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1.

To Open New File:

```
IDL> scan_info,0,/new
```

Select SPEC file
Highlight and select corresponding Pilatus folder (do NOT open folder)

Graph windows:

To pop up another graph window,

```
IDL> window, #(number)
```

To see the result from the new window

```
IDL> "command" , /wnew
```

To resize the window, for example,

```
IDL> window, 0, xsiz=1000, ysiz=800
```

To see the explanation about a specific command:

Example: pd_xr

```
IDL> doc_library, 'pd_xr
```

2.

Need to read any big text file? Use IDL

You can read the isotherm txt file or any big text file easily with IDL

```
IDL> anytext = rascii() and choose the file

IDL> head, anytext   You'll see the head part of the text

IDL> help, anytext   You'll see the array info of the text

IDL> plot, anytext[1,*], anytext[5,*] Plot x=first column, y=fifth column
```

3.

For Scan & Slit Info:

```
IDL> scan_info,s_no,/slits
```

Example:

```
IDL> scan_info,111,/slits

Scan header :     S 111 ascanb dth 11.5 13.5 40 30 0
Date/time   :     Fri Jul 25 11:51:53 2008\
```

Slit Data

Slit	Top	Bottom	Left	Right
S0	0.150	0.150	1.5000	1.5000
S1	0.010	0.010	1.4999	1.4999
S2	1.500	1.500	2.0000	2.0000
S3	1.500	1.500	1.9998	1.9998
S4	999.000	999.000	0.3000	0.3000
S5	999.000	999.000	0.3000	0.3000

4.

<u>For XR</u>:

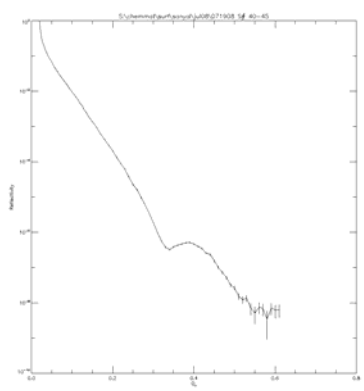
1. `IDL> pd_xr,s_no,sli=sli,/log, back=#, (snorm=#)`

   `(back=)` `#` is what the background angle(in degree) was set at .

   "snorm= # of direct beam scan" options gives you the count normalization.

   <u>Example</u>:

   `IDL> pd_xr,'40-45',sli=[23,11],/log, back=0.5, snorm=39`



`sli=[23,13]` is better for Niels' experiment(Lee group) check with pd_xr_view

2. `IDL> pd_xr_view,s_no,f_no,sli=sli,back=#`

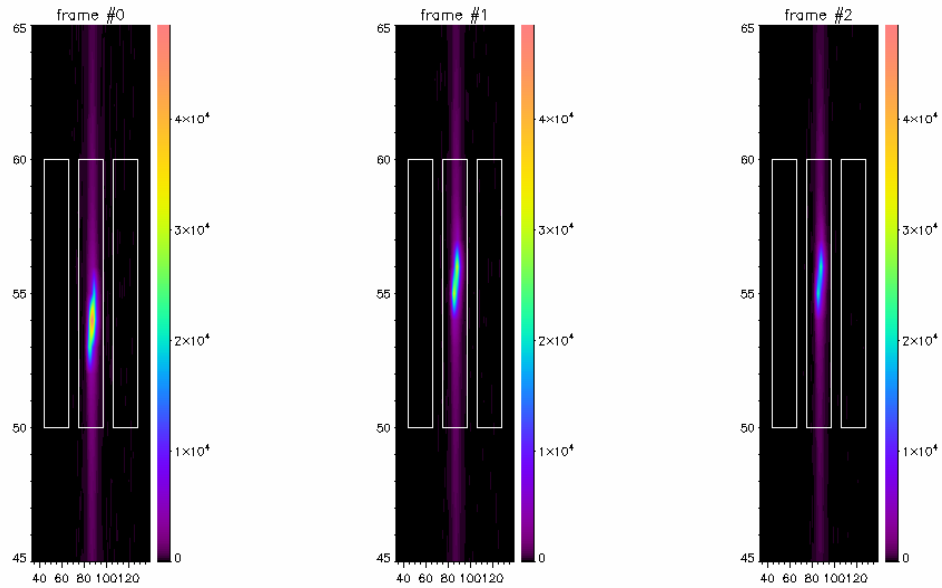
   `f_no` is the frame number in this scan

   `#` is what the background angle was set at

   <u>Example</u>:

   `IDL> pd_xr_view,16,'0-2',sli=[23,11],back=0.3`

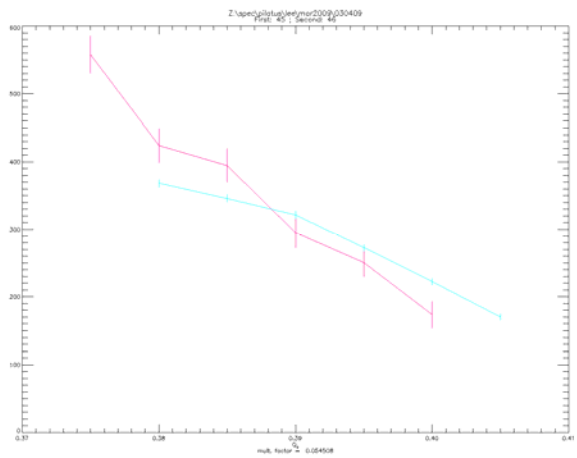
`'0-2'` means to show the first 3 frames among all the frame in scan #16. If you put ",min=0.02" at the line end, for example, the minimum value of background is set to 0.02




```
IDL> pd_xr_match,s_no#1, s_no#2, sli=sli,back=#
```

Example:

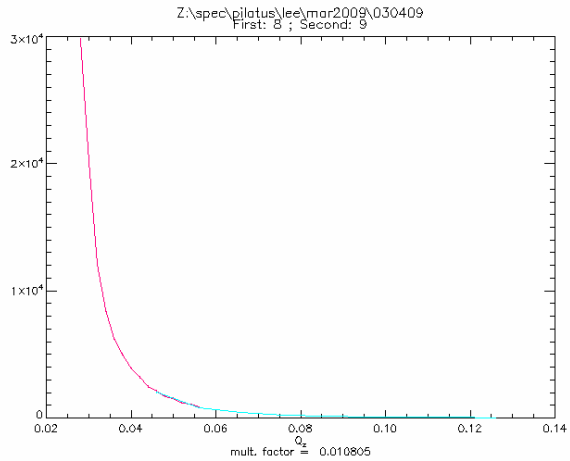
```
IDL> pd_xr_match, 45,46, slit=[23,13], back=0.5,/zoom
```



3. You can see the whole scanning range without "/zoom" command
   Or put ".run pd_xr_match" and rerun the line without "/zoom" in the IDL command line

   Example:

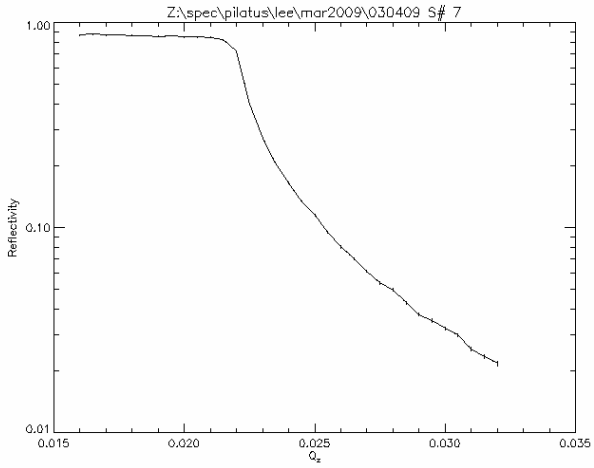
```
IDL> pd_xr_match,8,9,slit=[23,13],back=0.5
OR  if it doesn't work,
IDL> .run pd_xr_match
IDL> pd_xr_match,8,9,slit=[23,13],back=0.5
```



4. If you want to check your reflectivity factor with the direct beam scan,

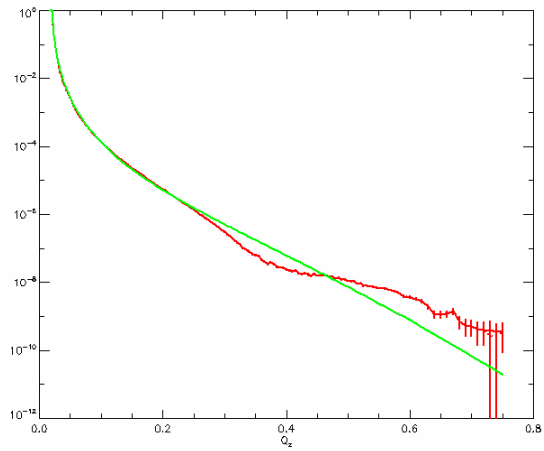
Example:

IDL> pd_xr, 7, sli=[23,13],/log, back=0.5, snorm=6 (6 is the direct beam scan and #7 is the start number for XR scan)



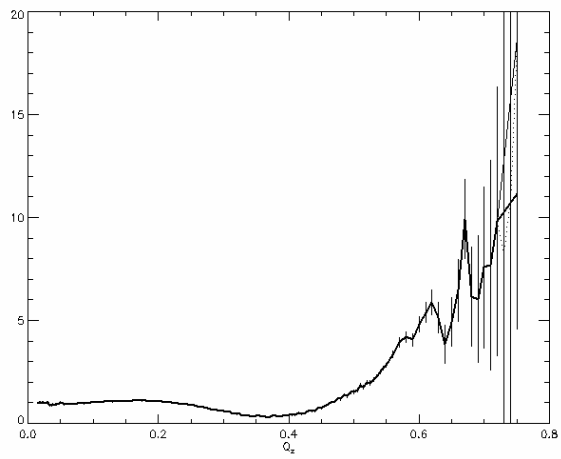
5. If you don't have any method for fitting your data with Rf(Fresnel reflectivity), use the following,

Example:
IDL> pd_xr, '7-15', sli=[23,13], back=0.5, res=whatever
Putting the result to 'whatever' directory.
IDL> reffit, whatever /sho



R/Rf can be obtained by the command

```
IDL> reffit, whatever
```



6. If you want to save the XR result to the ASCII file, let's say, "r18",

Example:

```
IDL>pd_xr, '18-25', sli=[23,13],/log, back=0.5, res=r18
IDL>wascii, r18
```

Then you will see the "select a file for writing" window,

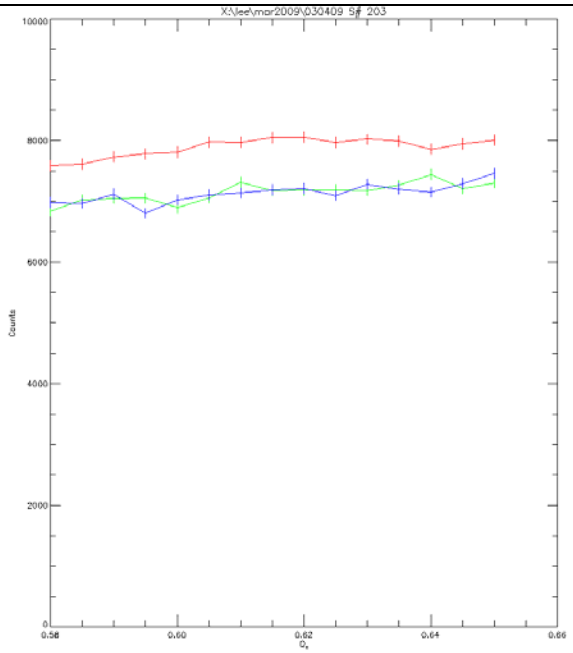
For more data info for the file you put, for example, "r18",

```
IDL>help, r18
```

7. If you compare the counts with background,

Example:

```
IDL>dum = scan_pd_xr(203,sli=[23,13],back=0.5,/show)
```



Red line is the main counts

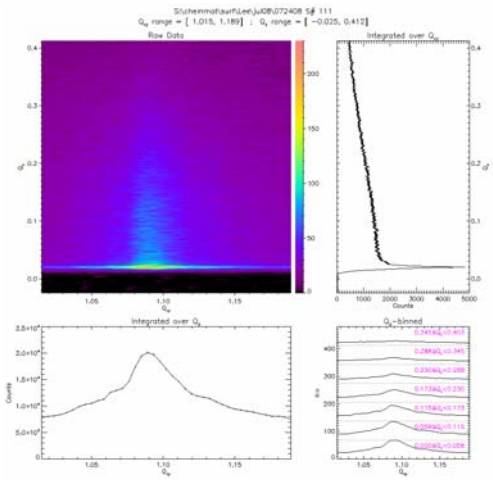
5.

<u>For GID</u>:

1. pd_gid,s_no

<u>Example</u>:

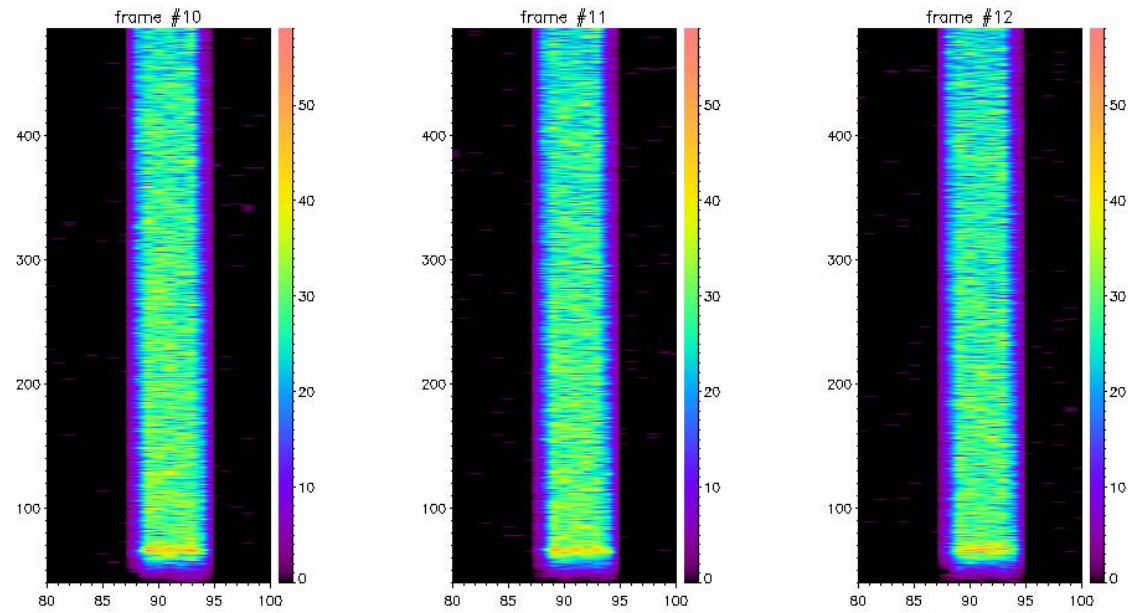
```
IDL> pd_gid, 111
```



2.pd_view

<u>Example</u>:

```
IDL> pd_view, 192, '10-12', hroi=[80,100], vroi=[40,500]
```



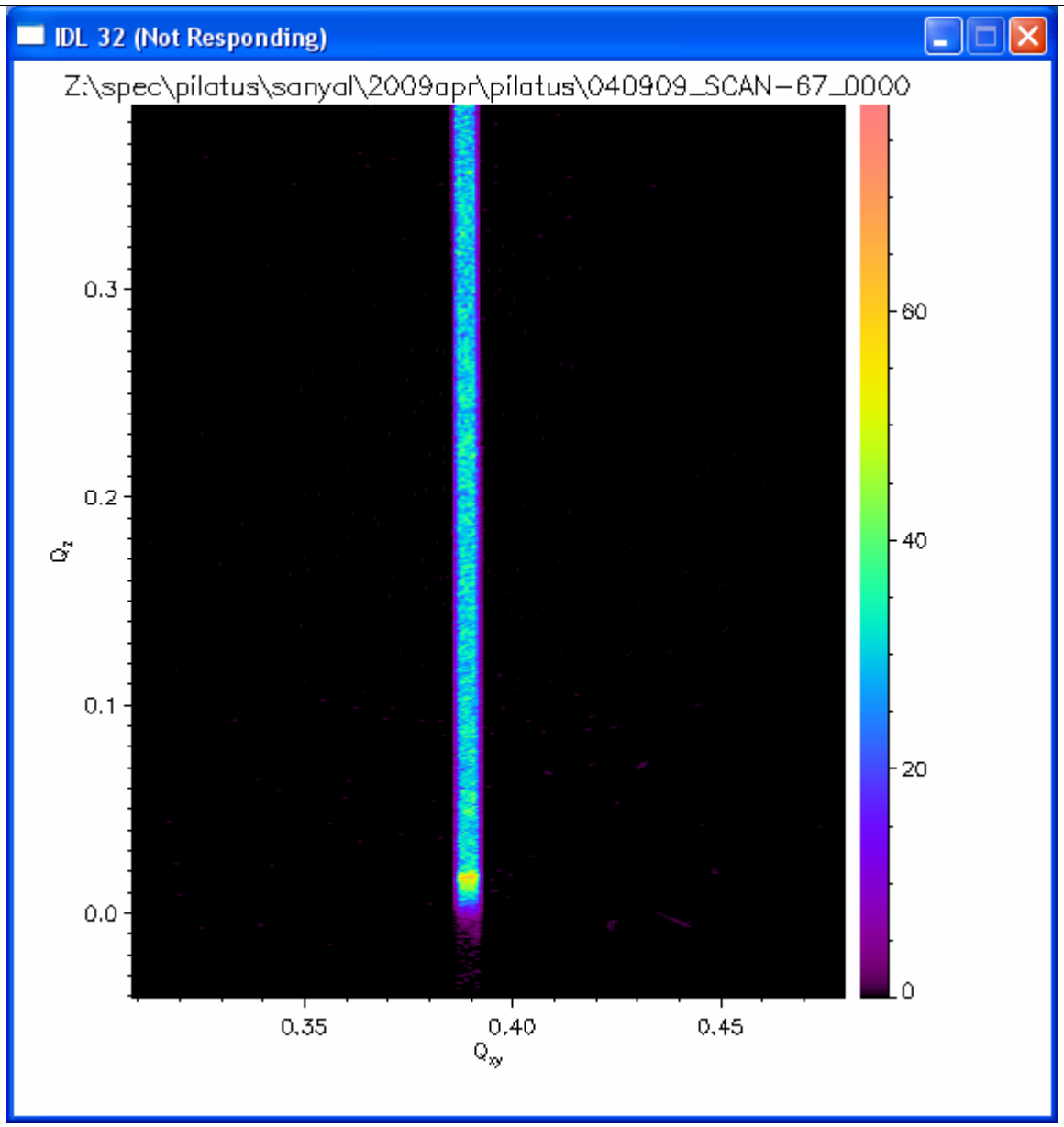
3. pd_movie,s_no, /indiv, /wait

Gives you the individual scans one by one. Select the options on the command line.

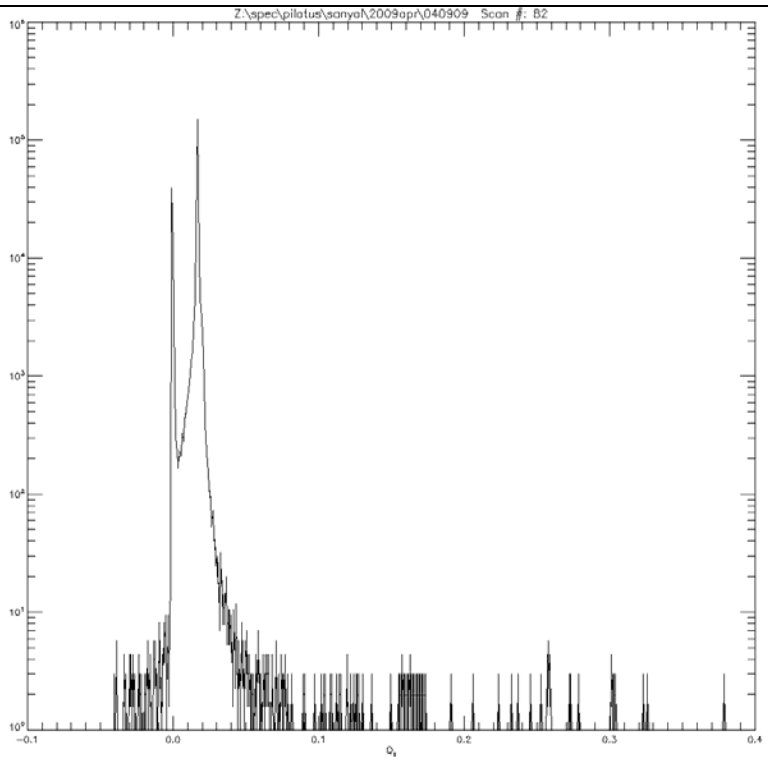
Example:

```
IDL> .run pd_movie
IDL> pd_movie, 67, /indiv, /wait
```

Hit "Q" to exit, "P" for previous, any other key to continue

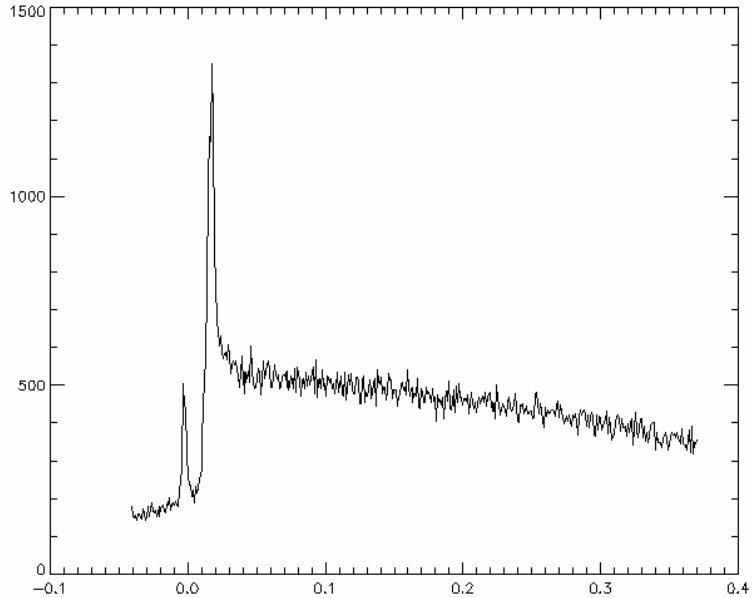



```
3. pd_locate
IDL> pd_locate

4. pd_kscan (previously pd_ks)
IDL>wascii, ks,'ks_133_139_sli27_3'
IDL> pd_kscan, '133-139', sli=[27,3], res=ks
IDL> scan_info, 133, /slits

5. pd_patch_z

IDL> pd_patch_z, 82, /ylog
```



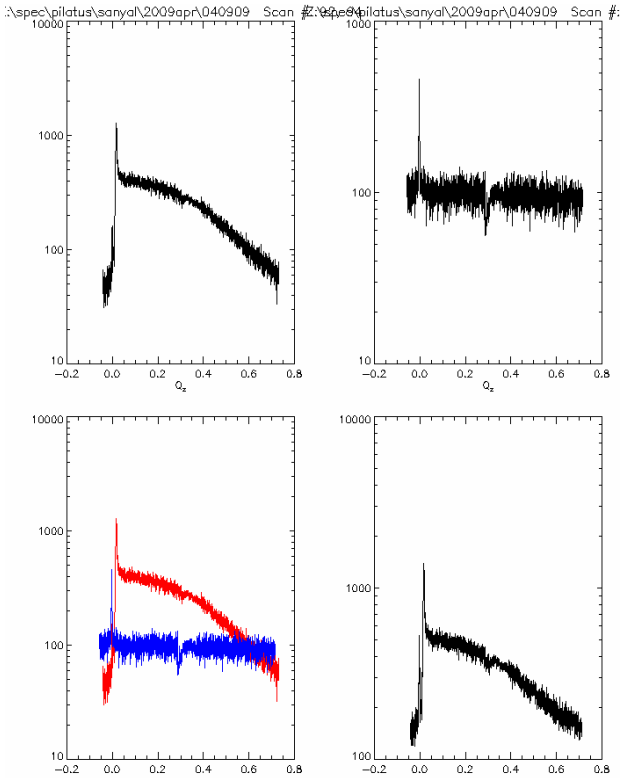
6. GIXOS / Bragg Rod related

```
IDL> .run plot_gixos
IDL> f=plot_gixos(85,86)
IDL> plot, f[0,*], f[1,*]
```




```
IDL> f=plot_gixos('92,94','93,95')
```

```
GIXOS command in EPIC
umi 0.1 0.1
dscanb dth 0 0 1 100
```



6.

<u>For Pinhole</u>:

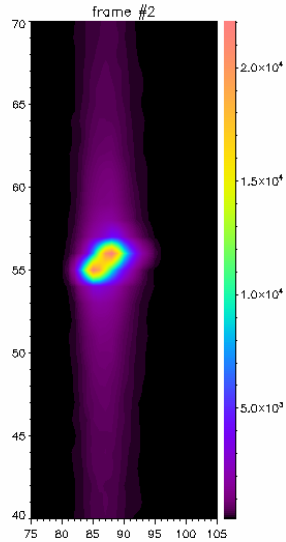
1. pd_view

```
IDL> pd_view,s_no,f_no,vroi=[vrmin,vrmax],hroi=[hrmin,hrmax]
```

Select a specified area (in pixel coordinate) from a whole image `vroi=[vrmin,vrmax],hroi=[hrmin,hrmax]` could be applied to all the 'PD_*' commands.

<u>Example</u>:

```
IDL> pd_view,16,'0-2',vroi=[0,100],hroi=[70,110]
```

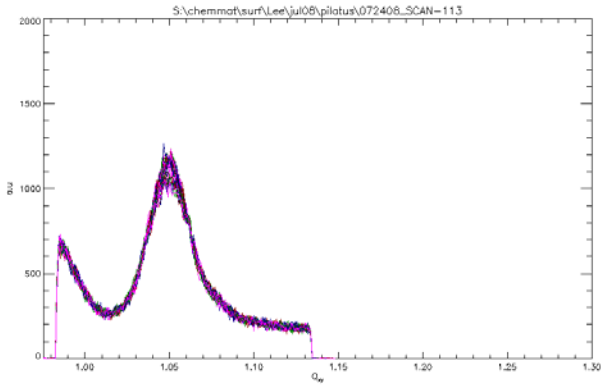



```
IDL> pd_view,s_no,/z_int,/no,/qval,xrange=x_r
```

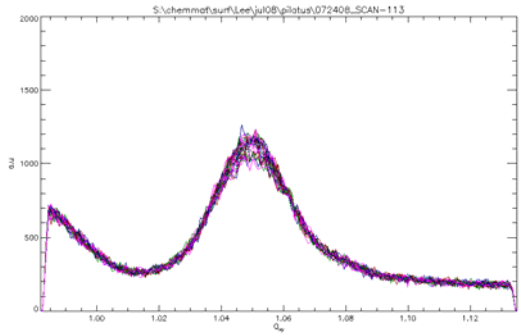
First specify only scan number to determine appropriate range; then run command again, this time specifying range as well

<u>Example</u>:

```
IDL> pd_view,113,/z_int,/no,/qval
```



```
IDL> pd_view,113,/z_int,/no,/qval,xrange=[0.982,1.135]
```



To view each line separately, add `,wait=-#` to view for # seconds or `,/wait` to view at own pace by pressing key

2.pd_pin

```
IDL> pd_pin,s_no
IDL> pd_pin,s_no,/limits
```

```
/LIMITS
; Switch. If set, the limits of the observable region, as defined by the
; beam's footprint and the slits, are superimposed on the image. Active
; only when a single scan is displayed.
```

The point is, there are two separate limits, namely:

1) The projection of the beam footprint on the Pilatus, through S4.

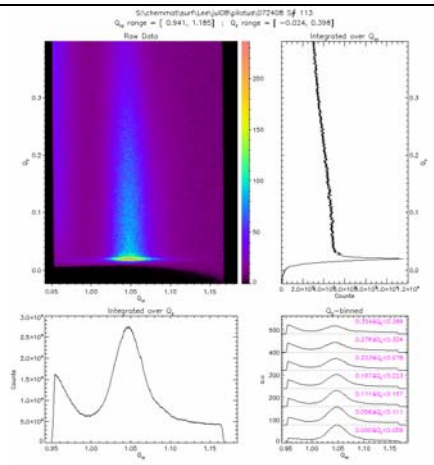
2) The projection of S5 on the Pilatus (note that S5 is not as wide as the Pilatus, even at full opening).

The keyword /limits always displays the smaller (i.e. more constraining) of the two. Whatever you have on the detector beyond the limits is sure not coming from the sample.

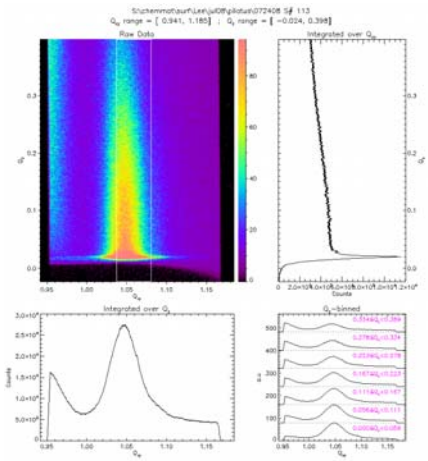
Note that to see the limits you must also use the keyword /raw with pd_pin.

<u>Example</u>:

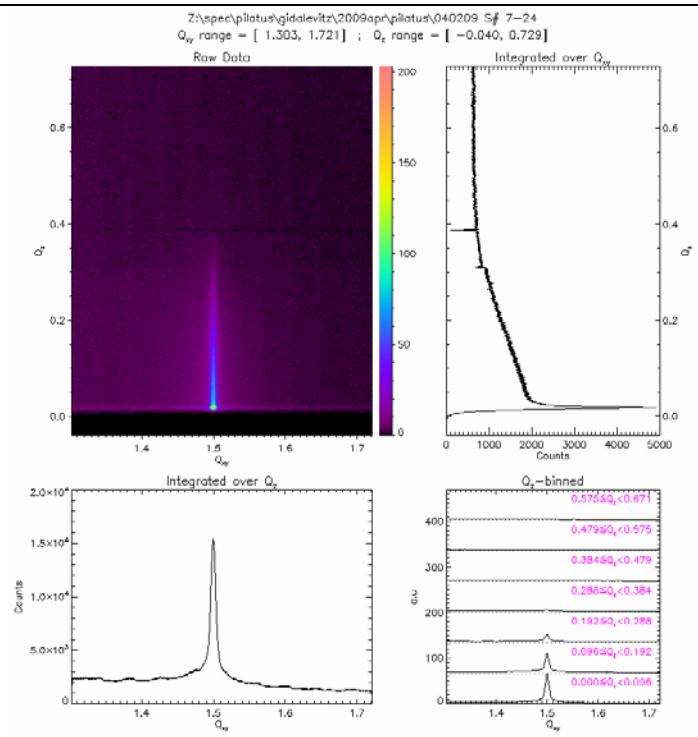
```
IDL> pd_pin,113
```



```
IDL> pd_pin,113,/limits
```

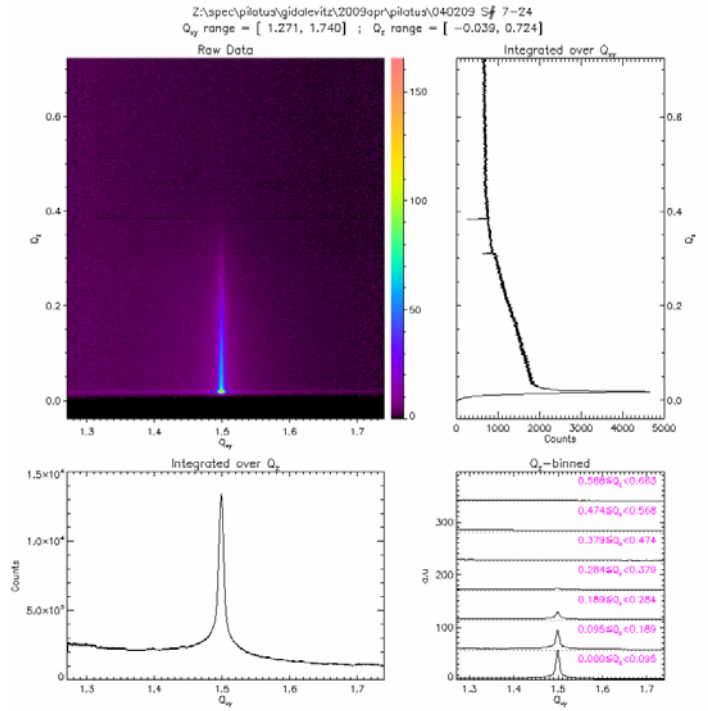


```
IDL> pd_pin, '7-24', hroi=[75,135]
```



The upper picture shows artificial groove features.
You should tweak 'hroi' range to get a better picture. For example,

```
IDL> pd_pin, '7-24', hroi=[50,150]
```



To eliminate the bad pixels, try, for example,

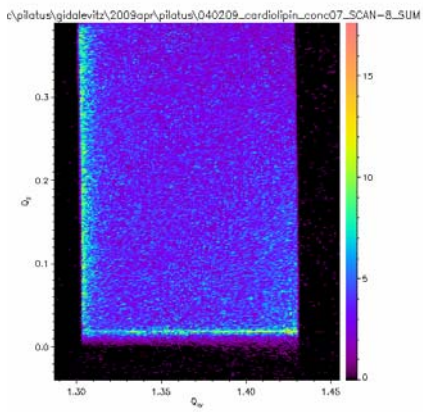
```
IDL> pd_pin, '7-24', hroi=[50,150],/bad,z_res=z130
```

3.pd_sum

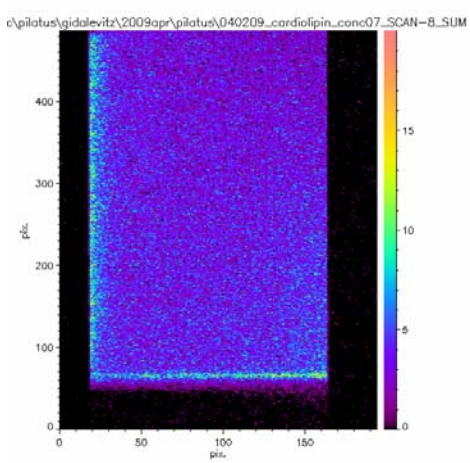
Pd_sum command displays a sum of Pilatus detector scans and frames.

Example:

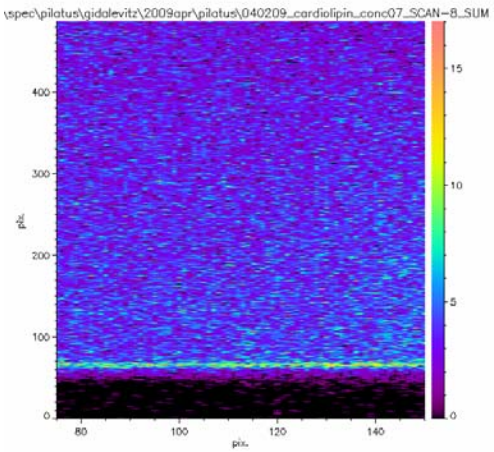
```
IDL> pd_sum, 8
```




```
IDL> pd_sum, 8, /raw
```




```
IDL> pd_sum, 8, /limits, /raw, hroi=[75,150]
```


\spec\pilatus\gidalevitz\2009apr\pilatus\040209_cardiolipin_conc07_SCAN-8_SUM
400
300
200
100
0
pix.
80
100
120
140
pix.
15
10
5
0

7.

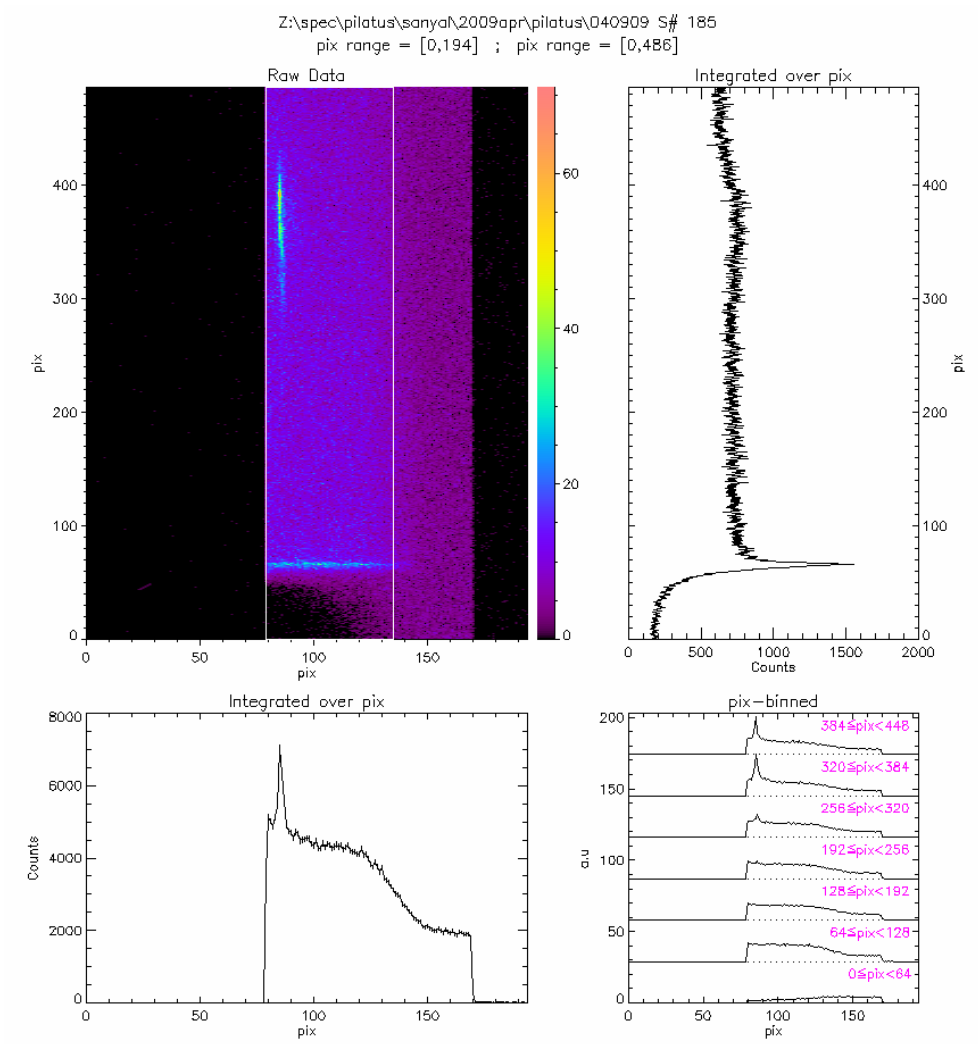
ADVANCED COURSE

Comments about /limit, /diffuse, /kscan, and /locate options using in pd_xr, pd_gid, pd_pin commands

1. **/lim**

Example: to see the single frame #53,

```
IDL> pd_pin, 185, fram=53, /raw,/lim
```



"/lim" option determines the effective slit sizes of Pilatus.
If the a and b values of Hroi=[a,b] exceed the limit shown on the results(pixel 75~135 roughly), please correct the values within limit lines (a>75, b<135).

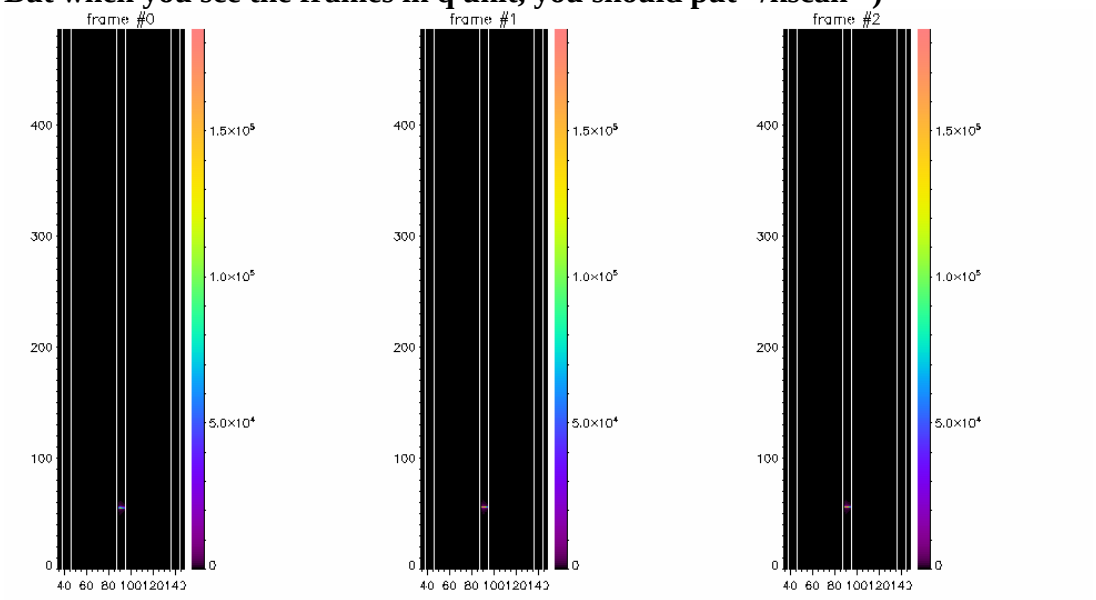
2. /diffuse and /kscan

```
IDL> pd_view, 136
```

shows you all the frames in scan #136. Then,

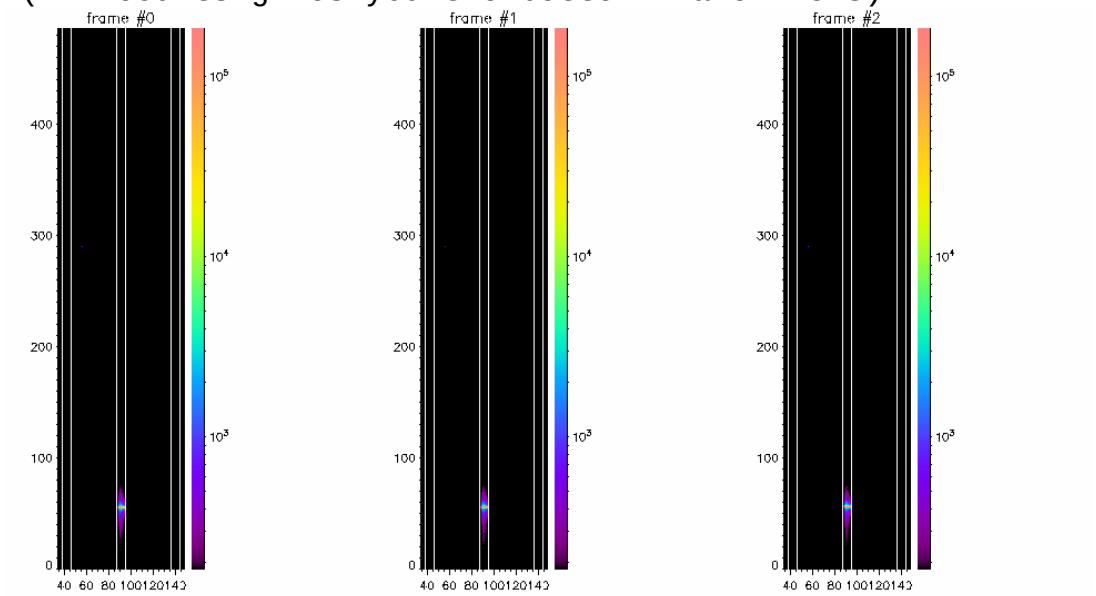
```
IDL> pd_xr_view, 136, '0-2', sli=[9,3], bac=0.5, /diffuse, /kscan
```

(background at 0.5 degree. No effect of "/kscan" option. "/diffuse" only OK But when you see the frames in q unit, you should put "/kscan")



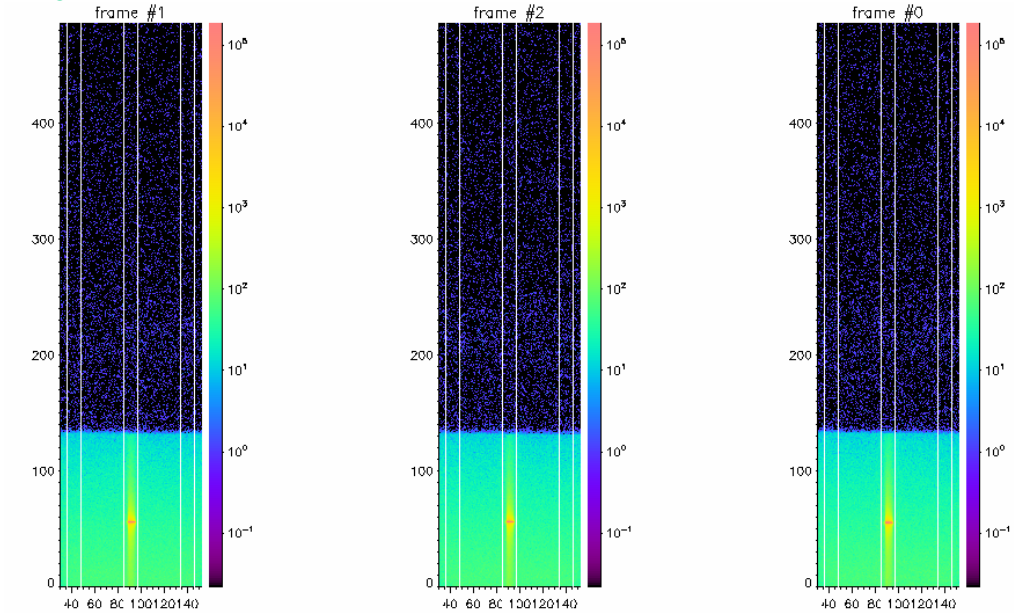

```
IDL> pd_xr_view, 136, '0-2', sli=[9,3], bac=0.5, /diffuse, /kscan, /log,
min=1e-3
```

(Min counts gives you the better frame views)

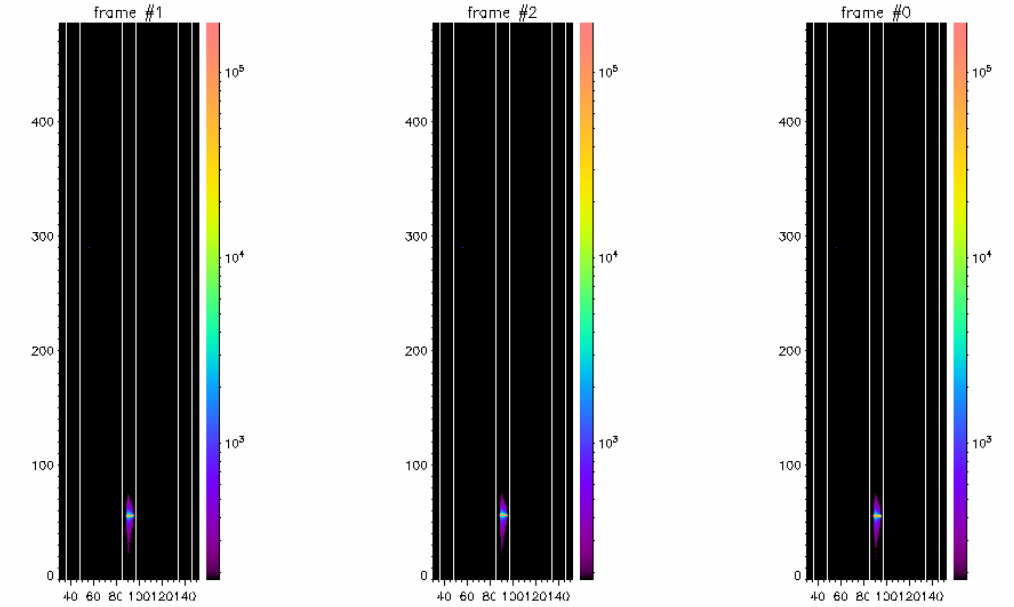



```
IDL> pd_xr_view, 136, '0-2', sli=[13,3], bac=0.5, /diffuse,
```

```
/log
```




```
IDL> pd_xr_view, 136, '0-2', sli=[13,3], bac=0.5, /diffuse, /log, min=1e-3
```



/diffuse only OK
But in q unit, you should put /kscan

[FYI:]
sli=[a,b] : a,b odd numbers, otherwise IDL automatically add 1 to the value

3. /locate

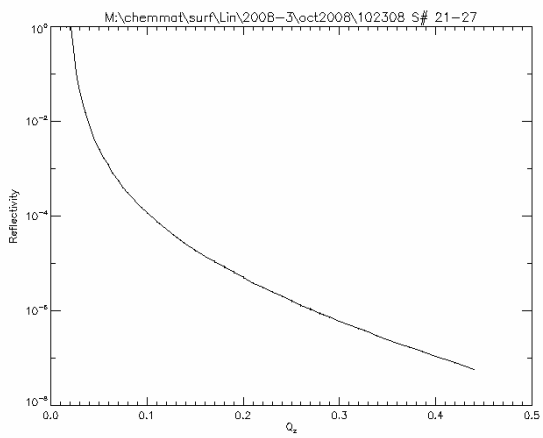
```
IDL>print, scan_pd_center(133)
      91       61
```

XR default take the reflected beam center from the first scan of the sequence of xr scans. Let's see

```
IDL> dump= scan_find(0, typ='ref',/show)

21,22,23,24,25,26,27
29,30,31,32,33,34,35,36,37
53,54,55,56,57,58,59,60,61
123,124,125,126,127,128,129,130,131
369,370,371,372,373,374,375,376,377,378,379,380,381
405,406,407,408,409,410,411,412,413,414,415,416,417
496,497,498,499,500,501,502,503,504,505,506,507
512,513,514,515,516,517,518,519,520,521,522,523,524
550,551,552,553,554,555,556,557,558,559,560,561
```

In this case, the beam center is selected at #21 during scan# 21 to 27 automatically.

```
IDL> pd_xr, '21-27', sli=[23,11], bac=0.5, rcenter=cent
```




```
IDL> print, cent
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
```

To reset the beam center,

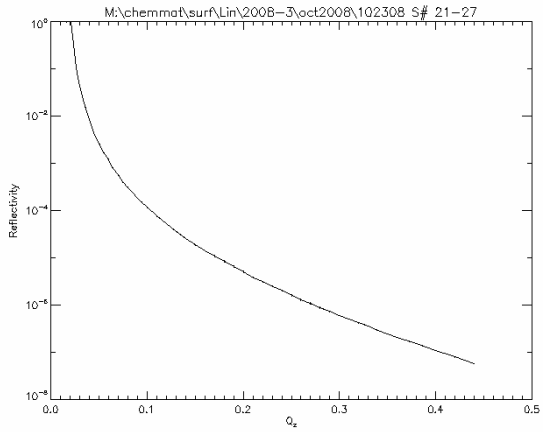
```
IDL> pd_xr, 136, sli=[23,11], /locate
```

:reset the beam center scan by scan

```
IDL> pd_xr, 136, sli=[23,11], /locate, /free
```

:reset the beam center frame by frame

```
IDL> pd_xr, '21-27', sli=[23,11], bac=0.5, rcenter=cent
```




```
IDL> print, cent
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
 91.0000      62.0000
```

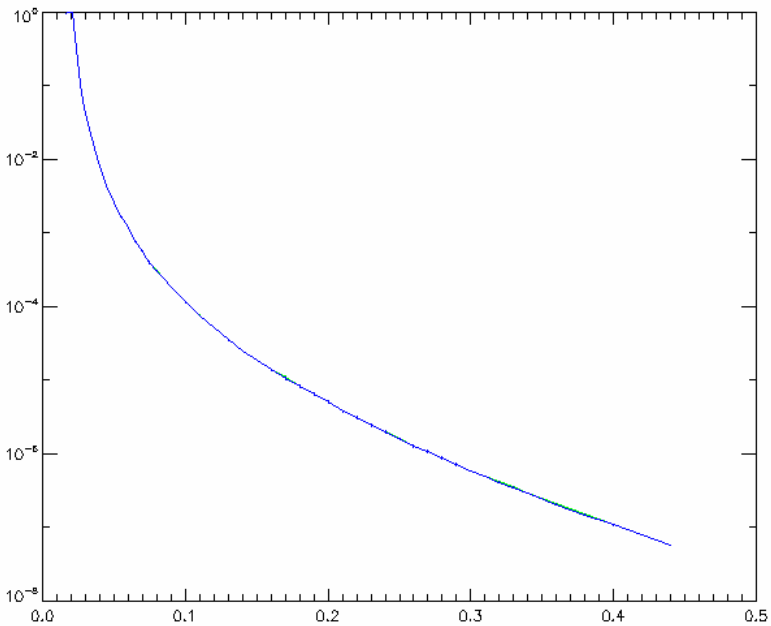
We can see no change of the beam center using ”/locate, /free” option

To see the specific beam center, type

```
IDL> print,scan_pd_center(21)
 92      62
```

To compare the effects of ’/locate’ and ’/locate, /free’

```
IDL> pd_xr, '21-27', sli=[23,11], bac=0.5, rcenter=cent, res=res1
IDL> pd_xr, '21-27', sli=[23,11], bac=0.5, rcenter=cent, res=res2, /locate
IDL> pd_xr, '21-27', sli=[23,11], bac=0.5, rcenter=cent, res=res3,
/locate,/free
IDL> scan_show, res1, res2, res3,/ylog, lcol=[!pcol.red, !pcol.green,
!pcol.blue]
```



8.

<u>For GIXOS</u>:

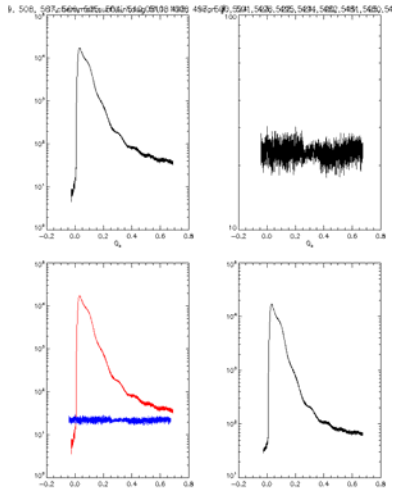
Copy plot_pd_snapshot IDL source file to your working directory. The file can be acessed from: \\epics\pilatus\plot_gixos

Note this file includes the '/bad' command for removing bad points but in cases where there are very sharp peaks this may need to be removed.

```
IDL> f=plot_gixos,sig_scan_no,bac_scan_no
```

<u>Example</u>:

```
f=plot_gixos('479-482,494-497,498-501,504-507,508-511','485-488,490-493,518-521,522-525')IDL> f=plot_gixos('479-482','485-488')
```



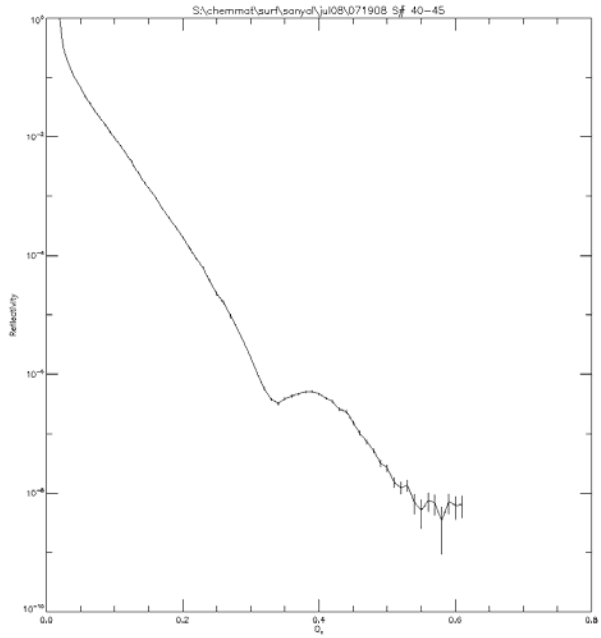
Note:

```
pro plot_pd_snapshots, s_no=s_no,x_r=x_r,fname=fname
;s_no=177
;x_r=[.91,1.025]
;fname='_Dchol_25C_30mN_pin'
s_no_s=strtrim(string(s_no),1)
scan_info,s_no,/slits
if keyword_set(x_r) then pd_view,s_no,/z_int,/no,/qval, xrange=x_r $
else begin
      pd_view,s_no,/z_int,/no,/qval
      pd_pin,s_no,z_result=z,/wnew
      wascii,z,'S'+s_no_s+fname+'.txt'
end

end
```

(\\cars5\Data\chemmat\surf\Lee\jul08\jul08 IDL Data\plot_pd_snapshots)

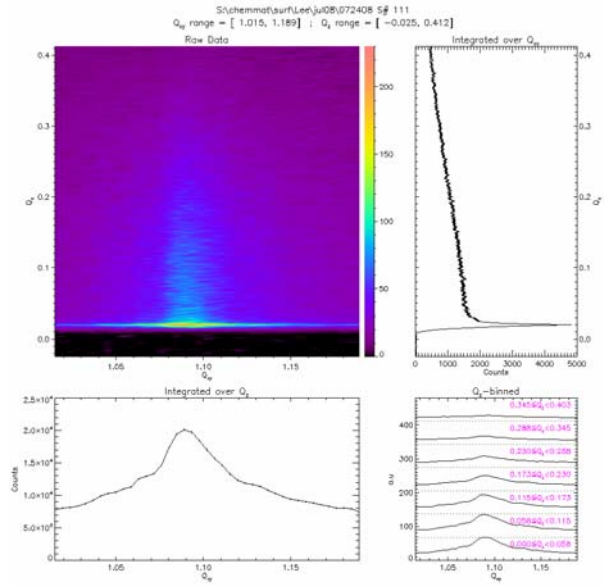
```
function plot_gixos,sig_scan_no,bac_scan_no ;,coe=coe

window,10,xsize=700,ysize=900
!p.multi=[0,2,2]

snum = Range_proc(sig_scan_no)
bnum = Range_proc(bac_scan_no)
sfram = total((Scan_field_read(snum,'ncr'))[*,1])
bfram = total((Scan_field_read(bnum,'ncr'))[*,1])

coe = [1.,sfram/bfram]

pd_patch_z, sig_scan_no, res=sig, /ylog
pd_patch_z, bac_scan_no, res=bac, /ylog
scan_show,sig,bac,lcolor=[!pcol.red,!pcol.blue],/ylog

zsig = [min(sig[0,*],max=max),max]
zbac = [min(bac[0,*],max=max),max]
zran = [zsig[0] > zbac[0], zsig[1] < zbac[1]]

dif = scan_lc(sig, bac, coef=coe,/inter)
dum = where((dif[0,*] ge zran[0]) and (dif[0,*] le zran[1]) and (dif[1,*] gt
0))
dif = dif[*,dum]

scan_show, dif, /ylog
!p.multi=0
return,dif
end
```

XR Scan



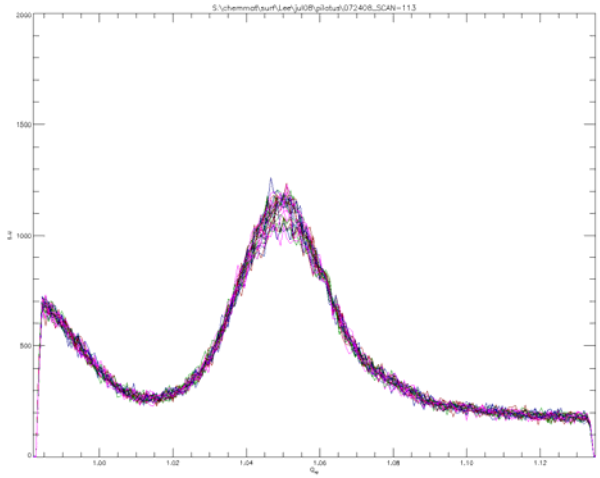
```
IDL> pd_xr,'40-45',sli=[23,11],/log,back=0.5
```

GID Scan

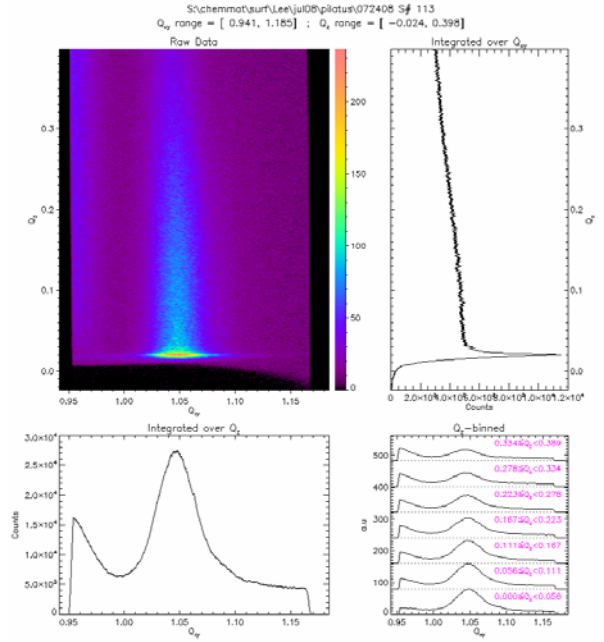


```
S 111 ascanb dth 11.5 13.5 40 30 0
Fri Jul 25 11:51:53 2008
S1        0.010        0.010
S2        1.500        1.500
S3        1.500        1.500
S4      999.000      999.000
S5      999.000      999.000
IDL> pd_gid, 111
```

Pinhole Scan



```
S 113 ascanb dth 12 12 23 10 0
Fri Jul 25 12:41:57 2008
S1        0.010        0.010
S2        1.500        1.500
S3        1.500        1.500
S4      999.000      999.000
S5      999.000      999.000
IDL> pd_view,113,/z_int,/no,/qval,xrange=[0.982,1.135]
```



```
IDL> pd_pin,113
```