Liquid Surface X-ray Scattering
## User Help

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1. Instrumentation Schematics

1a. Beamline Optics Diagram
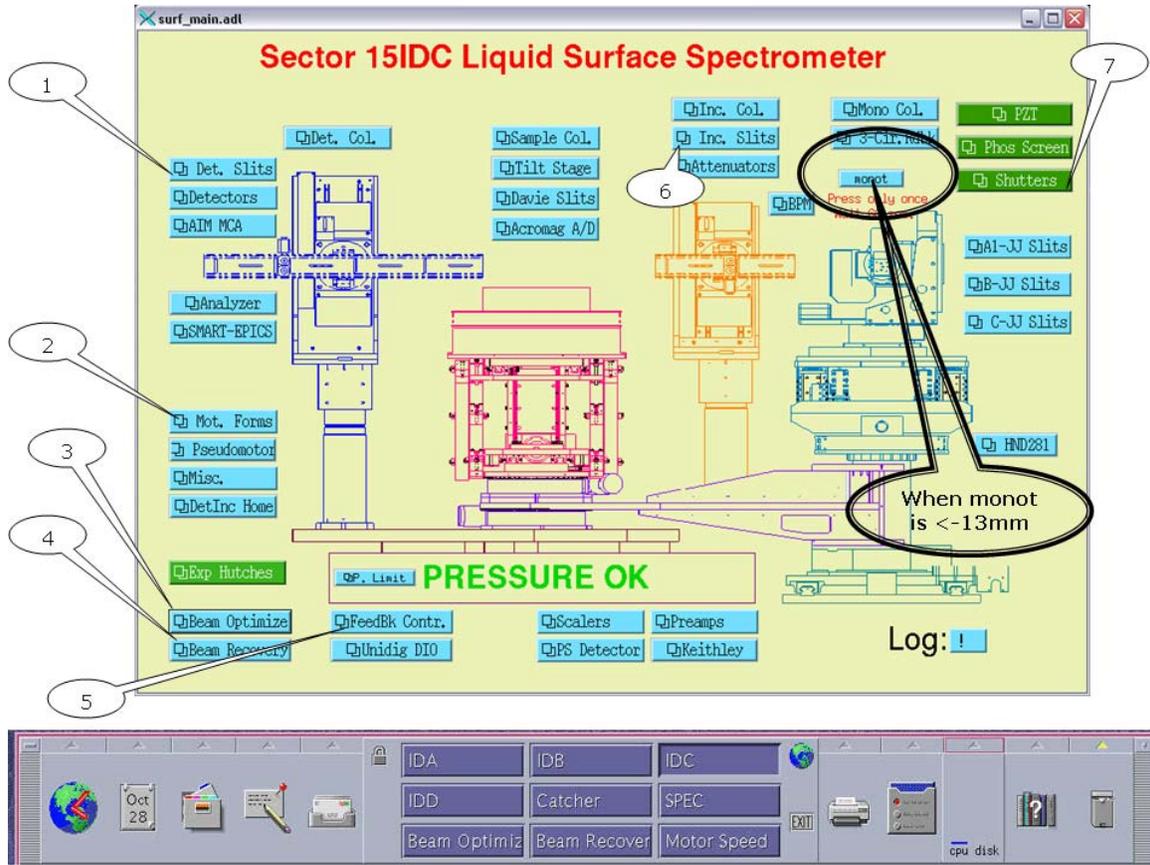
Beam Line Optics Diagram

*NB: Distances shown are not to scale
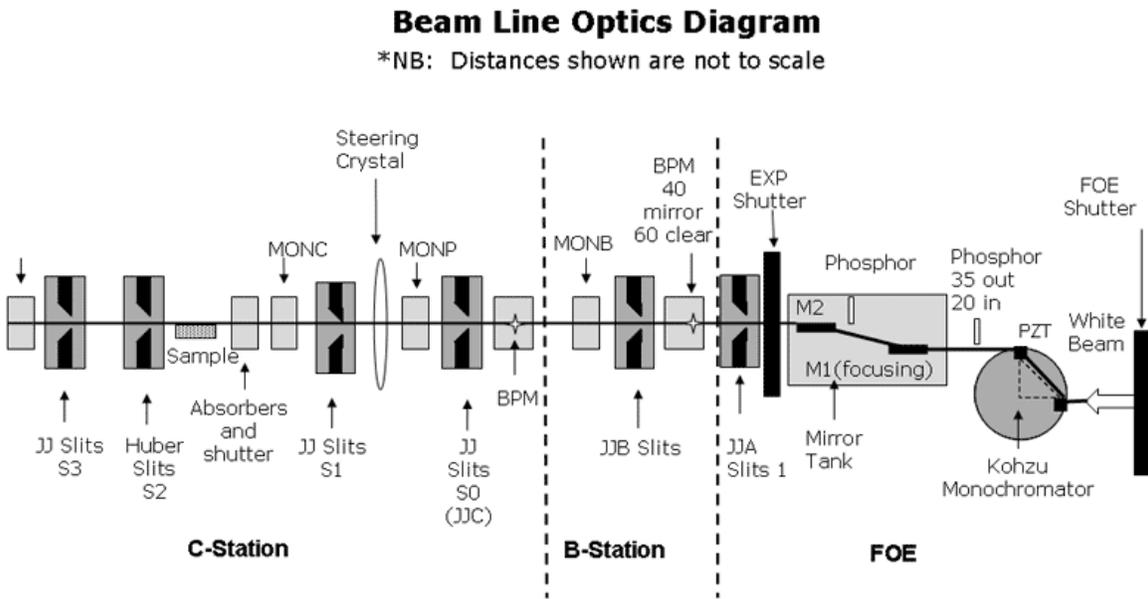
1b. Liquid Surface Spectrometer Layout
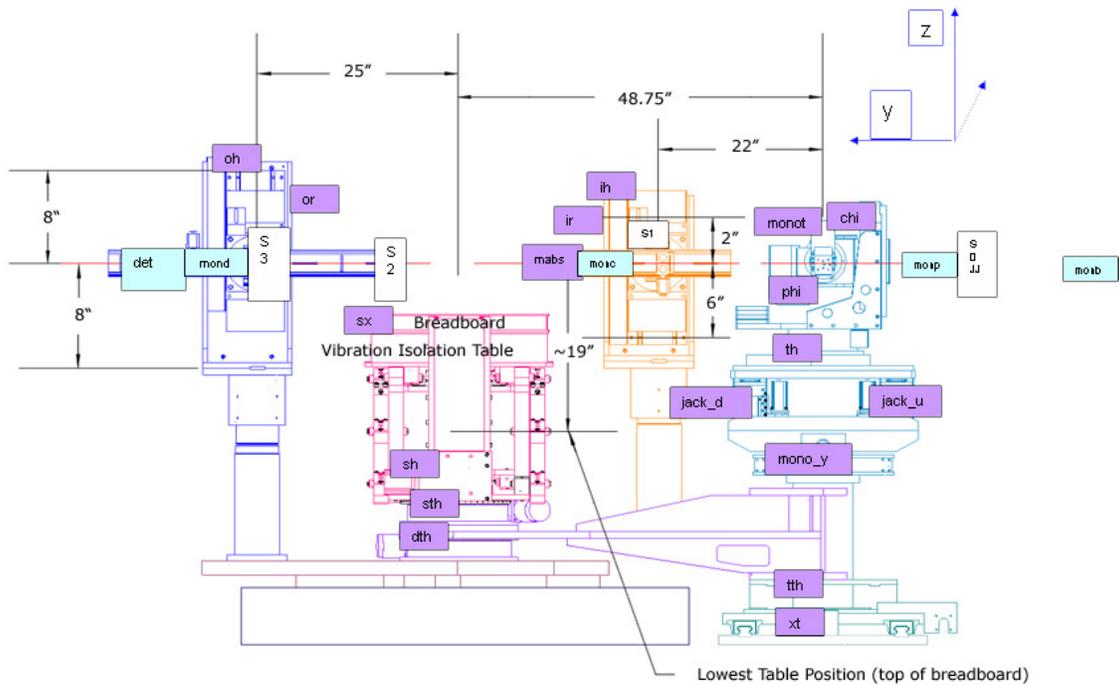
2. Software

2a. EPICS (MEDM windows for users)

IDC Liquid Surface Spectrometer Main Page

SPEC Command Window

Beam Optimization Window

3. Beam Optimization

To optimize the beam when
1) Intensity drifts
2) Intensity feedback is off
3) after recovering from a beam dump

15IDC Surface Beam Optimize X: 0.013 Y: 0.003

X 10 mm   X 10 mm

1 Turn Feedback off   Feedback On

2 Set DAC voltage to 0   0.9566

3 Set this to 3.00 → 0.600 / 0.600
Tweak this: MonoTheta2
Readback: 7.05907 arcsec
Set this value to 0.01.
to maximize this: 330632   MONB
Set this to 0.60 → 0.600 / 0.600

Beam Position

4 Tweak this: Mirror2 Theta
Readback: 2.200 mrad
Set this value to 0.001.
to maximize this: 216949   MONP

5 Tweak this: SLOWLY Mirror2 Chi
Readback: 1.500 mrad
Set this value to 0.2.
to maximize this: 216949   MONP

X zero -23.6   X offset -0.134
Y zero -13.8   Y offset 0.160
To reset, Click Help   Help

7 Set DAC voltage to 5   Turn Feedback On
DAC Voltage --> Feedback
0.9566   On

6 Set to 100 → Press button → Fdbk Setpoint
90.000   100% Scale   90.000

Intensity

HHL MONOCHROMATOR
Energy (keV): 30.0001   lambda (A): 0.41328
Undulator Energy (keV):   30.217
Beam Info: Beam Current =   101.4   A
Pinhole Position: Xp = 1.000
Yp = 36.000

	H SIZE	V SIZE		H SIZE	V SIZE		H SIZE	V SIZE
A1 JJ Slits	10.000 / 10.000	10.000 / 10.000	IDB JJ Slits	3.000 / 3.000	0.600 / 0.600	IDC JJ Slits	3.000 / 3.000	0.300 / 0.300
H CENTER / V CENTER	-0.000 / 0.000	38.244 / 38.244		-0.045 / -0.045	37.605 / 37.605		-0.000 / -0.000	-0.000 / -0.000

Beam Dump Recovery Window

4 Beam Recovery

After the beam comes back from a dump, follow the procedure to recover the beam

1 If the FE valve is closed or EPS is in FAULT, call a beamline scientist.
If ok, continue to step 2.

EPS FAULT STATUS
EPS-major Ok
Vacuum Ok
FE Valve Open

2 Check machine current (if 0 no beam).   Current: 102.2 ma Lifetime: 7.1 Hours
Machine status (should be user operations).   Machine Status : USER OPERATIONS
Check operating mode (should be beam deliverede). Operating Mode : Delivered Beam
Check shutter status (should be enabeled).   Shutter Status : Shutters Enabled
If all of the above are correct goto step 3.
Otherwise ask floor coordinator when beam will return. If long time, go home.

3 Check to see if FE and FOE shutters are open. If not go to PSS panel on Hutch and open them.
Station A: FE Shutter Open
Station B: FOE Shutter Open

4 Check gap and energy to make sure that it is closed to the proper energy. If not, close gap.
Gap (mm) Energy (keV)
Start   Stop
Access Mode : User
Energy [keV]
Current 30.217
Check 15IDA Logbook for the desired value
Place value here ----> 30.221

5 Insert Phosphor Screen Low High → Turn off feedback Adjust to maximize beam intensity
Out of Beam   On

6 Go to Beam Optimization screen
Or click button to call up screen ---> Beam Optimize

Surface Motor Speed

2. Motor Speeds

Check or change the speeds circled in red; the setting indicated are for sample scans which are slower than in alignment

Note: do not change Max speed and Base speed

motor_form_idc_speed.adl

PV Name	Mnemonic	Max Speed	Speed	Base Speed
		(UNIT/S)	(UNIT/S)	(UNIT/S)
15IDC:m58	chi	4.00000	2.00000	0.50000
15IDC:m59	phi	8.0000	4.0000	1.0000
15IDC:m57	th	3.000	2.000	0.500
15IDC:m60	monot	1.0000	1.0000	0.1000
15IDC:m18	mono_y	1.0000	0.5017	0.1000
15IDC:m20	jack_u	1.0000	0.9998	0.1000
15IDC:m19	jack_d	1.0000	0.9998	0.1000
15IDC:m26	tth	0.3000	0.0300	0.0010
15IDC:m17	base_x	1.0000	1.0000	0.5000
15IDC:m52	ih	0.5000	0.5000	0.0099
15IDC:m53	ir	1.0000	0.1000	0.0100
15IDC:m61	sh	0.5000	0.1000	0.0100
15IDC:m21	sth	0.5000	0.5000	0.1000
15IDC:m54	oh	0.5000	0.5000	0.0099
15IDC:m55	or	1.0000	0.1000	0.0100
15IDC:m23	dth	0.5000	0.1000	0.0050
15IDC:m41	xtalro	1.000	1.000	0.001
15IDC:m42	xtalli	0.500	0.500	0.001
15IDC:m25	sx	1.0000	0.2500	0.1000
15IDC:m56	tilt	1.0000	0.5000	0.0100
15IDC:m45	BPMlin	2.0000	2.0000	0.0500

IDA   IDB   IDC

IDD   Catcher   SPEC   EXIT

Beam Optimiz   Beam Recover   Motor Speed

Oct 28

cpu disk

2b. SPEC Commands in Brief

General Help
prdef *command*- prints the command usage. Or, just type command without any arguments.
history or **!** allow you to look at past commands (eg. "!d" looks at all past commands starting with d)
onsim/offsim – In simulation mode: no motors move, no permanent changes made, calculations only.
ca   (e.g. ca 0 0 1)   Calculates all angles and heights for specified qx,qy,qz
wh   Lists positions of the 10 real motors.
wm   *motor* lists complete info for up to 6 motors. (Example: wm oh)

Scans
DET=monc   - sets the detector to ion chamber, monc
plotselect   - choose desired input (Example: plotselect monc)
setplot   - Allows you to plot data in real time or after scan is completed.

ascan *(motor*   *start**   *finish**   *intervals*   *time)*

Task: Scans absolute position of specified motor. *mm or degrees.
Example: ascan oh -0.2 0.2 20 1

dscan *(motor   start*   finish*   intervals   time)*
Task: Scans relative position of specified motor. *mm or degrees.
Example: dscan oh -2 2 10 1

shscan *(halfwidth   intervals   time)*
Task: moves sample and detector heights together.

oscan *(halfwidth   intervals   time)*
Task: Moves detector in a "circle" around the sample.
Comments: Involves simultaneous motion of the or and oh motors

P CEN – prints the center position of a scan.
umv tth CEN - moves motor to center position of last scan
set tth 7.406 - resets tth motor so that current position reads 7.406

Other Useful Macros
ct *(time or monitor_counts)*
Task: Counts for a set period of time (positive) or to monitor counts (negative).

mv *(motor   angle/position)*
Task: Moves motor to absolute position specified.
Example: mv tth 50
Comments: **mvr** moves motor by a relative amount from current position.
             umv updates motor position to screen as motor moves.
           umvr Moves motor by relative amount, updates motor position in real time.

umi (*alpha beta)*   and   **umk** *(qx, qy, qz)*
Task: Change spectrometer alpha and/or beta angles. Many motors involved!
Examples: umi   0.2   0.0   umk 0 0 0.2

Slit Macros
wslits   Displays slit widths

s1v 0.1 0.1   *(mm below and above center position)*
Task: Opens slits to +/- 0.1mm about a center position

s2vscan 1 0.2 10 1 *(total_scan_range   slit_gap   intervals   time)*
Task: Scans the height of slit2, maintaining a constant opening of 200 microns.

Operating Linear Detector

mcavert *(time or monitor counts)*   Task: Collects data from the linear detector

2c. IDL Cheat Sheet

1) Make sure that chemmat28 us connected to the computer in use
2) Go to 'preferences" and check below
        startup file: chemuser\MIDL\startup_mm.pro

Path setting: c:\RSI\IDL\lib
Z:\Chemuser\MIDL

General Info

Important: All the data processing routines used here employ the concept of a "current file". The current file can be changed at any moment by adding a **,/new** to any of the statements. This will prompt the user to identify, interactively, the new file (with the previous one being "forgotten"). Note that one should not use **,/new** unless it is needed since there is a time overhead at reading a file.

Keywords: The actions taken by the various routines can be modified using keywords and some of these keywords are common to many of the routines. In the interest of brevity these keywords are listed here, instead of being repeated, over and over again, in the descritions of the individual routines. A reminder to new IDL users, IDL keywords come in two varieties, the "switch keyword" which is either "set" (by invoking its name preceded by /)or "not set", such as the /**new** mentioned above, and keywords which move values into and out of routines (these may be further subdivided into input and output keywords). The following is a partial list of common keywords used here. The routines used in the examples will be explained later

columns   An input keyword used by various routines which need to pick specific data columns from the data block in a scan in a Spec file. **columns** accepts as input a 2 or 3 element integer input, with the first number representing the x-column (the scan variable), the second, the y-column (usually detector reading) and the optional third one representing the normalization column (usually *monc* output). The columns can be numbered either from left (starting at 0 and going up) or from right (starting at -1 and going down). For example, in the call:

scan_show, columns = [0,-1]

the x-values are read from the first (from left) column, the y-values are read from the last column and no normalization is done. In the call

scan_read, columns = [2,-1,-2]

the x-values are read from the third column (typical in reflectivity scans), y from the last and normalization from the one before the last.

/**new**   As mentioned above, this is a switch which forces reading in a new spec file.

/**output**   Switch, used by all the routines which generate screen graphic output. When /**output** is set, a copy of the screen graphic is sent to the current printer. The size of the printout can be controlled using additional switch keywords (active only in conjunction with /**output**). These are:

/**full**	obvious
/**half**	ditto
/**quarter**	ditto
/**blin**	intermediate between half and quarter.

The size keywords are sticky, meaning that whenever one is used, it'll determine the size of all subsequent plots until the next time the size is changed.

result   This is an output keyword, enabling one to write the data processed by various routines into an IDL variable. For example the routine **patch_z** (described later) is used to patch together reflectivity scans and display the result on the screen, as in

patch_z, 45, 47, 50

(the numbers are scan numbers, explanation later). When called instead as

patch_z, 45, 47, 50, result = whatever

the result of the patching is put in the variable **whatever** and is available for further processing.

Important: The data is present in the variable in our standard data format. This is a 3-column array, where the coulms, in order, contain x-values, y-values and y-errors.

The list above is by no means exhaustive, but it'll do for now.

Note: All the routines generating graphic output accept all the usual IDL graphics keywords as well

To read in a SPEC file

SPEC file can be read in in a variety of ways, usually the most convenient is using **scan_info**. This routine provides information about a chosen scan in the current file, or, optionally, the file itself. Example:

      IDL>psyms, 0   (define symbols, optional)
      IDL>pcols   (define plot colors, optional)

These (optional) commands need to be issued only once per session.

      IDL>scan_info, 0, /new   (gives file info for new file)
      IDL>scan_info, 0   (gives file info for the current file)

Typical output from the above looks like

IDL> scan_info, 0

Filename   :   P:\MIDL\Surface\Data\11.14.03

Date/time   :   Thu Nov 13 23:29:16 2003
  177 scans present

Listed local parameters:

Chi In_Ht In_Rot Sample_H Det_Th Out_Ht Out_Rot Phi

an_Sam_H cpm ns dtoffset Theta

_____

IDL>scan_info,26   (basic info for scan 26)

Typical output looks like

IDL> scan_info, 26

Filename   :   P:\MIDL\Surface\Data\11.14.03

Scan header   :   S 26 hklscan 0 0 -0.0055 -0.0045 0.250001 0.250001 3 -3.2e+06
Date/time   :   Fri Nov 14 02:07:44 2003
11 columns,   4 rows

G_L1   : 559.441 ;   G_L2   : 1237.806 ;   G_L3   : 645.580

Q_vector = [0.000000, -0.005499, 0.250001]

Peak location   :   -0.00483333 ;   Peak intensity   :   105520.
COM =   -0.00485209 ; FWHM =   0.000499316 ;   CEN =   -0.00533265
LAMBDA = 1.1269

_____

Scan info accepts a number of keywords, as follows:

/**pars**   Switch, when set a list of tracked parameters with their value is displayed.
/**slits**   Switch, when set the list of all the slit values is displayed.
/**full**   Switch, when set all the gory details of the scan, as written in the file, are shown.

Reading SPEC Scans

Data from any *single* scan can be read into an IDL variable using the function **scan_read**. The basic syntax is

        IDL>res = scan_read(s#, columns = col)

where **s#** is the number of the scan wanted and **col** is a 2-3 element vector (see keyword **columns** in "General Info"). Optionally, one may live out **columns**. In such case IDL will ask for the column numbers, interactively.

The function returns the read data in the standard [x,y,y_error] format. **scan_read** accepts a number of keywords, most of them not of interest for the general user. The ones worth knowing are:

/**err**   Switch, when set the return variable contains [x, y_error/y,0] (the third column is
                   zeroed.
header   Output keyword, can be used to return the header of the data block. For example

                   IDL> res = scan_read(18,col=[0,-1,-2],head=head)
                   IDL> print, head

H K L Epoch monb monp mond mca Seconds monc det

Displaying SPEC Scans

Data from single scans or groups of scans can be displayed using **scan_show**. The basic syntax is

      IDL>scan_show, s#, columns = col

with **s#** and **columns** same as above.

It is possible to display multiple scans at once, for example the command

      IDL>scan_show, 5, 8, 15, 12, 2, columns = [0,-1,-2]

Will display on a single plot the data from the five scans numbered 2,5,8,12,15 (the order in which the numbers are provided doesn't matter), using the first, last and before last columns for [x,y,e_error], for <u>all</u> scans (it is, of course, the users responsibility to make sure that all scans are of compatible type and the column assignment is valid for all of them).

More generally, whole ranges of scan numbers can be combined, as in

      IDL>scan_show, '6-13, 16, 18-22', columns = col

In this case all the scans from #6 through 13, scan #16 and the scans from 18 through 22 will be used. Note that the scan number entry in this case is a <u>single</u> character string, not numeric.

As a last possibility, actual scan data in our standard data format (a [3,n] array) can be provided. For example, one can have

      IDL>a = scan_read(4, columns = col)
      IDL>b = scan_read(32, columns = col)

      IDL>scan_show, a, b

Note that **columns** entry is not required in this case. This mode of use is valuable when one wants to display together scans from different SPEC files, or processed data (not original scans).

1)To view individual spec scan results, say for scan #27—has to be a dsan or ascan,
      IDL>scan_show, 27, col=[0,-1,-2], psym=-8,/output,/quart&wshow
            (col=[x,y,monc], output for printer, optional)
2)To read a scan 9 data into IDL for data analysis
      IDL>res=scan_read(9,col=[0,-1,-2])

Patching together spec scans taken with different absorbers, scaling appropriately
      (1) for GID

IDL>patch_xy, '100-107, 109', /force   (linear scale)
IDL>patch_xy, '100-107, 109', /force, /ylog   (log scale)
Note that scan numbers must be listed in the order of increasing theta values

(2) For reflectivity
IDL>patch_z,95,96,97,[-98,99,-100],res=a,/output,/quarter(negative is for background
scan whose count is ½ count of the specular scan

plot options:
       /new/ylog,xran=[0,1],yran=[1,2]..

Detector linear fit

IDL> detfit, 126, /pil, tit= 'Have a nice day!', /new ($$$$ should print scan file title)

CCD related (temp)

   1) dth scans
IDL> lee_dth_scan, '3-7', ran=[1,3],step=.5

Using g_l1, g_l2, g_l3
g_l1,[154,155,156]
g_l2,[154,155,156]
g_l3,[154,155,156]

;========================Demostration:
Listings in CARS5\users\chemuser\MIDL\Surface\Data\Listings.txt

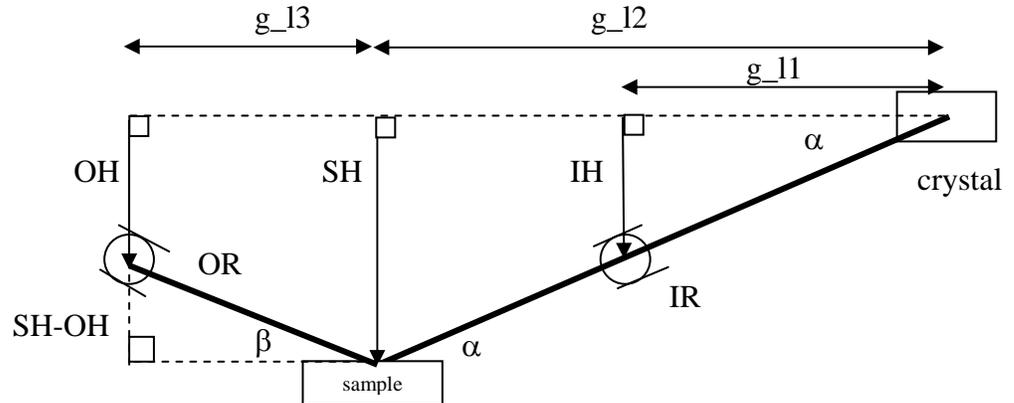File 08.20.03 contains Q_xy set of scans, # 25-33
File 11.16.03 contains Q_y set of scans, # [71-76,77-82,83-88]
File 11.14.03 contains Q_z set of scans,
#, 59,60,61,62,63,64,65,[66,-67,-68],[69,-70,-71],[72,-73,-74]

3. Geometric Alignment for the Liquid Surface Spectrometer

## 3.a   Determining Geometry Parameters and Zero Angle Correction

Find g_l1. For this parameter only, you don't need to have the sample in place. It's essential that beam is centered on the steering crystal. Select four different α angles and record IH for each angle (perform iscans here; these involve simultaneous motion of both the incident height and rotation). Vary α by up to 5 degrees. Use MONC to measure intensity. In IDL, perform a linear fit to determine g_l1. The y-intercept should be very close to zero.

$$\text{IH} = (g\_l1) \tan(\alpha)$$
$$\text{IH} \sim (g\_l1)\,(\alpha)$$
$$\text{Therefore}\quad g\_l1 = \text{slope of IH versus } \alpha$$

Zero Angle Correction insures that beam is parallel to the interface. This should be a very small correction since the beam and the interface are very close to horizontal to begin with. See the figure below.
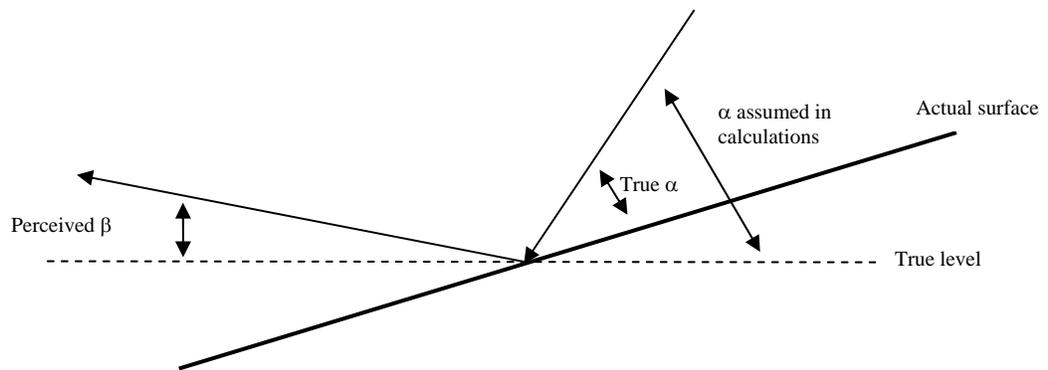
First, move sample out the way and scan oh with nominal α equal to zero. Set oh center to zero. Then move spectrometer to some small angle (qz=0.05) and move sample into place. Don't pick too small of an angle since there is a risk that you will detect transmitted beam in addition to the reflected beam. Perform an shscan to center the sample. Perform an oscan with the detector slits open fairly wide. In this way, minor curvature in the sample surface will deflect the beam away from the true specular direction, but will still be captured by the detector. If the slit is open too wide, you may capture transmitted beam. Perform macro zero_angle to take the measured β and estimate a correction to α (half the difference in β). The correction can be based on a single angle α.

Measured β Offset	Calls for…
Small and random	A smiling face, Good!
Constant with increasing angle needed	Correction to zero angle correction
Increasing with increasing angle needed	Correction to geometry parameter

Find g_l2. Perform sample height scans for a number of different α's (like 0.03, 0.05, 0.10, 0.15) and determine the sample height (negative number) corresponding to the center of each scan. Determine g_l2 in same manner as g_l1.

Find g_l3. Perform an oscan for four different α's and determine OH for each angle. Perform a fit, using the value of g_l2 that you determined in the previous step.

$$\tan\alpha = (SH-OH) / (g\_l3)$$
$$\alpha = (SH-OH) / (g\_l3)$$
$$\text{but,} \quad SH = (g\_l2)\tan\alpha = (g\_l2)(\alpha)$$
$$\text{so,} \quad \alpha = [(g\_l2)(\alpha) - OH] / (g\_l3)$$
$$OH = (g\_l2 - g\_l3)(\alpha)$$

Therefore, for linear fit to graph OH versus α, the slope $= (g\_l2 - g\_l3)$

3.b SPEC Cheat Sheet for the Geometric Alignment of the Liquid Surface Spectrometer

(Align the beam to be parallel with the surface of the sample and determine g_l1, g_l2 and g_l3)

A) Alignment for g_l1
   a. SURF> g_trck=0;pa (to disable oh or sh)
   b. SURF>s1v 0.01 0.01,s1h 1.5 1.5
   c. SURF>DET=monc; plotselect monc
   d. SURF>umk 0 0 0
   e. SURF>dscan ih –0.3 0.3 20 1
   f. SURF>umv ih CEN;set ih 0
   g. SURF>umk 0 0 0.05
   h. SURF>dscan iscan –0.5 0.5 20 1
   i. SURF>umk 0 0 0.1
   j. SURF>dscan iscan –0.5 0.5 20 1
   k. …continue (Repeat the iscan to an angle as far as your experiment requires.)
   l. SURF> g_trck=1;pa (enable oh or sh)
   m. Use IDL to obtain g_l1 value (see IDL cheat sheet), input g_l1 in SPEC, and then check the alignment at a few angles.

B) Zero_angle procedure
   a. (mv sh to cut incident intensity by ½ and set sh 0)
   b. SURF>s1v 0.01 0.01; s1h 1.5 1.5;s2v 1 1;s2h 2 2;s3v 1 1;s3h 2 2
   c. SURF>DET=det;plotselect det
   d. SURF>abs 41
   e. SURF>umv sh -2
   f. SURF>dscan oh –1.5 1.5 20 1
   g. SURF>umv oh CEN;set oh 0
   h. SURF>umi 0.35 0.35
   i. SURF>wh

j. SURF>abs 20

k. SURF>shscan 0.4 20 1

l. SURF>umv sh CEN; set sh NOM

m. SURF>dscan oh -1.5 1.5 20 1

n. SURF>abs 40

o. SURF>zero_angle

p. Record mi value on the screen to note the correction for alpha.

q. Repeat from a) to n)

C) Alignment for g_l2 and g_l3

    a. SURF>s1v 0.01 0.01; s1h 1.5 1.5;s2v 1 1;s2h 2 2;s3v 1 1;s3h 2 2

    b. SURF>DET=det;plotselect det

    c. SURF>abs 41

    d. SURF>umi 0 0

    e. SURF>umv sh -1

    f. SURF>dscan oh –1.5 1.5 20 1

    g. SURF>umv oh CEN;set oh 0

    h. SURF>umk 0.35 0.35

    i. SURF>wh

    j. SURF>abs 20

    k. SURF>shscan 0.7 20 1

    l. SURF>umv sh CEN; set sh NOM

    m. SURF>oscan 1.5 20 1

    n. SURF>umi 1 1

    o. SURF>wh

    p. SURF>abs 10

    q. SURF>shscan 1.2 20 1

    r. SURF>umv sh CEN

    s. SURF>oscan 1.57 20 1

    t. SURF>umi 2 2

    u. SURF>wh

    v. SURF>abs 0

    w. SURF>shscan 2.4 20 1

    x. SURF>umv sh CEN

    y. SURF>oscan 1.5 20 1

    z. SURF>umi 3 3

    aa. SURF>wh

    bb. SURF>abs 0

    cc. SURF>shscan 2.4 20 1

    dd. SURF>umv sh CEN

    ee. SURF>oscan 1.5 20 1

    ff. Continue the measurements until shscan measurement is impossible.

    gg. Use IDL to find g_l2 and g_l3 (see IDL cheat sheet), input them in SPEC, and then check the alignment at a few angles.

4. Detectors

4.a   Ion Chamber Detectors

Ion chamber setup

(esp. <u>monc</u>, the beam normalization detector on the Incident Arm)

1) Preamp Offset: Keep dark count (no beam) lower than 100
2) Preamp Sensitivity: Select gain so the count rate is >5000counts/second and <500,000 counts/second (to keep the error <2%)
3) Use N_2 for photon Energy between 8-30keV. Check N_2 supply everyday (or Ion chamber's count is wrong)
4) Ion chamber high voltage: For photon energies less than 25keV use a voltage of 2 kV. For higher energies, use 1.5 kV

How to calculate absolute current output from ion chamber

Ratemeter (if set to "1x") gives an output of 100,000 cts/s for every volt out of preamp.
The preamp converts current from the ion chamber to a voltage.

(high sensitivity; 5nA/V => only 5 nA required to produce 1 volt output.
Low sensitivity; 5 microA/V => a much larger current required to make same 1 volt output)

For example:
2,300,000 cts/s gives 2.3 volts. If the preamp sensitivity is set to 5 microamps/volt, this means that 11.5 microamps are produced by the

4.b Scintillator Detector (Cyberstar 1000)

- Use MCA to check the window, gain and HV settings
- Check linear range
- Check hutch noise (put lead tape in front of S2 with beam on)

5. Troubleshooting

1) <u>IF monb and monp count rates are normal but monc rate is abnormally low,</u> check monot position on TV for "Newport Control"—last number of the four numbers on the TV. If monot is equal to ~ -13.5, go to MEDM panel "LIQUID SURFACE SPECTROMETER" in Sun window IDC (see graph 2.a.1) , and click the **"monot"** button on the right. After ~1 minute, monot should go to the position marked on at the TV monitor. If monot fails to go to the designated position but at a position > -11, then use SPEC to mv monot 0.

2) <u>If monb and monp count rates are fluctuating,</u> there are two possible reasons. One may be due to the malfunction of the intensity feedback, and the other may be due to the instability of the synchrotron beam. Turn the intensity feedback off to see if the fluctuation persists. If it does then the synchrotron beam is unstable. Call the floor coordinator to complain. Otherwise call the beamline scientists.

3) <u>If monc count rate fluctuates but monp and monb are normal,</u> check phi (third number) or chi (second number) on the TV to see if they fluctuate. If they do then move phi or chi back and forth a few times. These are servo motors so they hunt all the time and sometimes may get into a bad spot.

4) <u>After a refill,</u> turn off the feedback and go to MEDM panel "SURFACE BEAM CONTROL" in Sun window Beam Optimization (graph 2.a.3). Follow the instruction from 1-8 on that panel.

5) <u>If the intensity feedback is drifting constantly,</u> follow the instruction in 3) for beam optimization after a refill.

6) <u>After a beam dump,</u> pull out MEDM panel "Dump Recovery" in Sun Window Beam Recovery (graph 2.a.4). Follow the instruction from 1-5. Then use Beam Optimization to optimize the beam intensity.

7) <u>If Surf Froze,</u> open a new console (see graph 2.a.2) and change to your working directory, then start surf.