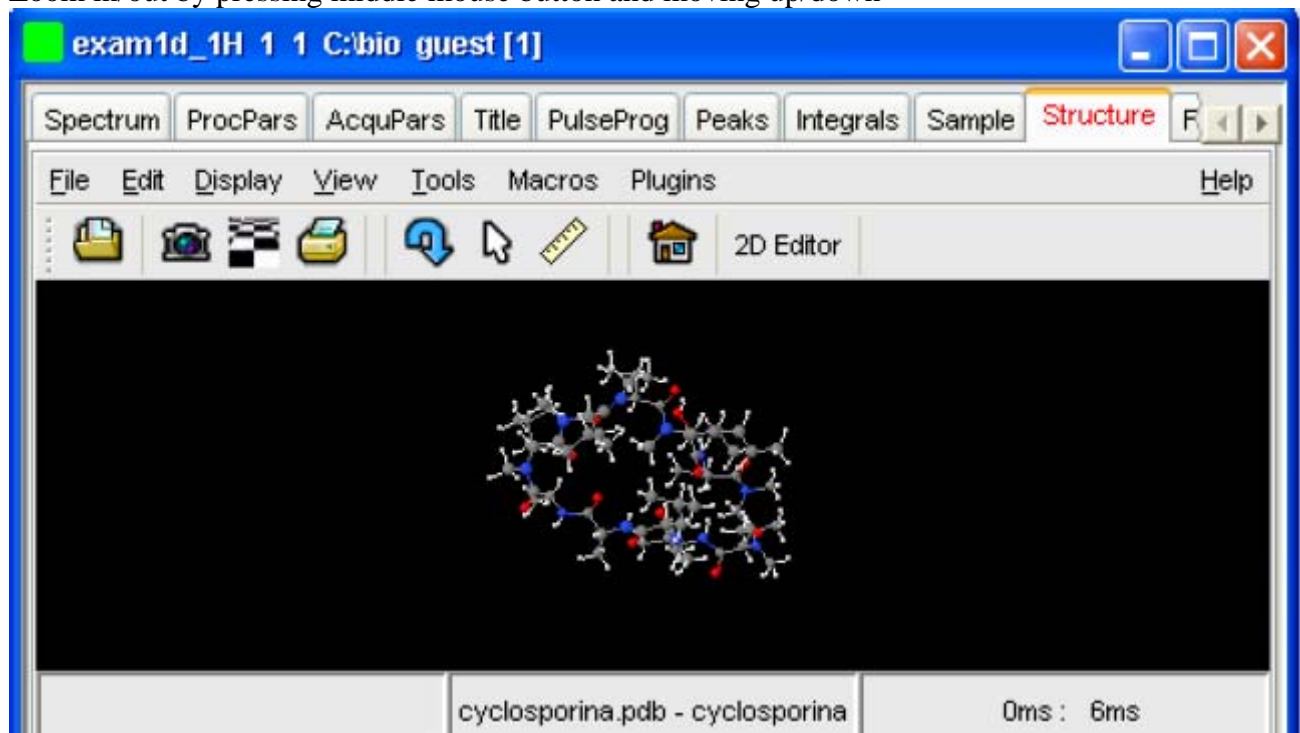
The viewer displays the structure file that resides in the **expno** of current dataset.

Following structure files are supported : .xyz, .mol, .pdb, .cml, .out, .mmlgp, .res, .cif, .gprm .hin, .nwo


Rotate a molecule around x and y axis by left mouse dragging Left/Right, or up/down.

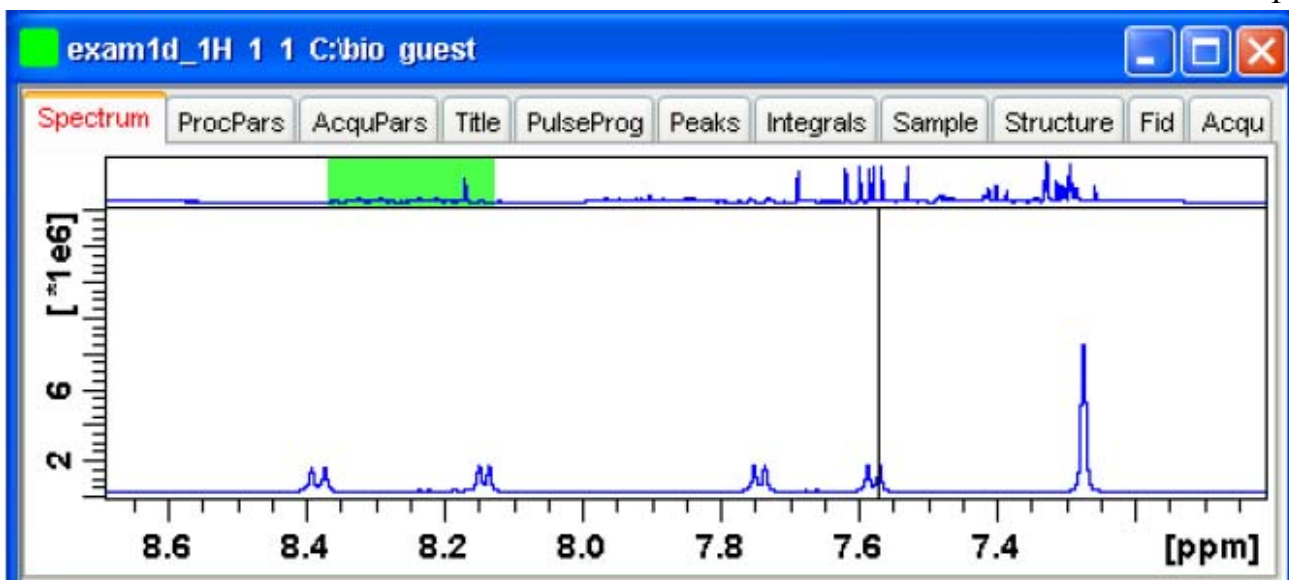
Rotate a molecule around Z by pressing middle mouse button and moving left/right.

Zoom in/out by pressing middle mouse button and moving up/down



Spectrum Overview:

To toggle spectrum overview click on  in the tool bar.



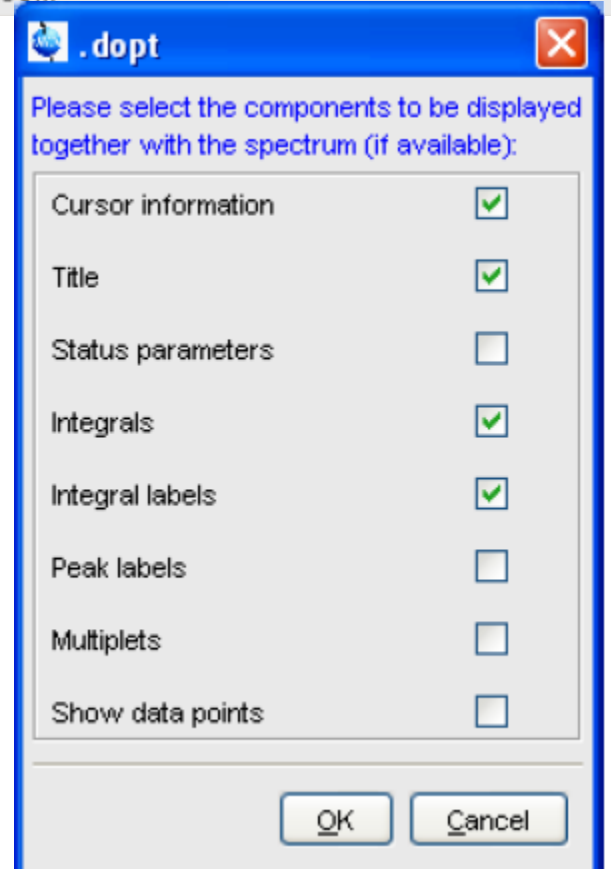
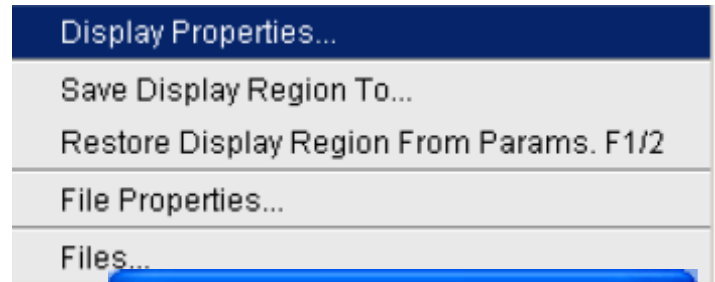
The zoom region is shown in green. To shift the spectra, simply drag the green region on the overview.

Display properties:

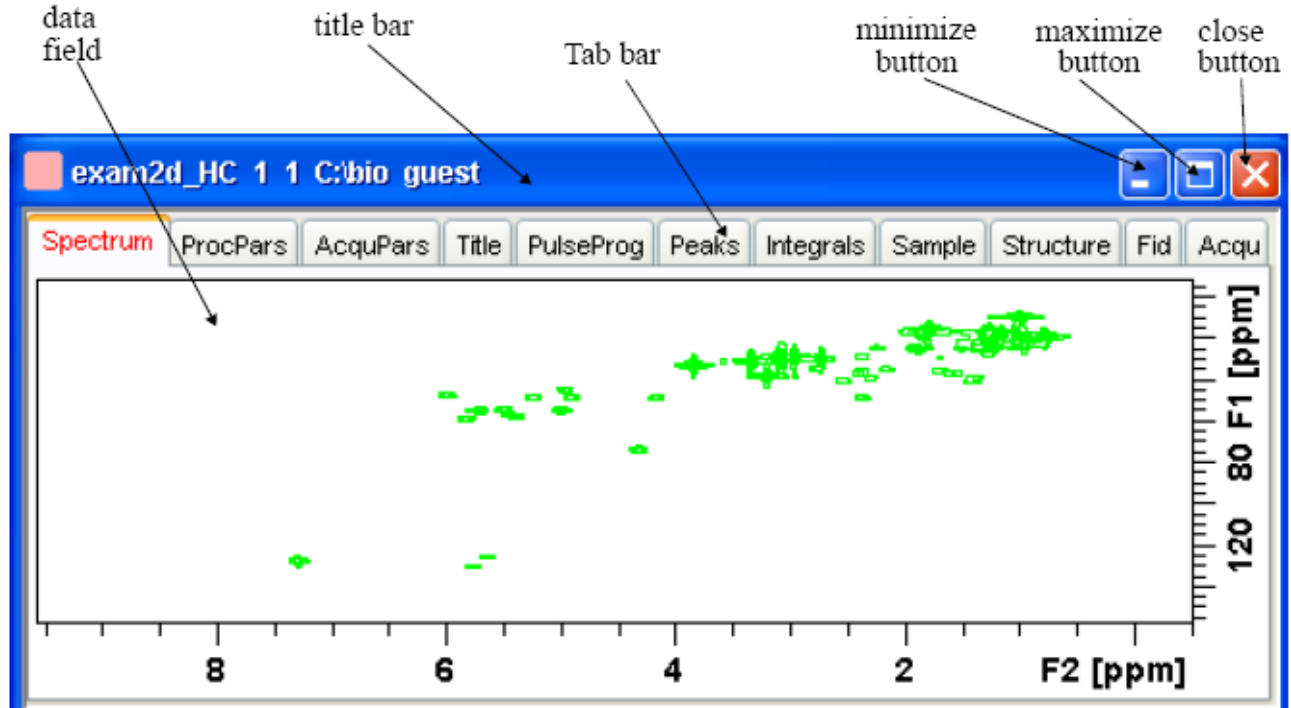
If you right click on a spectra and select Display properties ..., You can select component you wish to display.

To superimpose cursor information in the data window, select that item.



You can decide to display the title, the parameters, the integrals, the integral labels, Peak labels, Multiplets, etc...





2D Display



To change intensity scaling:

Use scale buttons of lower tool bar :  like in 1D. Use the  button to change distance between levels.

Click on  to change # contours. Use the +/- button to toggle positive and negative contours. The  button save the contour levels to disk

Use the mouse wheel to change the intensity when mouse cursor is in the graphics region.

You can also toggle square 2D layout ON/OFF with right mouse.

Zooming:



Reset Full spectra horizontal window
 Reset Full spectra vertical window
 Reset full spectra

Increase Zoom
 Decrease zoom
 Enter Zoom with Dialogue box
 Go to previous zoom


Retain Vertical and Horizontal zoom to display another data set

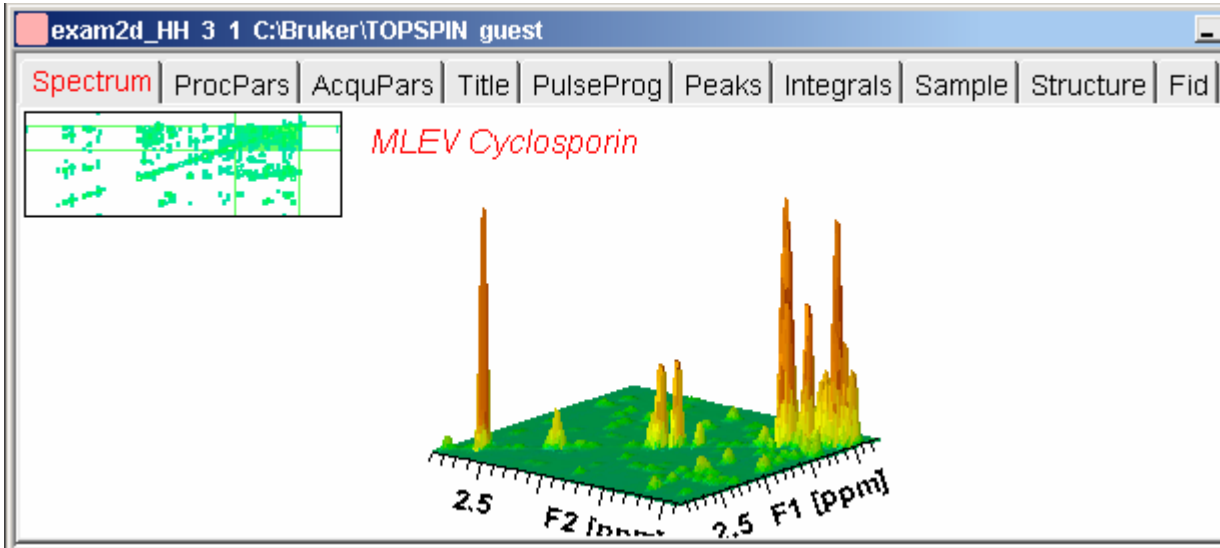
You can also zoom using left mouse drag in the data set.

The Left and right arrow: shift spectra in direction of the arrow.

You can use the “4-arrows” button to shift the spectra around by dragging.

The Up and Down arrow shift the spectra up and down.

The 3 last buttons apply to projection  data: where you can rotate the oblique view in various direction



If you Right-click inside 2D, popup menu can allow to display properties, Edit contour levels etc...



Various display options can be set in the **Options → Preferences → spectrum**

To display peak list:

Click on “**Peaks**” tab to display peaks.

Peaks can be calculated with the command “**pp**”

The list is similar to the 1D spectra. The difference is that there are 2 columns for the shifts in the 2 dimensions.


Integral in 2D


Click on “**Integrals**” tab to display integration.

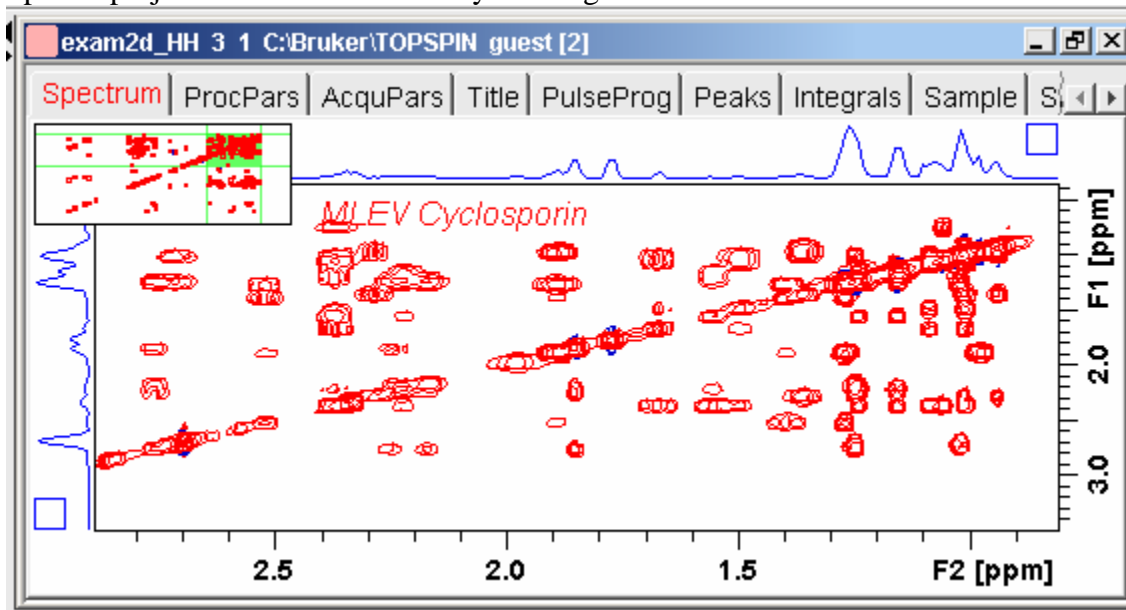
Peaks can be integrated with the command “**int**”

The list is similar to the 1D spectra. The difference is that there are 2 columns for the shifts in the 2 dimensions.

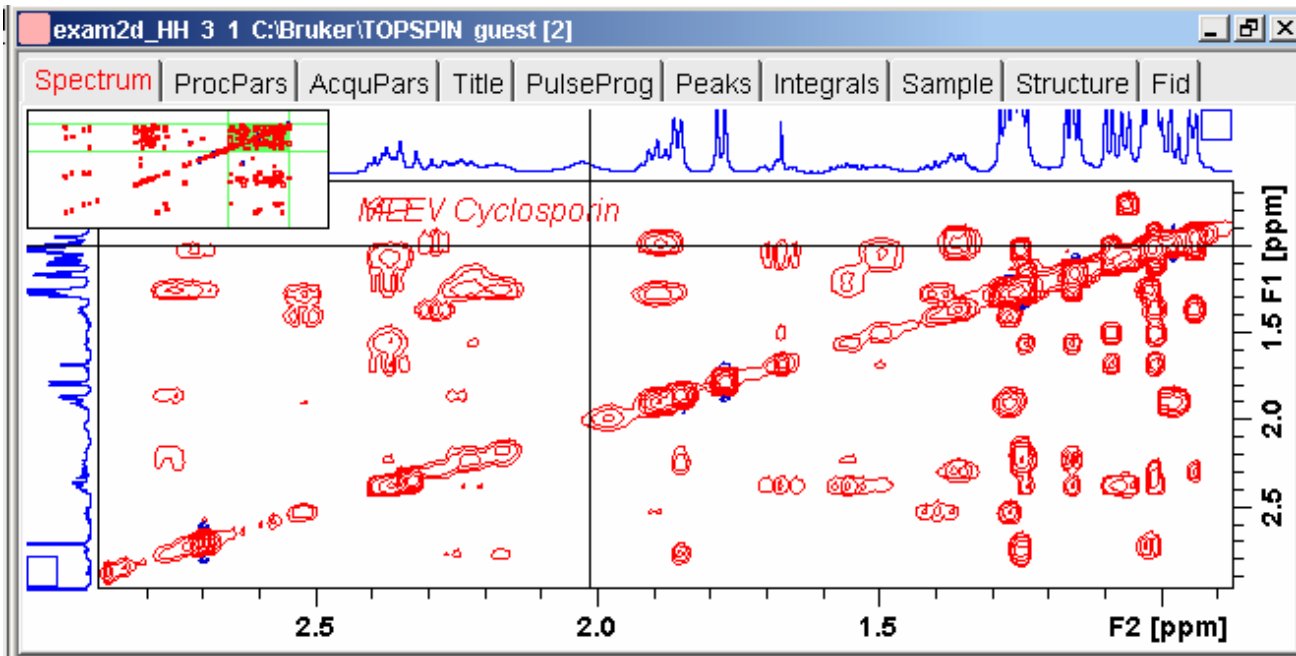
Spectrum overview

You can switch spectrum overview with the button: . The overview displays in green the zoom region. You can move the region with the mouse.


Spectra projection can be obtained by clicking on : 




By Right clicking in projection area, One can select a 1D data set instead of projection. The little square shown in the projection area serves to activate the 1D trace for vertical scale adjustment.



Display options

To display contour, use the button  in the upper toolbar.

In the lower toolbar, the button  allow you to control the contour levels by opening the following window.

exam2d_HC 1 1 C:\bio guest

1	9990701.0	-9990701.0
2	17983261.9	-17983261.9
3	32369871.4	-32369871.4
4	58265768.4	-58265768.4
5	104878383.2	-104878383.2
6	188781089.7	-188781089.7
7	339805961.5	-339805961.5
8	611650730.7	-611650730.7
9	0.0	0.0
10	0.0	0.0

Required parameters

Calculation method

Multiply with increment
 Add increment

Contour level sign

Positive & Negative
 Positive
 Negative

	Positive	Negative
Base level	5669127.1	-5669127.1
Level increment	1.800	1.800
Number of levels		8

Fill Clear Apply


OK Cancel


You can calculate levels by selecting first:

“**multiply with increment**” : to create geometrical sequence of levels

“**Add increment**” : to create equidistant sequence of levels

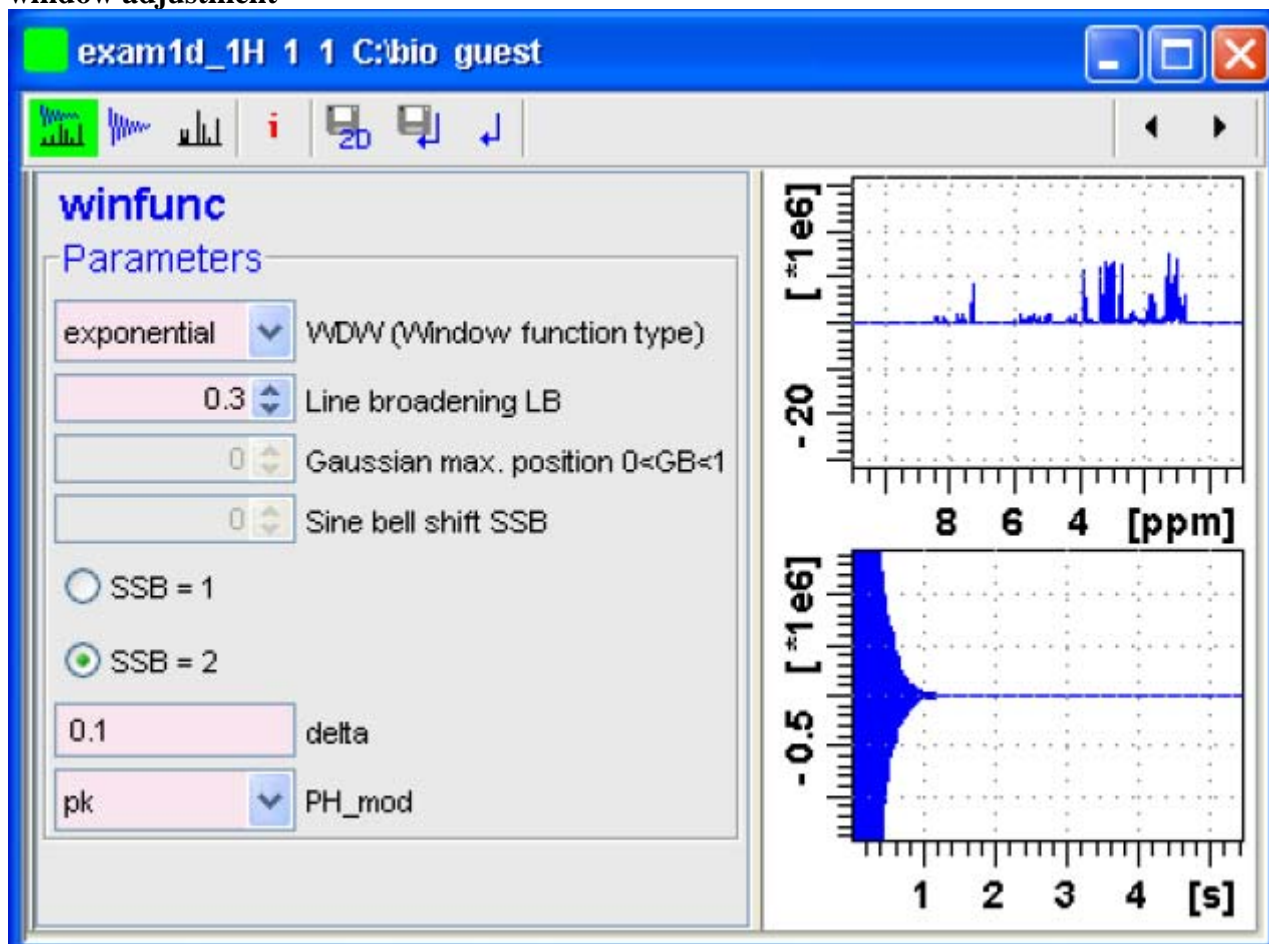
- After selecting mode of calculation, enter the **Base level**, **Level increment** and number of levels
- Click “**Fill**” to activate the sequence
- Click “**Apply**” to update the display (or **OK** to store levels, update the display and close dialogue box).

The button :  found on the lower toolbar store the levels after interactive manipulation of the intensity with scale buttons.


The button :  switch contour between, positive, negative or both.

Interactive manipulation (1D)


Interactive Window multiplication : **Processing** → **Window Multiplication** → enable **Manual window adjustment**



The new window shows parameters on left, Spectra and FID on the left

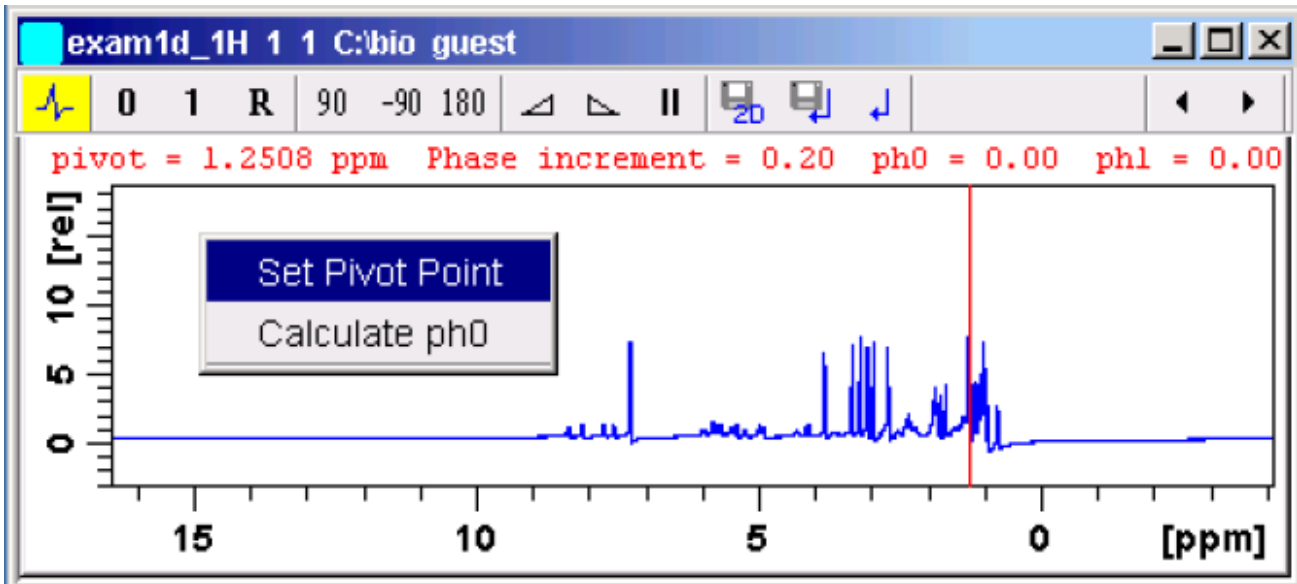
The first buttons above the window  can be used to select Spectra and FID together, Spectra alone or FID alone.

The info button  switches cursor information on/off.

The saving buttons  can save parameters to 2D or 1D data set or simply return without modification. (for 2D the 1D dataset was extracted using 'rser').


Interactive Phase correction:

In the upper toolbar, use the phase button :  to enter in the phase mode.



The Yellow button indicates that you are in phase correction mode. Some button turn green when they are clicked. As long as a button is green, it is active.




To perform phase correction:

1. Click-drag the **0** button and move the mouse until the reference peak in red is correctly adjusted.
2. Click-drag the **1** button and move the mouse until the whole spectrum is well phased
3. Click on  to save phase correction and return.

By default the pivot point is set on biggest peak. To change the pivot point, Right-click on desired pivot point, and choose “*set pivot point*” from popup menu.

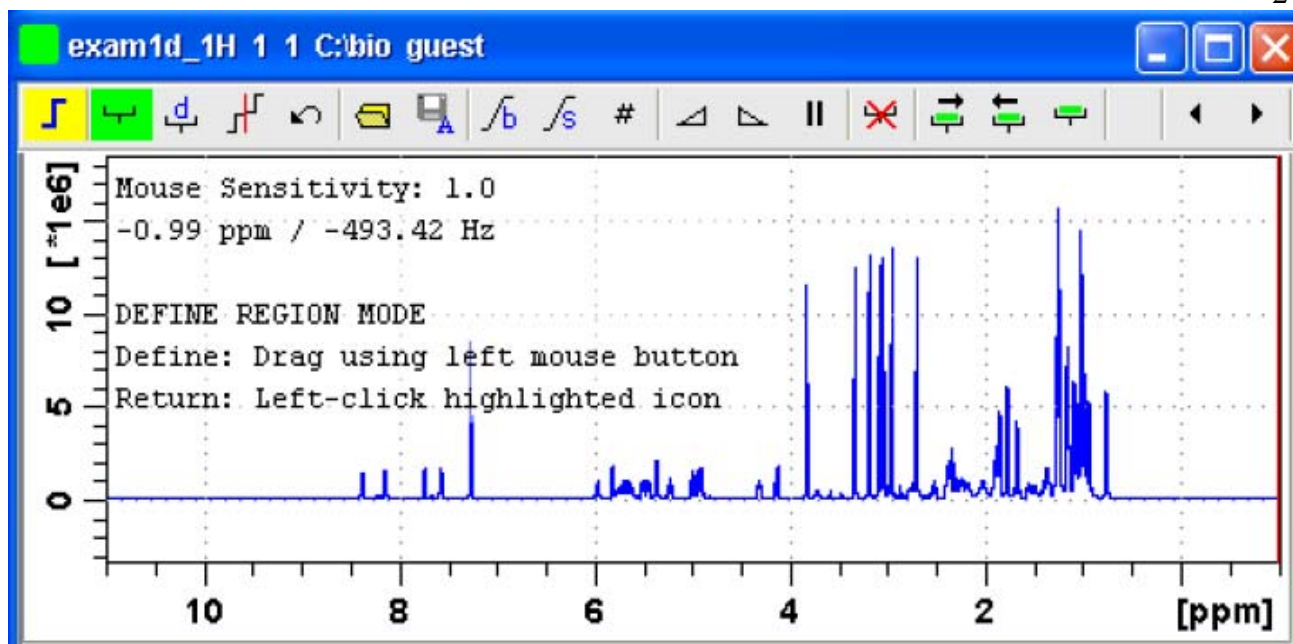
To perform 90° or 180° phase correction use the correct button : **90 -90 180**

To reset the phase to default value, use the **R** button.

The saving and return buttons    can save phase to 2D or 1D data set or simply return without modification. (for 2D the 1D dataset was extracted using ‘rser’).


1D integration


Click in integral button  to enter in integrate mode.



The yellow button in the active window toolbar indicates that the window is in the integral mode. Any button that turn green indicate that it is activated.

To define an integral interactively:



1. click on define integral button  (it will turn green)
2. Put the red cursor at the beginning of the region you want to integrate and left drag to the other end.
3. Define other regions in the same way. When finish deactivate the “define integral button” (become gray)


To define integral exactly: click on  and enter the values for the integral region in the dialogue box

To select (or deselect) All displayed integral regions use :

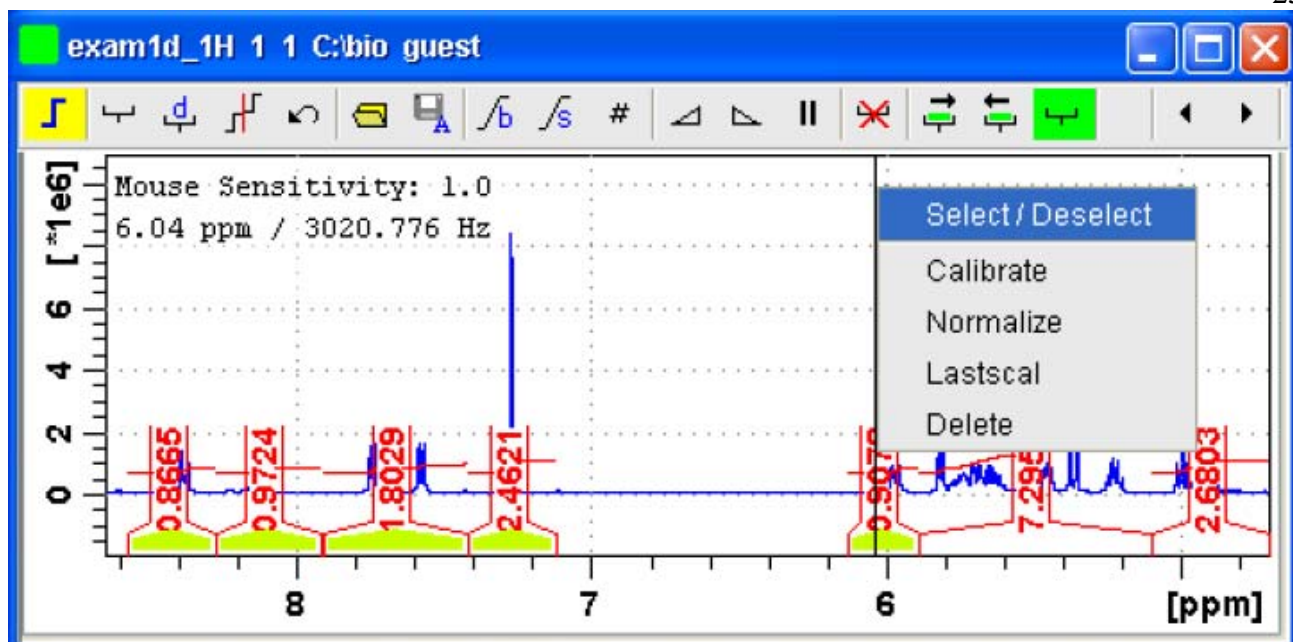



To **select/deselect** one integral, right click on it and choose select / deselect from popup menu.

To select the next or the previous integral, use   to correct button.

To select several integration and not other, use the select all integral , and by right click deselect a few integrals.

Selected integrals are painted in green.



To perform slope and bias correction, click-drag the button  until integration is well adjusted. The correction will occur on all selected integrals.

To calibrate and normalize integral:

Right-click in reference integral region and choose “*Calibrate*” in the popup menu. Type the desired value.

To Normalize integrals

- This will set the sum of all integrals to a value, and adjust individual integral accordingly.

Right click on an integral and choose “*Normalize*” in the popup menu. Type the desired value.

Normalize and Calibrate only affect the current data set.


To scale integrals respect to Different spectra:

1. Right-click in the reference region
2. Choose “**Lastcal**” from the menu

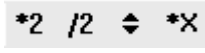
This make sense only for spectra that have been acquired using same conditions.


The scaling factor is stored in /prog/curdir/<user>/intscale

To delete integrals from the display:


Select the integral in the display and click on 


To delete only one integral: right click in the integral and choose “**Delete**” from the menu

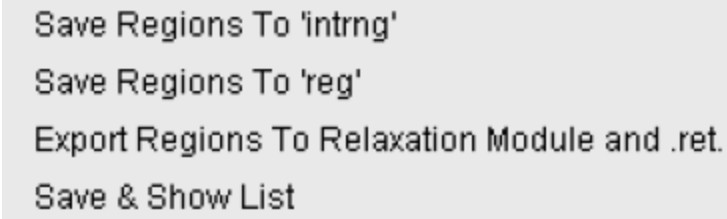
To scale selected or all integrals, use the scale buttons: . The *X button scale the integral by an amount that can be typed in.

The button , scale all integral to the same height, showing scaling factor above the integral. Click again on the button to go back to previous mode.


To adjust the integral baseline (offset) select one of the following buttons : 


To cut an integral region, use the  button to activate (it will become green) this mode, move the red cursor where you want to cut and click left mouse. When finish using deselect that mode.

To save integrals, use : a popup window will appear:




- **Save regions to 'intrng'** : save integrals with slope and bias values.
- **Save Regions to 'reg'** : save integrals to the file 'reg'
- **Export Regions to relaxation module and ret** : Use that on relaxation data only.
- **Save and Show list** : Save current integrals with slope and bias and show integrals on screen

Use  to save region to '**intrng**' and return.


Use  if you want to return without saving.

1D-Calibration

Click on  to enter in calibration mode.

Position the red cursor on the reference peak, Left-Click on the position, enter the value for that peak.

Multiple display

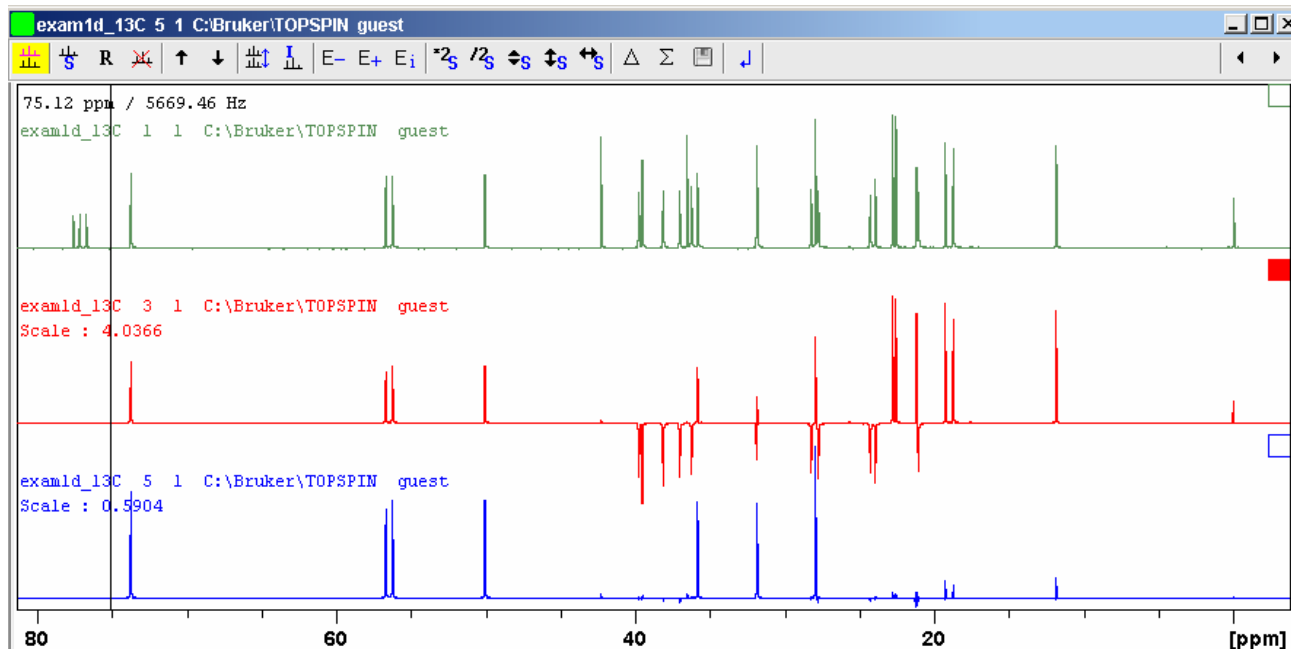
The Button  in the upper toolbar is used to create multiple display.


To add a data set you can:


- Left-drag the data from the browser
- Right-click and choose "**Display**" from popup menu
- Enter '**re**' (read) and specify *filename*

Another way is to read multiple data sets simultaneously:

1. In the browser: hold <Ctrl> and select multiple data sets or hold <Shift> and select first and last files of a series.
2. Right-Click any of the selected data files and choose "**Display**" Alternatively you can also select "**Display in a New Window**"



The Yellow button  in the data toolbar indicates that the window is in multiple display mode.

Some Buttons turn green  for as long as the button is active.

At the bottom of the browser, the datasets are displayed with the color they have in the data window. The data sets that are selected appear highlighted and in the data window, the data highlighted have full color square.

When no data set is selected: all data are selected.


To select / Deselect Datasets


Click on the spectra in the data window


Click on the small square in upper right of the spectrum window

Click on the small square in the lower left browser


The button  in the multiple display window deselect all data sets.


To remove a data set, select it and use the button  in toolbar.

The button  will show the difference between the first spectra and the sum of the other spectra.

The button  will show the sum of all spectra.

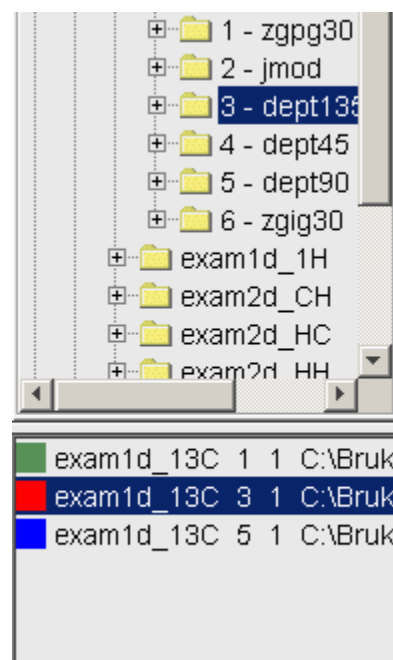
The button  will save the sum/difference spectra: you have to specify the process number.






The button  toggle between superimpose and stack display.

The button  toggle information on the spectra.

It is also possible to shift the baseline and scale of individual spectra in multiple display. To do this:

1. expand the region of interest




2. Select one spectra (you can also select a few spectra by clicking on them using the <shift> or the <Ctrl> key)
3. To change the scale drag the up/down button  or use the $\frac{1}{2}$  $\frac{1}{2}$ buttons.
4. To shift the baseline of the spectra, use .
5. To shift the spectra left or right, use .
6. To reset scale/shift on selected spectra use : 

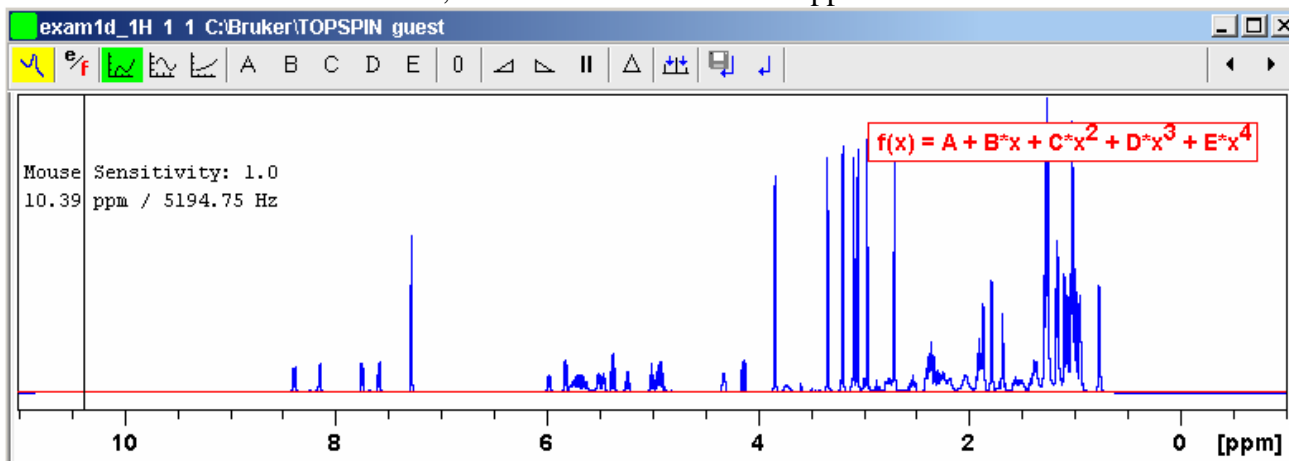
The last button of the toolbar :  go out of the multiple display mode.


To change the colors of the various datasets, click on **Options** → **Preferences** in the menu and change colors.

1D interactive Baseline Correction


Baseline correction can be done automatically by using 'abs' or 'absd' commands.

For interactive baseline correction, use the  button on the upper toolbar.




The yellow button  on the data toolbar indicate that baseline correction mode is active. The buttons that turn green indicate that they are active.

To perform Polynomial Baseline Correction


1. Click on 
2. Drag button A until the red line coincide with the first data point.
3. Continue by dragging buttons B, C, D, E until the red line coincide with the entire baseline on the spectra.

To perform Sine Baseline Correction



1. Click on 
2. Drag button A until the red line coincide with the first data point.


- Continue by dragging buttons B, C, D until the red line coincide with the entire baseline on the spectra

To perform Exponential Baseline Correction


- Click on 
- Drag button A until the red line coincide with the first data point.
- Continue by dragging buttons B, C, until the red line coincide with the entire baseline on the spectra

To preview Baseline corrected spectra

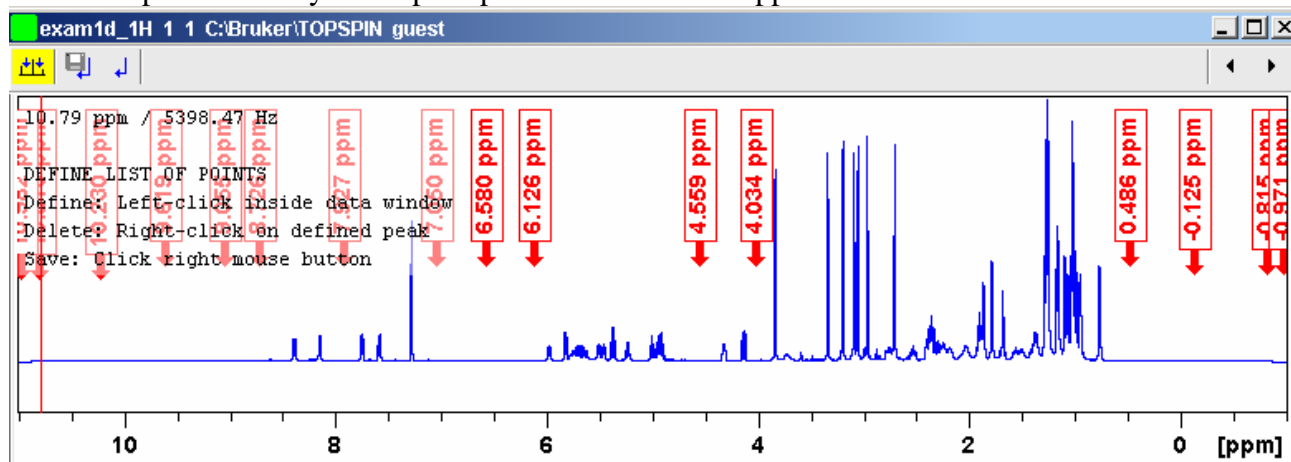
- Click on  to preview corrected spectra which will be shown in red.
- If baseline is correct, click on  to save correction
- If more correction is needed, deactivate the preview and correct more.



The button , reset correction line to zero.


To perform a Cubic Spline Baseline correction

Click on the button  to define points.

If a list of points exists you are prompted to overwrite or append to the list.




- To define baseline points: move cursor to baseline point and left-click that position
- Define at least 5 points
- To save those points, use the button  of the Spline toolbar
- To execute the Spline correction, use the  of the baseline toolbar.

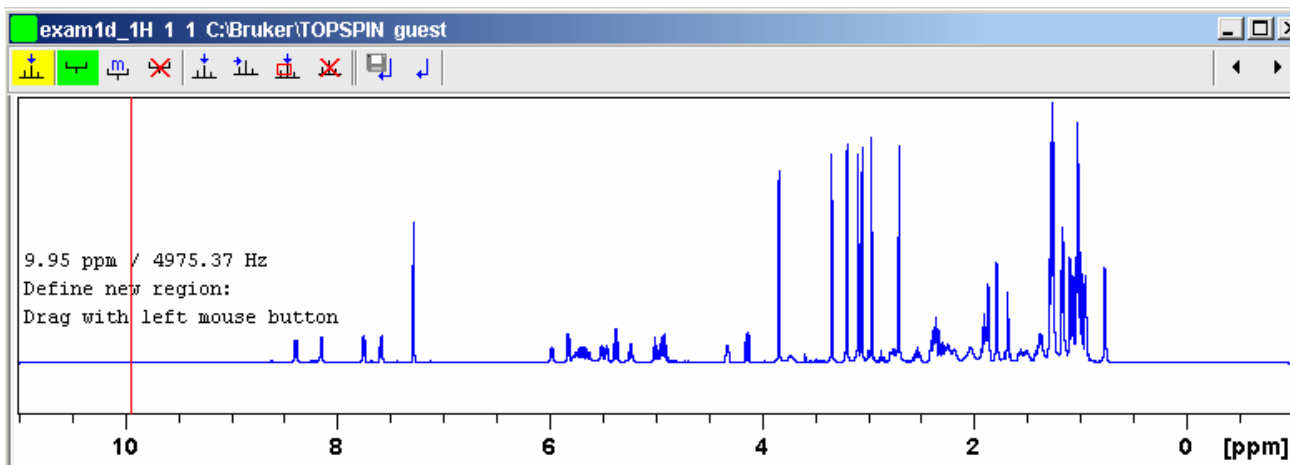
To return without saving, use the  return button


To delete a data point, click on the data point with the right mouse and chose 'Delete Current' from the Popup menu


Interactive Peak Picking

Peak picking is perform with the command "pps"


To interactively list peaks, select the button  in the top toolbar.




The yellow button  indicates that you are in peak picking mode. Any buttons in green indicate that they are active.


The button  indicate that define range is active.


To define a peak range:

1. Drag the mouse from the upper left corner to the lower right corner
2. This will mark the range in green and will set the maximum / minimum intensity in which pick picking occur. Peaks appear automatically.
3. Repeat step 1 and 2 for each range you wish to define
4. Click on the  button to leave define range mode.


To modify existing ranges:



1. Click on  to enter in the modify range mode
2. Put the cursor on the edge of a region and drag the green range to a new position. Peaks are updated automatically to respond to the new region.
3. Click again on the modify range to leave that mode.

To delete all peak ranges use the  button.

To define a peak manually, activate the  button and click on the peaks you want to list. When finished, deselect the define peak button to leave that mode.


To delete a peak from peak list, Right-click on a define peak and select “Delete peak under cursor” from the menu.

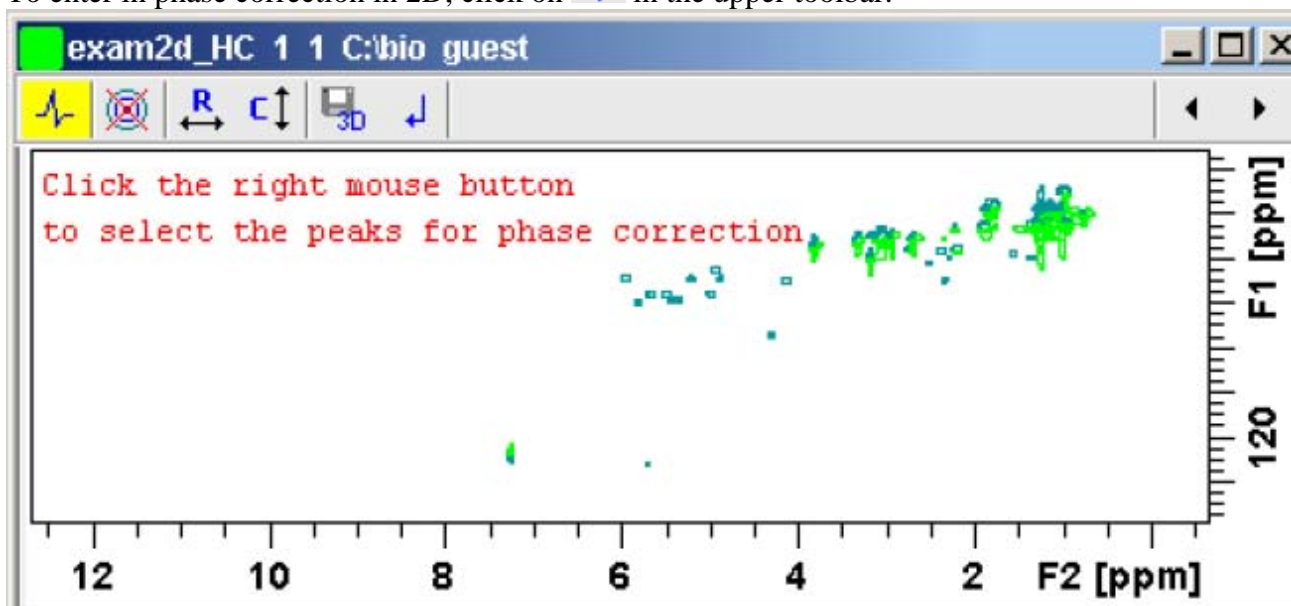
To delete all peaks, choose “Delete All Peaks” from the menu or click on  in the toolbar.

To save the peak region and peak list, use the button  on the toolbar. To discard the changes, use the  button.

2D Interactive manipulations


2D Phase correction


To enter in phase correction in 2D, click on  in the upper toolbar.




The yellow button  on top indicate that you are in phase mode.

The  button toggle contour display on/off

The  button switch to row phase correction of selected peaks


The  button switch to column phase correction of selected peaks

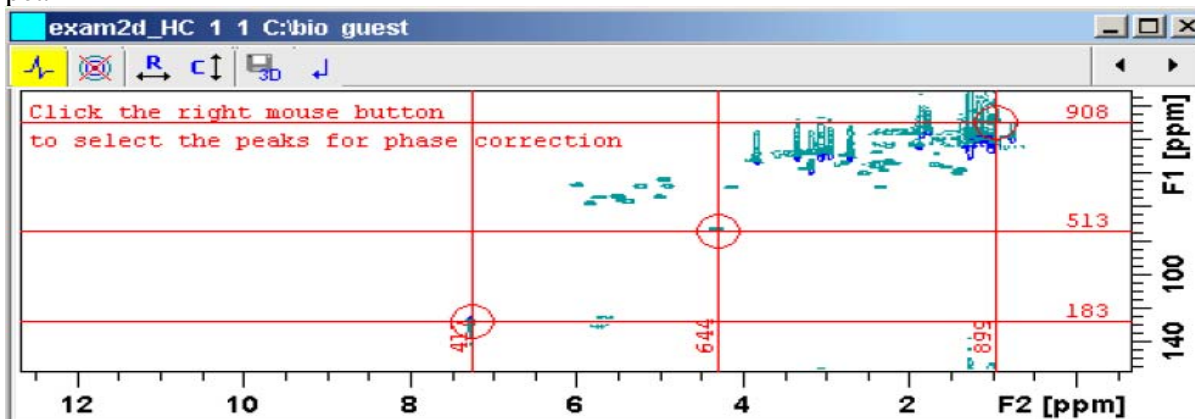
The  button save phase values to the 3D data set from which 2D plane was extracted

The button  : return out of that mode.

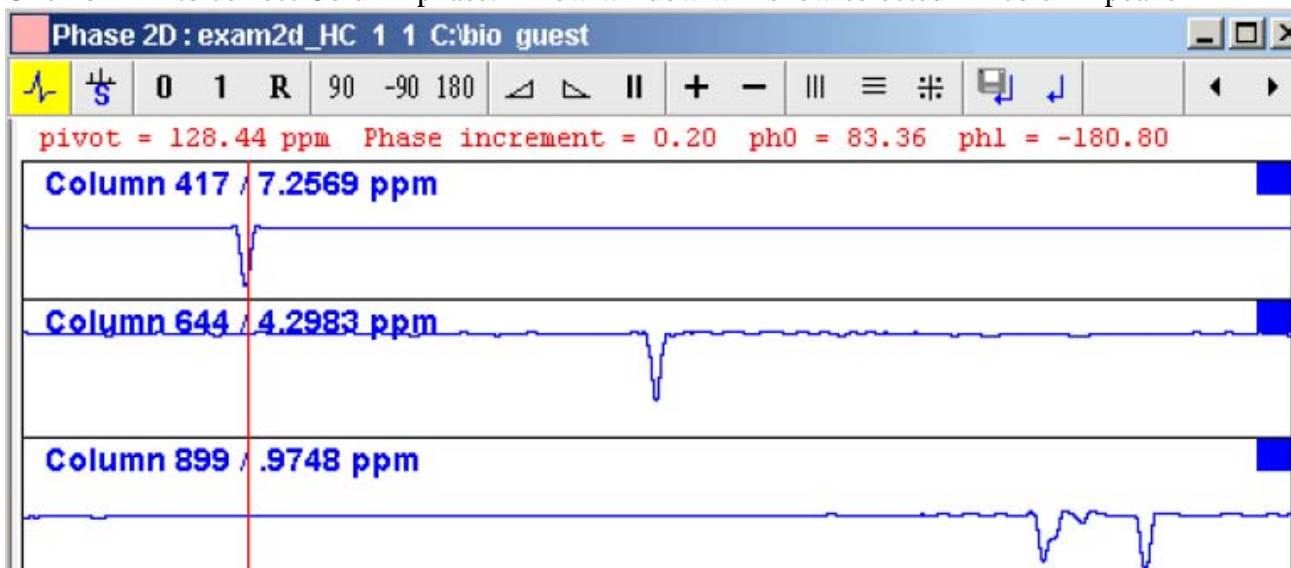
Typical phase correction:

1. Select 2 or more peaks in different part of the spectrum
 - a. Zoom on a peak – draw a box around it with left mouse
 - b. Right-click at the peak and choose “Add” from popup menu

- c. Click on  to go back to full spectrum and repeat step a. and b. to select another peak





2. Click on  to correct Column phase. A new window will show selected 1D column peaks




3. Drag the **0** button until red cursor peak (zero-order) is well phased
 Drag the **1** button until other column are well phased
 Click on Save Return to execute phase

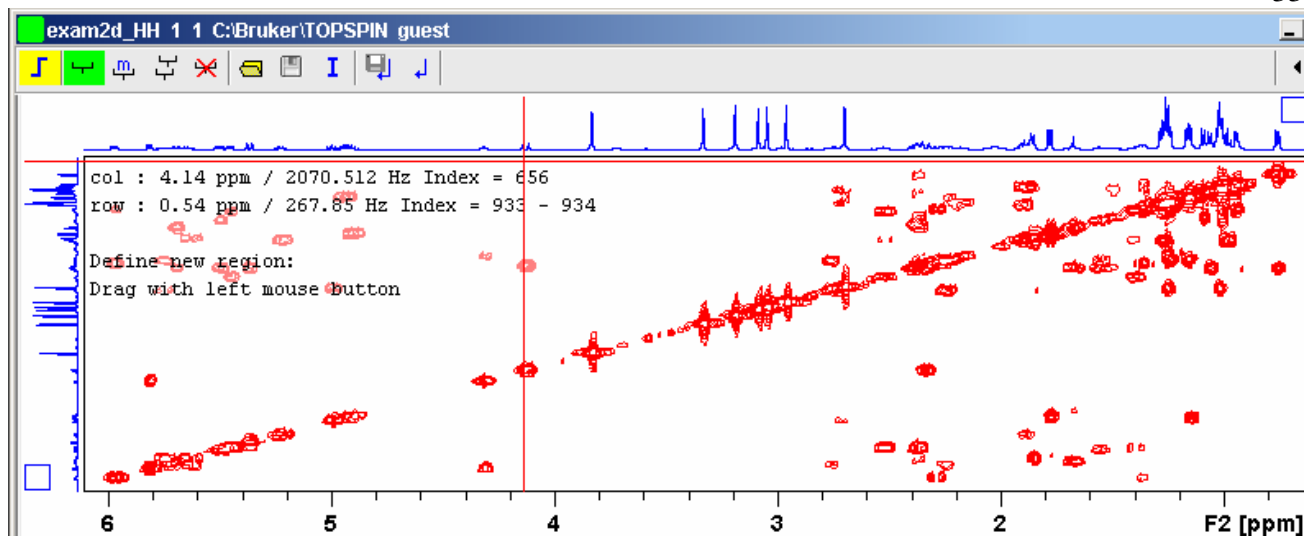
The  button arrange traces horizontally


The  button arrange traces vertically

The  button arrange traces in split window

Integration

To go in integration mode use the  button in the upper toolbar.




The  yellow button indicate that you are in the integration mode. Any button highlighted in green indicate that the function is active.

The  button define integral region (active when green)

The  button Move integral region



The  Copy a region

The  Delete all regions.


The next 3 buttons    : Read, Save and Define integral region.

The last 2 buttons :   are used to Save and Return, or Return without saving.

To Integrate:


1. Define integral by defining a box around a region
2. in the popup menu, choose one of the options
 - a. **Integrate:a** : add up all intensities in the region
 - b. **Integrate:+** : add up all positive intensities in the region
 - c. **Integrate:-** : add up all Negative intensities in the region
 - d. **Integrate:a+-** : add up all intensities in the region and store separate entries for *all positive* and *negative* intensities
 - e. **Integrate:a+** : add up all intensities in the region and store separate entries for *all* and *positive* intensities
 - f. **Integrate:a-** : add up all intensities in the region and store separate entries for *all* and *Negative* intensities
 - g. **Integrate:+-** : add up all intensities in the region and store separate entries for *negative* and *positive* intensities
3. Click on  button and choose “Integrate current regions” from pull down menu
4. Click on  again and choose “List integral values” from pull down menu

Alternatively, you can define a reference integral and integrate defined regions of the same or different dataset relative to this integral.

The  button offers following choices:

- **Integrate current regions rel. to reference** (you will be prompted for reference integral number and value)
- **List integral values** (list will show an additional column with normalized integral values)
- **Define current dataset as reference** (you will be prompted for reference integral number and value)
- **Integrate and use ref. dataset for calibration** (integral value on a reference dataset is used for calibration)


To move integral, click on  and left-drag the region to desired position.

To copy an integral region click on  and left-drag the region to desired position


The save button will save regions to the file “int2drng” in current PROCNO.

Multiple display in 2D

Any number of 2D and 1D spectra can be superimposed. Spectra are automatically aligned according to the selected axis unit. A superimposed 1D is automatically displayed in the direction of the matching nucleus.

Simply read a 2D dataset and click on multiple display button  in upper toolbar, then drag a 1D or a 2D dataset in the window.

Data in multiple display mode can be individually shifted. To do that,

- Select the spectrs in the lower part of the browser
- Click-drag using the  button.
- The button **R** reset scaling and shifting

Scan Rows / Columns

In multiple display mode you can scan for rows using  button or for column using .

Once the button is activated, simply move the mouse in the spectra.

To increase the scale, turn the mouse wheel up or click with the Left mouse. To scale down, turn the mouse wheel down or click on middle mouse button.


To grab a row/column (to keep it displayed), right-click once at the desired position and choose “Grab Row/Column” from the menu. The row/column will appear in the browser.

To go to the next or previous row / column, use the + and – button.


To extract a row/column, right-click once at the desired position and choose “**Extract Row/Column**” from the menu. A new window will appear where a new procno can be specified.

For referencing

You can use the command 'sref' for automatic referencing.

For manual referencing, Expand you reference peak on screen and use the  button on the upper toolbar. Enter the new reference value for both domains.

To measure distance between peaks

Use the  button in the upper toolbar to measure distance between peaks. Click on a peak and drag the mouse to another peak. Distance is displayed as dragging occur.
To quit this mode simply Right-click the mouse.