

WAND² Single Crystal Diffraction Scripts Manual

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Xiao Hu

Neutron Scattering Scientist

Oak Ridge National Laboratory



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I. Prologue

This manual provides an overview of the general workflow of **WAND² single-crystal data analysis** using Mantid-based scripts. The workflow consists of the following stages:

- **Data loading**
- **Data slicing**
- **Peak analysis**
 - Peak search, indexing, filtering
 - Peak integration

The **peak analysis** section describes how ready-for-refinement peak files – containing indices, intensities, and associated errors – are generated with Mantid-based scripts. Additional details on the underlying script mechanisms are included in the [Appendix](#).

Two methods of peak integration are included:

- **[Method 1](#) (Conventional Mantid algorithm)**
Utilize Mantid's built-in functions (e.g., IntegratePeaksMD). This method is well suited for rapid integration and quick peak inspection. However, its error propagation can be problematic.
- **[Method 2](#) (Detector image-based algorithm)**
A newly developed algorithm that performs peak integration directly from detector images. Although more sophisticated than Method 1, this approach resolves several limitations, such as handling adjacent peaks, irregular peak profiles, and aluminum powder ring contamination.

For general graphical user interface (GUI) instructions, please refer to the Remote Desktop Analysis platform at:

data → HFIR → HB2C → shared → WANDscripts → manual
and read the file *SCD reduction manual.pdf*.

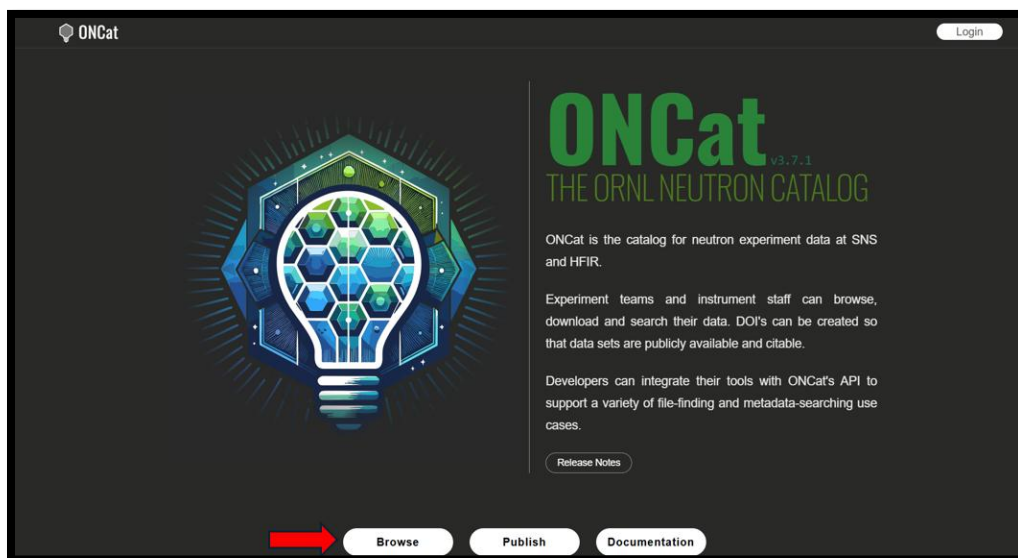
If you have any questions or feedback about this manual, please contact hux6@ornl.gov.

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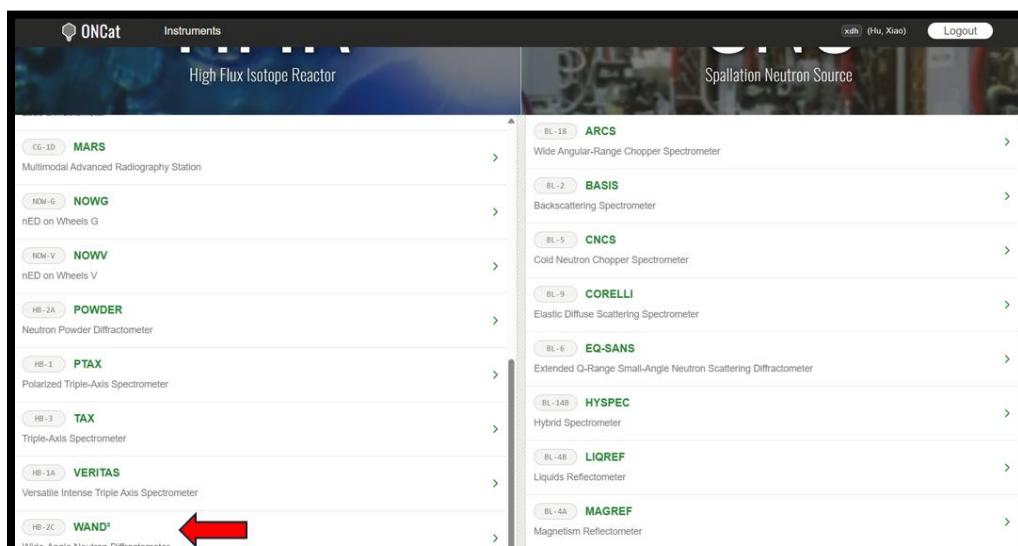
II. Locate IPTS and Run numbers & Open Mantid Workbench

(a) Find experimental data under proposal number (IPTS)

(1) Go to <https://oncat.ornl.gov/> to view your experiment information. Click “Browse” and log in to ONCat catalog with UCAMS.



(2) Find the instrument in the HFIR/SNS instrument list and click on WAND².



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(3) Search for experiment data through: Experiments → type in proposal number (IPTS).

Scans will be displayed along with run number (ID), sample information, and scan descriptions. Record run numbers you need for analysis.

WAND²
Wide-Angle Neutron Diffractometer
HB-2C

Experiments Runs Scans

IPTS	Team Member	Instrument Details
IPTS-7776	Fernandez-Baca, Jaime	WAND-Instrument time 1T-TiSe2 · 3D Printed collimator · BaTiO3
IPTS-22745	Frontzek, Matthias	WAND ² - Calibration and Standards Al2O3 · Aluminum ring and plug · H2O · KCl · NIST 640e Si · NaCl · Shielding material · Silicon · V SING

ONCat Instruments > HFIR / HB2C > Experiments

Filter by ID, Title, Team Member or Sample

IPTS	Team Member	Instrument Details
IPTS-7776	Fernandez-Baca, Jaime	WAND-Instrument time 1T-TiSe2 · 3D Printed collimator · BaTiO3 · Basanite · Boron coated carbon fiber · Ca2Ru(1-x)Fe(x)O4 · x
IPTS-22745	Frontzek, Matthias	WAND ² - Calibration and Standards Al2O3 · Aluminum ring and plug · H2O · KCl · NIST 640e Si · NaCl · Shielding material · Silicon · V SING

ONCat

Instruments

>

HFIR / HB2C

>

Experiments

>

IPTS-30754

>

Runs

xdh

(Hu, Xiao)

Logout

WAND² Info

Configure Tables

Download as CSV

ID	Sample		General		
	ID	Name	Created	Notes	Title
<div><div></div><div># 1,020,371</div><div>></div></div>	<div>87,904</div> <div>></div>	Ca0.6Sr0.4MnSb2	2023-06-09 19:51:09	-	Ca0.6Sr0.4MnSb2 T=10 K scan at Detz=0
<div><div></div><div># 1,020,370</div><div>></div></div>	<div>87,904</div> <div>></div>	Ca0.6Sr0.4MnSb2	2023-06-09 19:50:54	-	Ca0.6Sr0.4MnSb2 T=10 K scan at Detz=0
<div><div></div><div># 1,020,369</div><div>></div></div>	<div>87,904</div> <div>></div>	Ca0.6Sr0.4MnSb2	2023-06-09 19:50:39	-	Ca0.6Sr0.4MnSb2 T=10 K scan at Detz=0

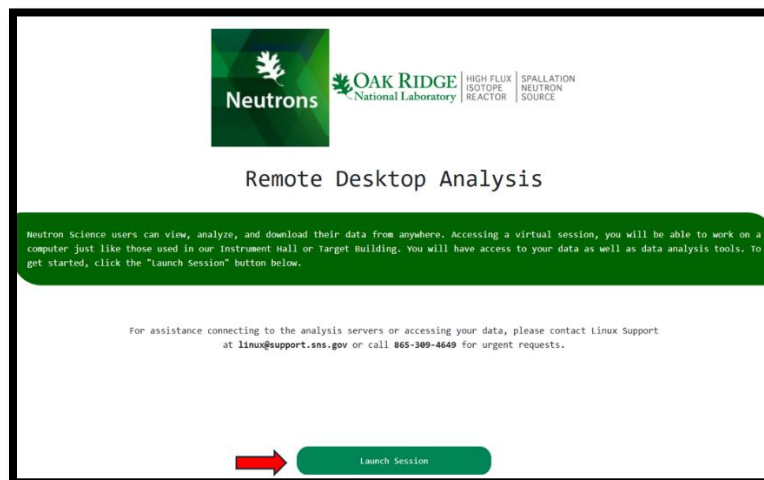
Note:

Vanadium calibration was usually performed before or at the beginning of each cycle. Users have access to the vanadium IPTS 23858. Use the vanadium run number that is closet (in timeline) to your beamtime.

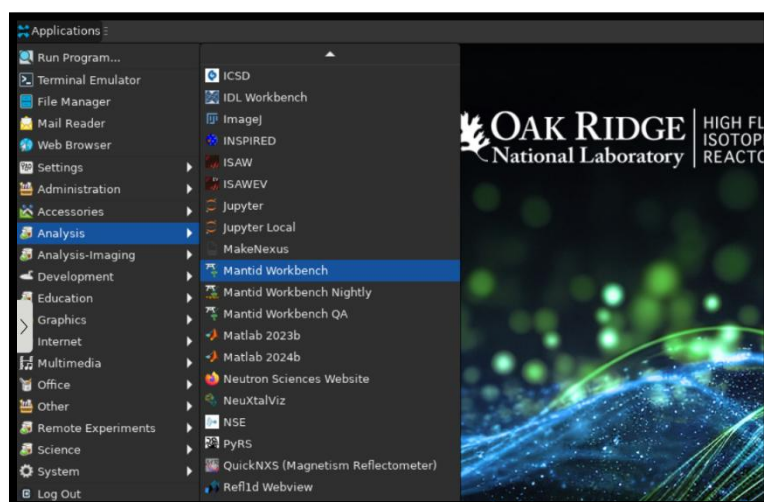
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(b) Open Mantid Workbench in analysis cluster

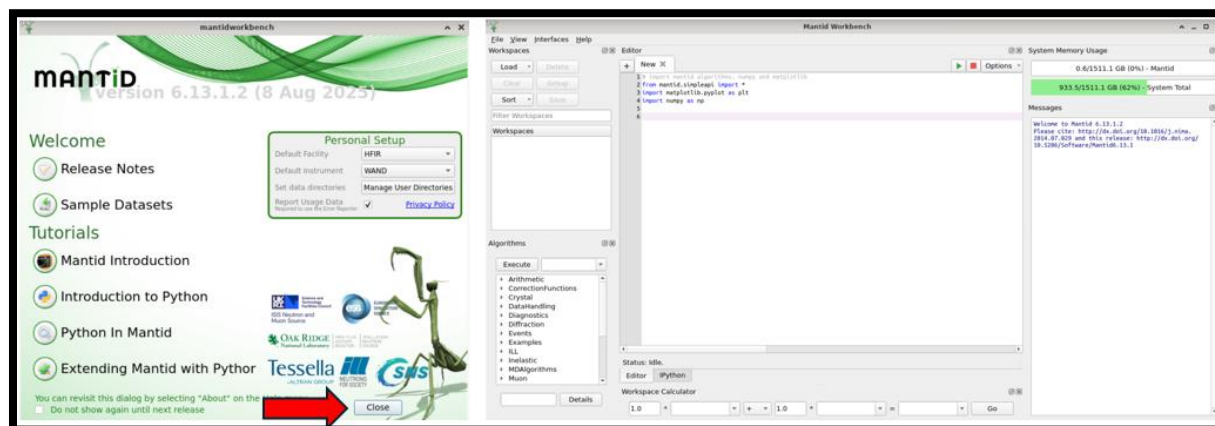
(1) Go to Remote Desktop Analysis at <https://analysis.sns.gov/> and log in with UCAMS username and password.



(2) Once logged in, on the left upper corner, go to Application → Analysis → Mantid Workbench.



(3) When Mantid Workbench opens, there will be an option to personalize the setup and tutorial available if needed. If a personalized setup is not necessary, close the Welcome window. You should see the Mantid graphical user interface on your screen.

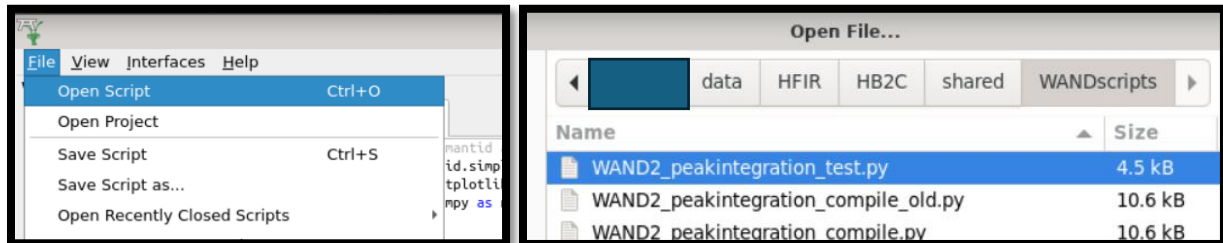


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III. Script execution in Mantid

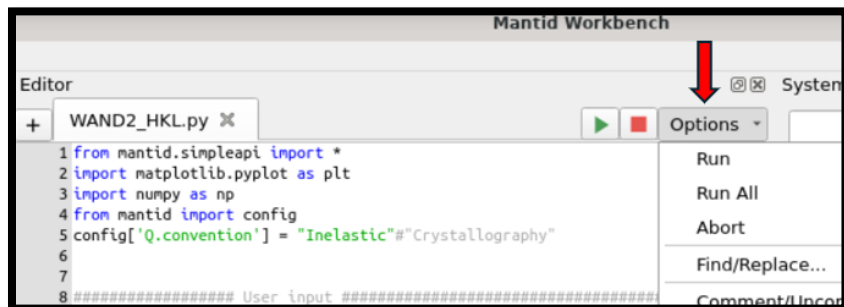
(a) Open script in Mantid

Go to **File** on the left upper corner of the Mantid interface and hit “**Open Script**” or **Ctrl + O**. Locate and open the target script.



(b) Execute (entire or part of) the script

(1) To execute the **entire script**, click **Options** on the upper right corner and select **Run All**.



(2) To execute **part of the script**, highlight the target part and click the **Run** button (**green triangle**).



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IV. Data slicing

There are two options for data slicing, involving two algorithms, respectively:

- **ConvertQtoHKLMDHisto**
- **ConvertWANDSCDtoQ**.

ConvertQtoHKLMDHisto uses data workspace (in reciprocal Q-space) generated during [peak analysis](#), but it does not deal with vanadium normalization properly. Thus, the other method involving **ConvertWANDSCDtoQ** is introduced here:

(1) Follow the path “data → HFIR → HB2C → shared → WANDscripts” and locate the script

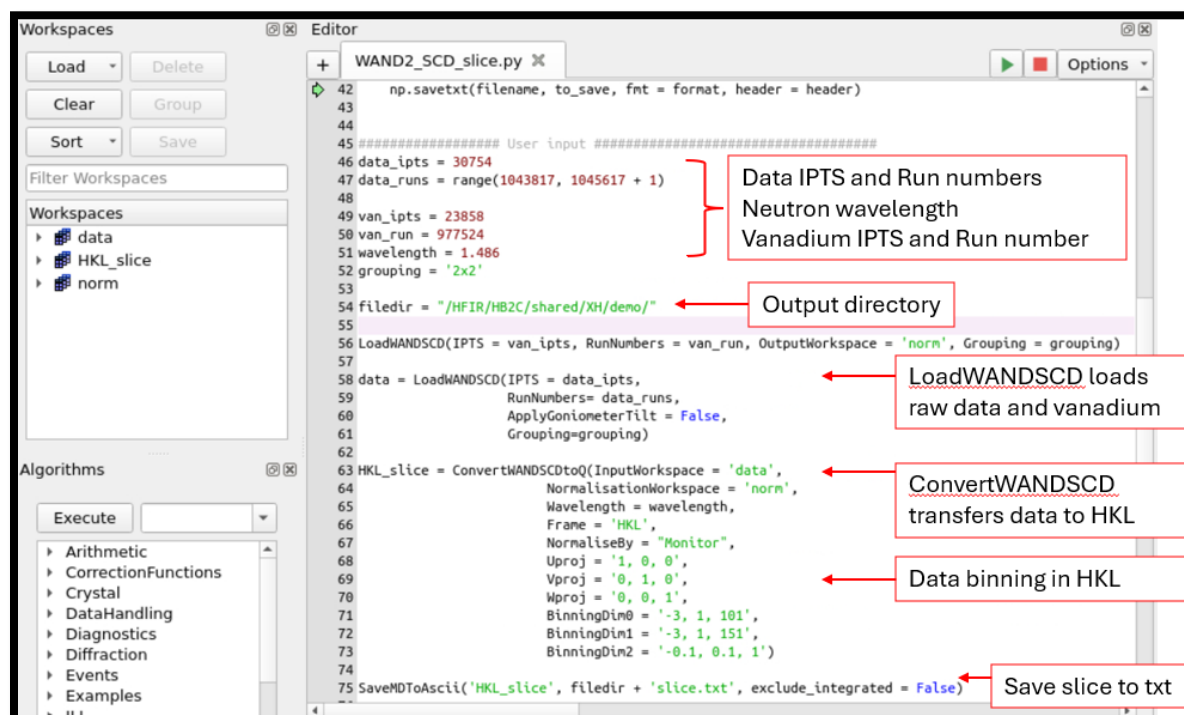
WAND2_SCD_slice.py

(2) Copy and paste it to your working directory.

(3) Open the script in Mantid by going to **File** on the left upper corner of the Mantid interface and hitting “**Open Script**” or **Ctrl + O**. Locate your working directory and select the script.

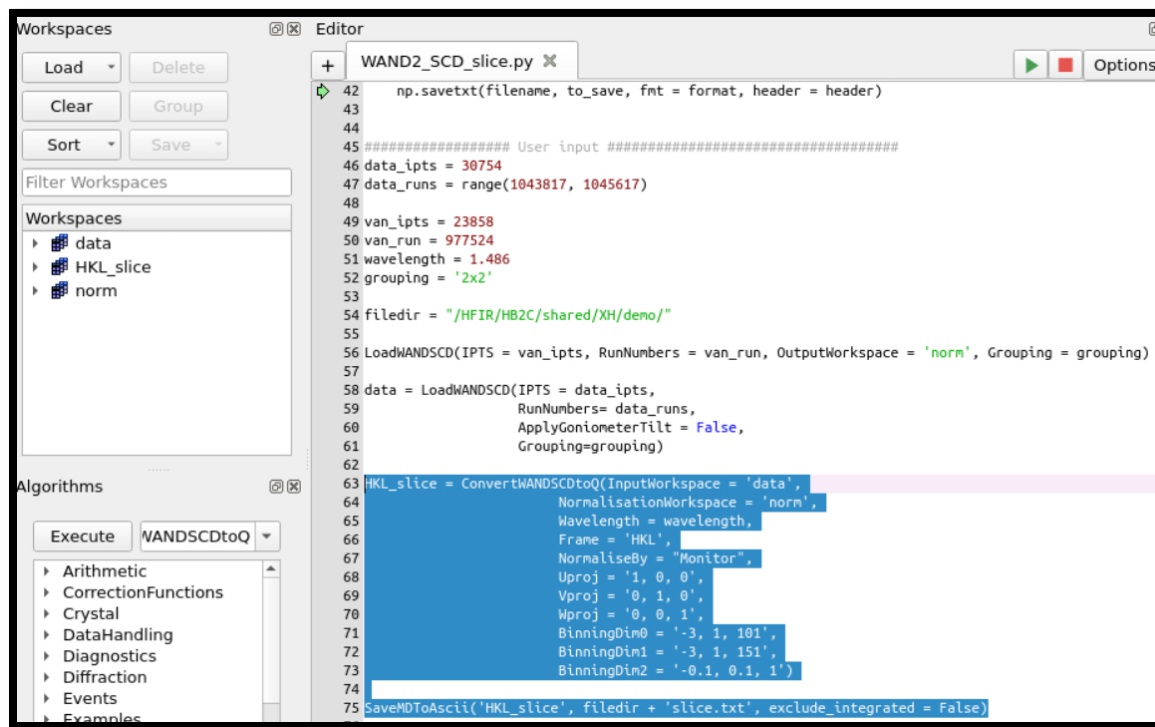
(4) The script looks like below. Command lines before line 43 define a file-saving function **SaveMDToAscii**. It saves the output to the customized directory in ASCII format.

(5) Modify relevant parameters (explained in the *Note* below) and execute the entire script by going to **Options** on the upper right corner and selecting **Run All**.



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(6) To revise the sliced data (e.g., binning size, Frame), modify relevant parameters in the **ConvertWANDSCDtoQ** command lines, highlight the relevant command lines (as shown below for example), and hit **Run** button (green triangle button) on the upper right corner.



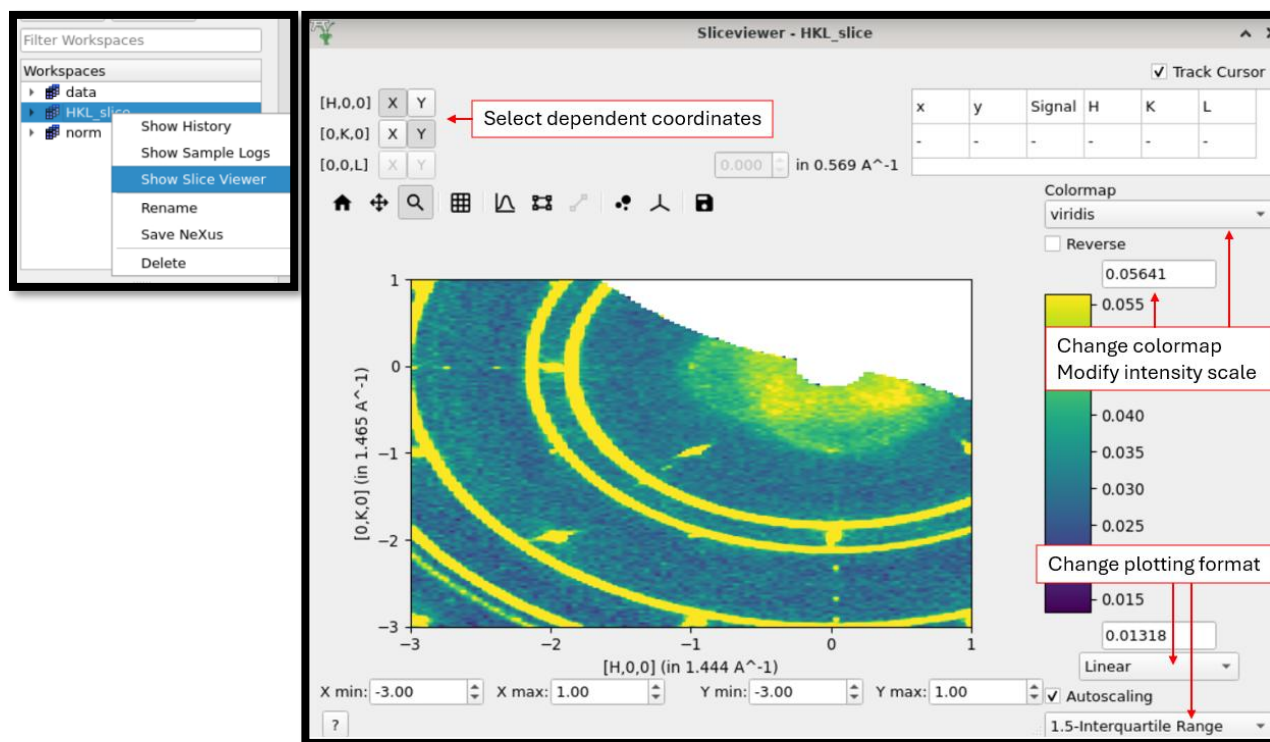
Note:

- Users need to input the **data IPTS** and **run numbers**, along with the **vanadium IPTS** and **run number**. Data run numbers are in the format of a python list. It could be
 - `range(start, end + 1)` (as shown in the screenshot above)
 - `[run1, run2, run3, ...]`
 - `list(range(start1, end1 + 1)) + list(range(start2, end2 + 1))`
- **wavelength** is the incident neutron beam wavelength. **grouping** is for faster data processing. It has options: "2x2", "4x4", "None". **filedir** is the directory path to save output files. Modify it to your working directory.
- **LoadWANDSCD** loads data and vanadium files into Mantid workspaces, **data** and **norm** here, which will appear in the left-hand side "Workspace" window after execution. Modify the name of the **OutputWorkspace** if necessary.
- **ConvertWANDSCDtoQ** will bin and slice data in a customized style.
 - Input data and vanadium workspace. (vanadium is for normalization)

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- **Frame** can be “HKL” or “Q_sample”. “Q_sample” has a unit of \AA^{-1} .
- **NormalizeBy** has multiple choices: “Monitor”, “Time”, “None”.
- **Uproj, Vproj, Wproj** are basis vectors defining data binning dimensions.
- **BinningDim0,1,2** refer to data binning sizes along **Uproj, Vproj, Wproj**, respectively. Format: “start, end, number of points”.
- **SaveMDtoAscii** saves output sliced data into ASCII files. In the example, the sliced data is the workspace **HKL_slice**.

(3) To view the sliced data in Mantid, right-click the data workspace in the “Workspaces” window on the left-hand side and select **Show Slice Viewer**. A slice viewer window will pop up (shown below).



Note:

The **Show Slice Viewer** visualizes the data in the reciprocal space, enables fast data inspection, and helps users do further data slicing/cutting. Move the mouse to each button and icon to see the pop-up illustration of its functionality.

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V. Peak analysis

(a) Data loading

(1) Follow the path “data → HFIR → HB2C → shared → WANDscripts” and locate the script

WAND2_SCD_peaks.py

(2) Copy and paste it to your working directory.

(3) Open the script in Mantid by going to **File** on the left upper corner of the Mantid interface and hitting “**Open Script**” or **Ctrl + O**. Locate your working directory and select the script. The script looks like below.

(4) Input data IPTS and run numbers, and incident neutron wavelength.

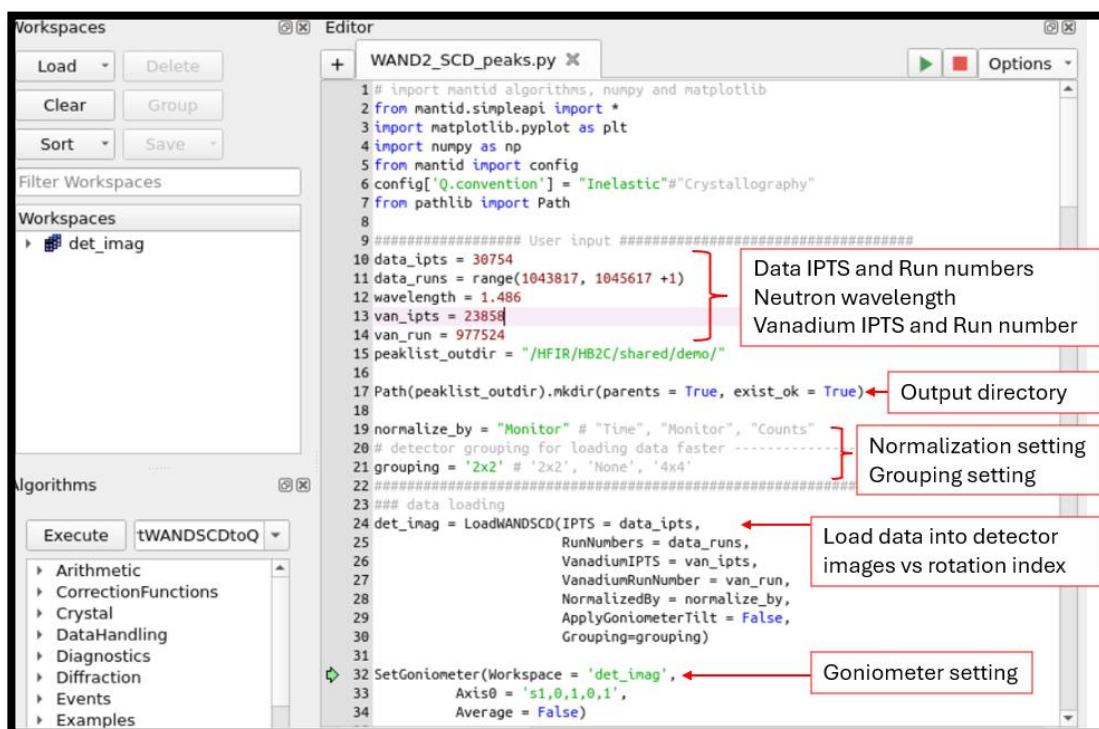
(5) Input vanadium IPTS 23858 and run number.

(6) Input the output directory path (to save output files).

(7) Choose **normalize_by**, “Monitor” or “Time” or “None”. “Monitor” and “Time” are commonly used.

(8) Choose **grouping**, “2x2” or “4x4” or “None”. It is recommended to use “2x2”.

(9) Highlight command lines (line 1 to 34) and hit **Run** (green triangle).

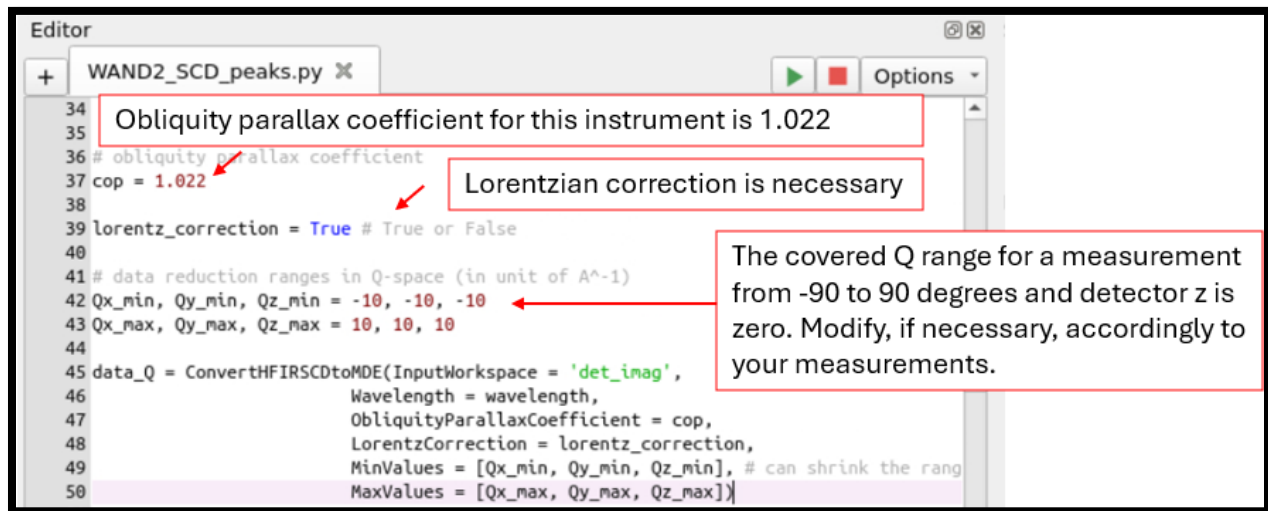


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Note:

- **LoadWANDSCD** loads data files into Mantid workspace, **det_imag**, as shown in the “Workspaces” window on the left-hand side of the interface. Modify workspace name as needed.
- **SetGoniometer** defines the goniometer rotation axis \rightarrow s1 motor rotation, about the vertical axis. Horizontal plane is the scattering plane at WAND².

(b) Convert data into reciprocal Q-space



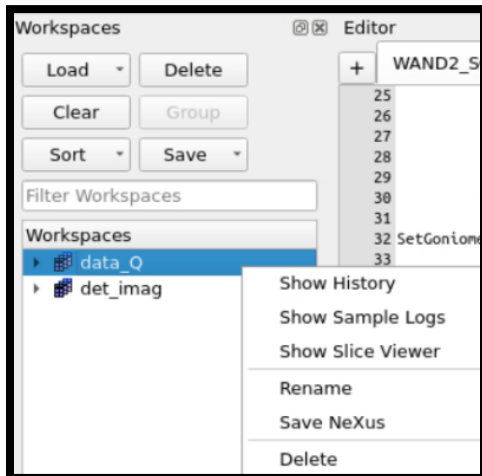
- (1) Set the obliquity parallax coefficient.
- (2) Set **lorentz_correction** = True.
- (3) Set Q-range for peak search. Unit: \AA^{-1} .
- (4) Highlight command lines (line 37 to 50) shown below and hit **Run** (green triangle).

Note:

- After it has finished running, a workspace **data_Q** appears in the “Workspaces” window on the left-hand side of the interface, which contains data in the reciprocal Q-space (**Q_sample**). Right-click on the workspace **data_Q** and select **Show Slice Viewer** to see what it looks like.
- Once the slice viewer window opens, there are several options to adjust the plot:
 - Select different dependent coordinates for 2D plotting.

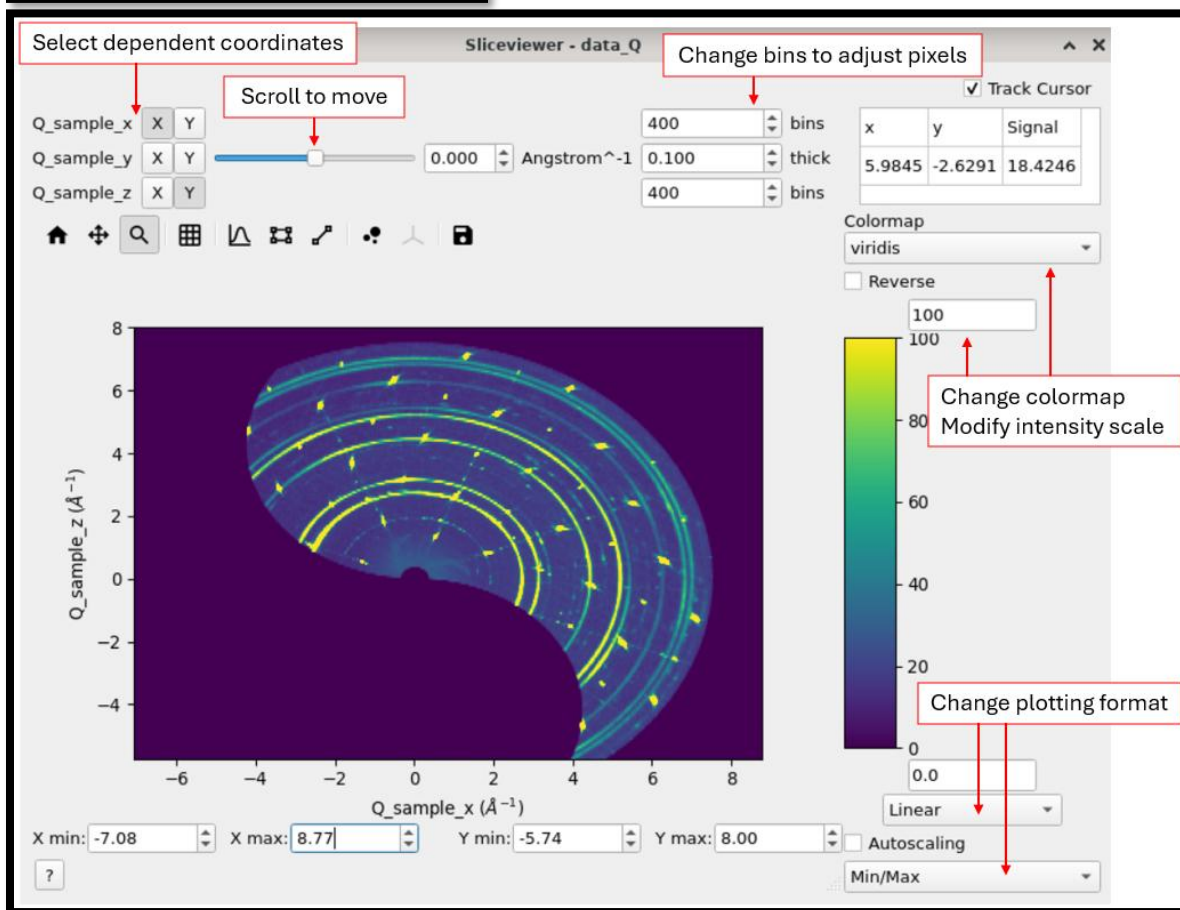
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- Scroll the 3rd coordinate to see different slicing.
- Adjust data bin size.
- Adjust intensity and colormap scales.



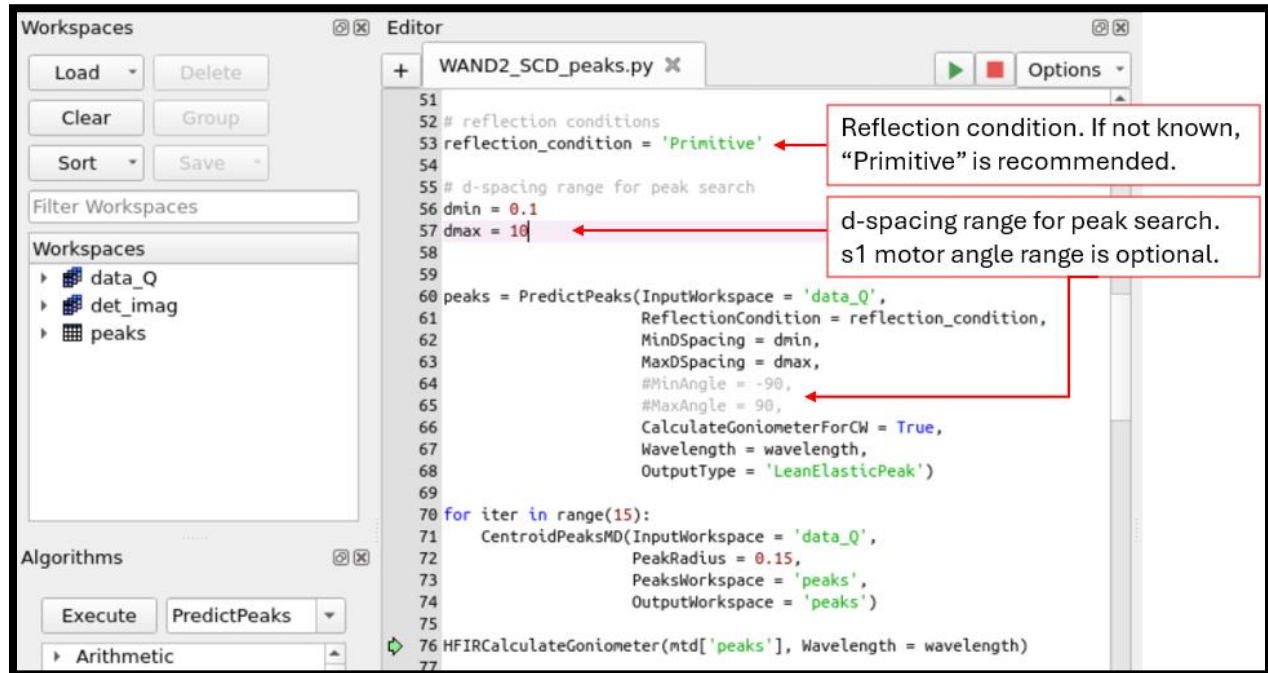
Note:

In the reciprocal Q-space (Q_{sample}), the goniometer tilting information is contained in the data. Usually, the sample is not perfectly aligned in the horizontal scattering plane, so we will see that the entire contour plot is “tilted” away from canonical xyz mesh grid.



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(c) Predict and index peaks



(1) As shown above, set **reflection_condition**. Available choices:

- "Primitive"
- "C-face centred"
- "A-face centred"
- "B-face centred"
- "Body centred"
- "All-face centred"
- "Rhombohedrally centred, obverse"
- "Rhombohedrally centred, reverse"
- "Hexagonally centred, reverse"

When not sure / want every possible peak, choose "Primitive".

(2) Set d-spacing range, **dmin** and **dmax**.

Or comment out "**MinDSpacing**" and "**MaxDSpacing**" lines, and use "**MinAngle**" and "**MaxAngle**" lines for peak search with a customized s1 motor angle range.

(3) Highlight command lines (line 53 to 76) shown below and hit **Run** (green triangle).

(4) A new workspace, **peaks**, appears in the "Workspaces" window. Right-click it and select **Show Data** to see its content → peak information summary (such as HKL index, wavelength, DSpacing, Qlab, Qsample).

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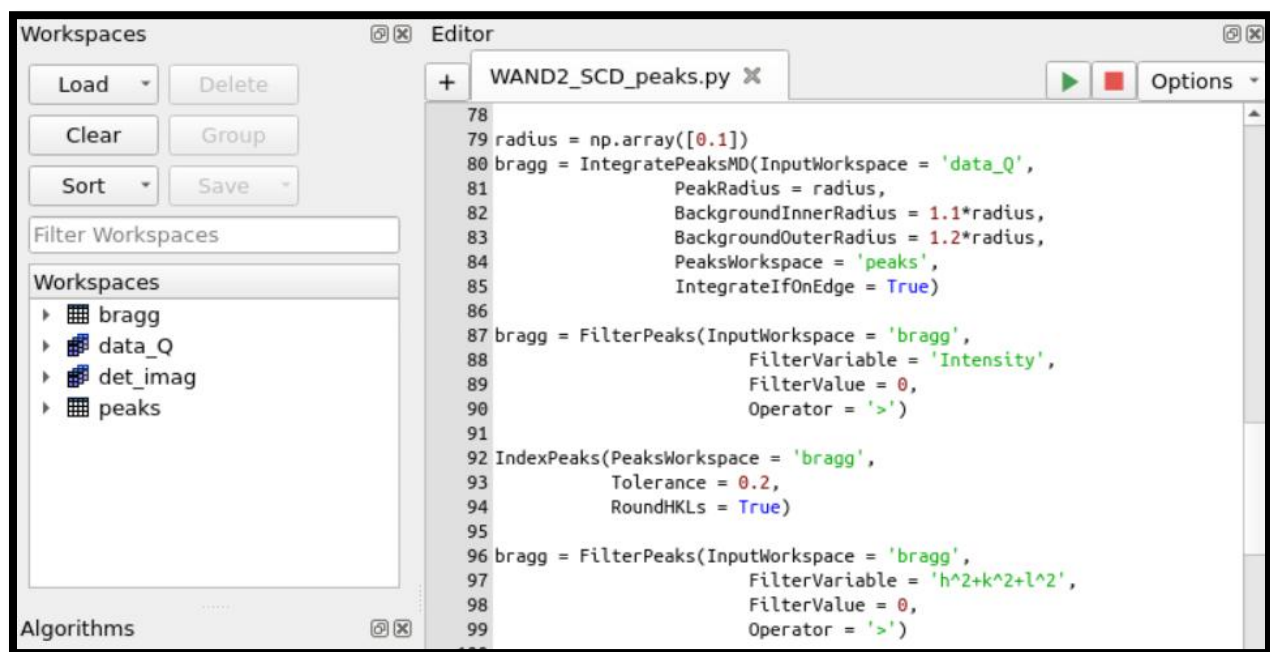
Note:

- **CentroidPeaksMD** algorithm helps optimize the peak center (“center of intensity”) for each peak in the Q-space.
- **HFIRCalculateGoniometer** algorithm recalculates the corresponding goniometer matrix for each peak with the incident neutron wavelength after peak center optimization.
- Peaks that are out of detectable range are also predicted. That’s the reason we need to filter them out next.

(d) Filter peaks (integer-HKL peaks)

(1) Set **radius** for parent peak filtering.

(2) Highlight command lines (line 79 to 99) shown below and hit the **Run** button (green triangle). A new workspace **bragg** will appear in the “Workspaces” window on the left.



Note:

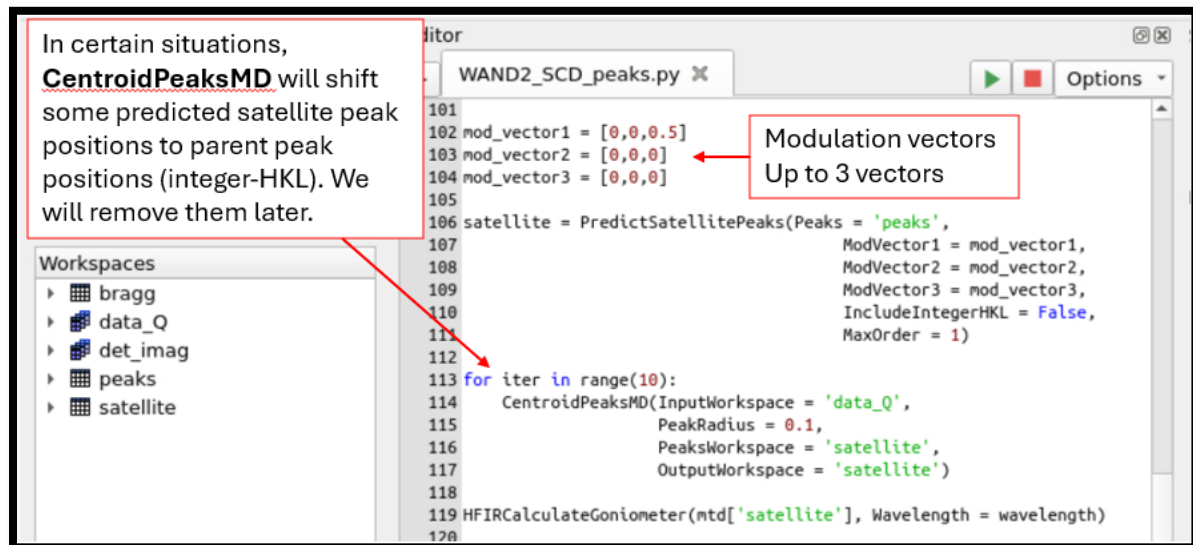
- This part of command lines works as an intensity filter for parent peaks (integer-HKL indices).

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- **IntegratePeaksMD** algorithm generates a sphere (or ellipsoid if a 3-number array is given to **radius**) centered at each peak with the preset radius (0.1 is sufficient. Unit: \AA^{-1}) and integrates data within the sphere. **BackgroundInner/OuterRadius** is used for background estimation. The algorithm returns an estimation of peak intensities.
- **FilterPeaks** algorithm filters peaks based on the **FilterVariable** and **FilterValue**. For example, **FilterVariable** = “Intensity” with **FilterValue** = 0 means only peaks with intensities > 0 are kept. This will remove those peaks that are out of detectable range. **FilterVariable** = “Signal/Noise” with **FilterValue** = 1 is also commonly used to filter peaks.
- **IndexPeaks** algorithm will index the remaining peaks with H, K, L within the tolerance. If a peak cannot be indexed, it will have H, K, L = 0, 0, 0, and will be filtered out by the subsequent **FilterPeaks** with constraint of $h^2 + k^2 + l^2 > 0$.

(e) Predict, index, and filter satellite peaks

- (1) Set modulation vectors for satellite peaks.
- (2) Highlight command lines (line 102 to 119) shown below and hit the **Run** button (green triangle).



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- (3) A new workspace **satellite** will appear in the “Workspaces” window. Right-click it and select **Show Data** to see its content.
- (4) Set **radius** for satellite peak filtering. Similar procedures as parent peak filtering.
- (5) Highlight command lines (line 121 to 145) shown below and hit the **Run** button (green triangle).

```

120
121 radius = np.array([0.1])
122 satellite = IntegratePeaksMD(InputWorkspace = 'data_Q',
123                             PeakRadius = radius,
124                             BackgroundInnerRadius = 1.1*radius,
125                             BackgroundOuterRadius = 1.2*radius,
126                             PeaksWorkspace = 'satellite',
127                             IntegrateIfOnEdge = True)
128
129 satellite = FilterPeaks(InputWorkspace = 'satellite',
130                         FilterVariable = 'Intensity',
131                         FilterValue = 0,
132                         Operator = '>')
133
134 IndexPeaks(PeaksWorkspace = 'satellite',
135            Tolerance = 0.2,
136            RoundHKLS = True)
137
138 no = 0
139 while no < satellite.getNumberPeaks():
140     p = satellite.getPeak(no)
141     [h,k,l] = p.getHKL()
142     if ((h==0)&(k==0)&(l==0)) | ((h%1==0)&(k%1==0)&(l%1==0)):
143         DeleteTableRows(satellite, Rows = no)
144     else:
145         no += 1

```

Remove 000- or integer-HKL peaks

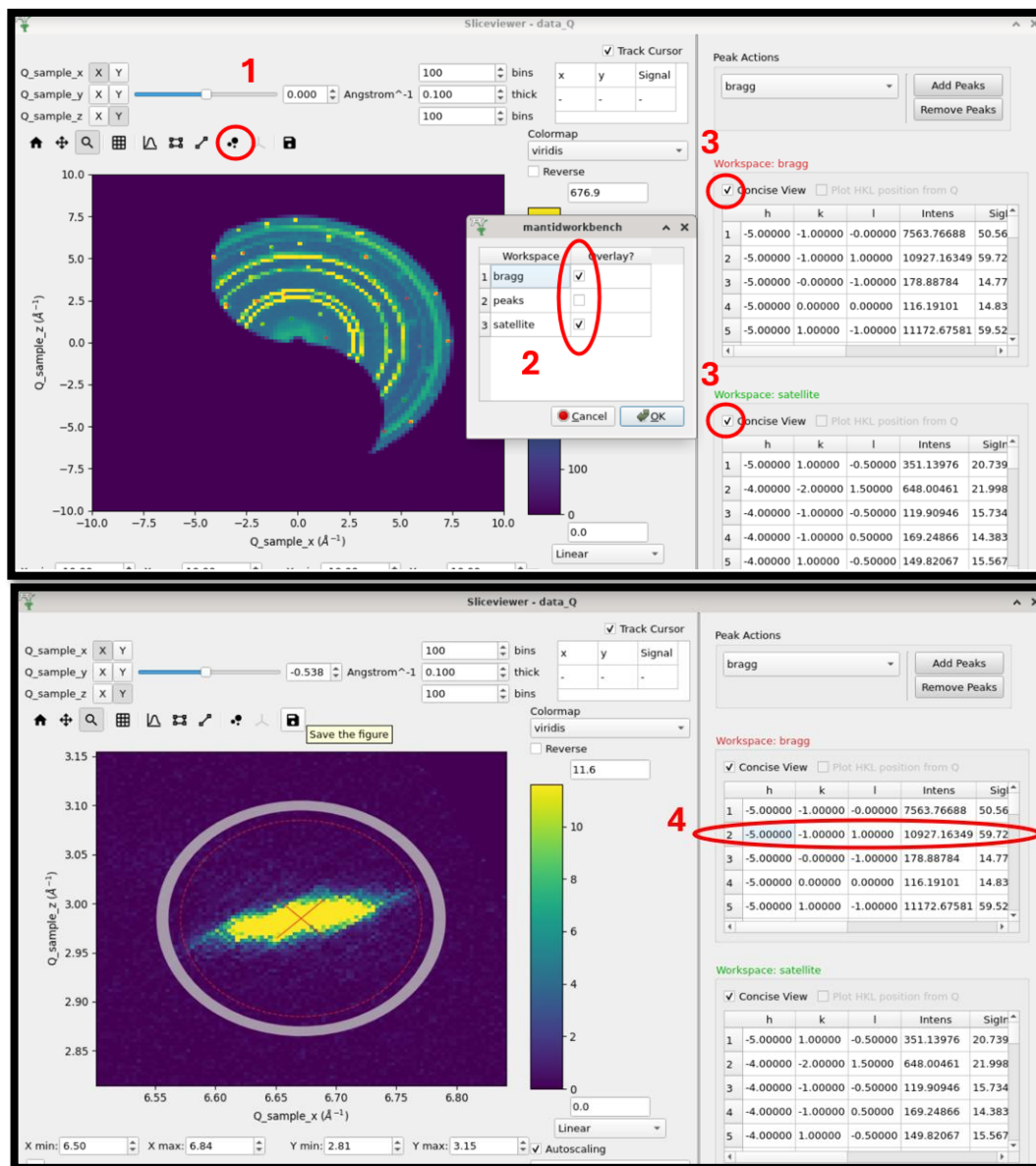
Note:

- **PredictSatellitePeaks** algorithm predicts satellite peaks based on the input modulation vectors and a parent peak workspace **peaks**.
- If there is no peak intensity at the predicted satellite peak position, **CentroidPeaksMD** may optimize them to the nearby parent peak position. That's why we use line 139 to 145 to remove them from the satellite peak workspace.
- Line 139 to 145 will remove peaks indexed as (000) or integer-HKL in the workspace **satellite**.

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(f) Inspect peaks in Slice Viewer

- (1) Right-click **data_Q** in the “Workspaces” window and select **Show Slice Viewer**.
- (2) In the slice viewer window, click “Add peaks overlays” button (step 1), shown below.
- (3) Check the target peak workspace (step 2) in the pop-up window and click OK. The workspace content will be listed on the right-hand side.
- (4) Check “Concise View” (step 3).
- (5) Click on any peak in the right-hand side window (step 4), for example (-5, -1, 1) here. The peak statistics will be highlighted in the left-hand side contour plot. The **red cross** in the plot is the peak center. Details will be covered in the later “Integrate peaks” section.

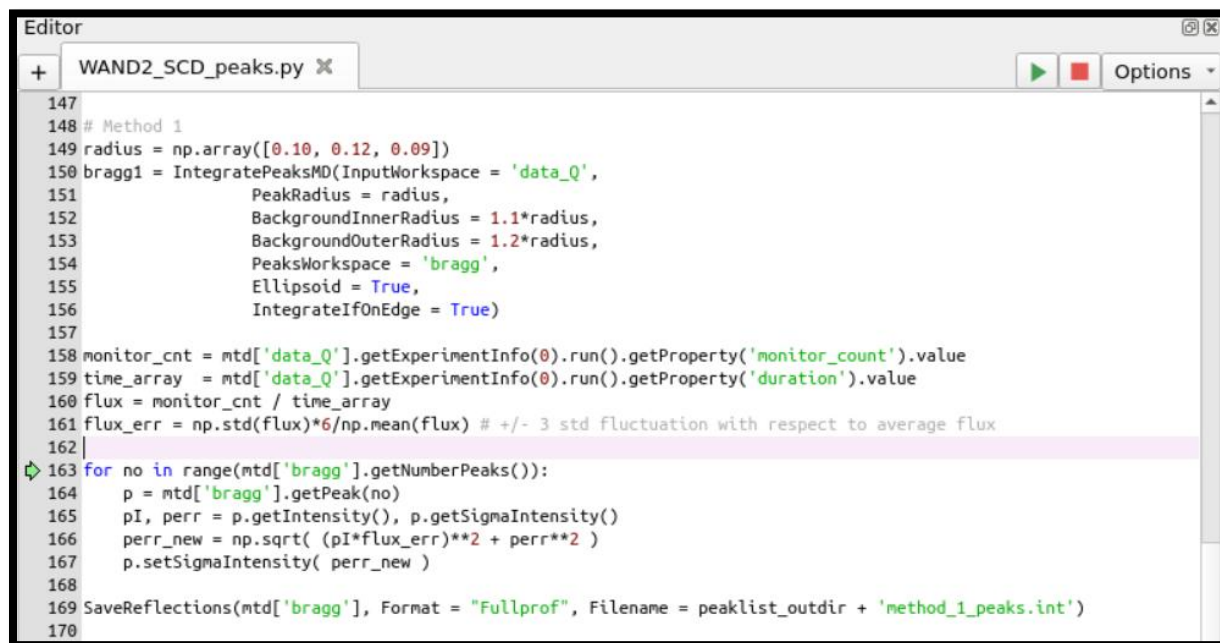


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(g) Integrate peaks

(i) Method 1: IntegratePeaksMD

- (1) Set **radius** for peak integration in the command lines (line 149 to 156) shown below. In practice, a Bragg peak in Q-space does not have a perfect spherical profile. Instead of sphere, we use a 3D ellipsoid to do peak integration (as shown below, the command line “**Ellipsoid = True**” in the **IntegratePeaksMD** algorithm). The ellipsoid calls for 3 radii, which are semi-axis in Q_sample_x, Q_sample_y, Q_sample_z directions. Make sure the ellipsoid is big enough to cover the peak.
- (2) Adjust **BackgroundInner/OuterRadius** coefficients. (Here are 1.1 and 1.2, respectively)
- (3) Highlight these command lines (line 149 to 169) and hit **Run** (green triangle).
- (4) Replace all **bragg** strings with **satellite** strings and change output file name when integrating satellite peaks in the same way.
- (5) The for-loop (line 158 to 167) is to revise the errors of peak intensities, considering the uncertainty (%) of neutron beam flux.
- (6) If the peak integration is not ideal, consider changing **radius** to re-integrate the peaks.



```

147
148 # Method 1
149 radius = np.array([0.10, 0.12, 0.09])
150 bragg1 = IntegratePeaksMD(InputWorkspace = 'data_Q',
151                             PeakRadius = radius,
152                             BackgroundInnerRadius = 1.1*radius,
153                             BackgroundOuterRadius = 1.2*radius,
154                             PeaksWorkspace = 'bragg',
155                             Ellipsoid = True,
156                             IntegrateIfOnEdge = True)
157
158 monitor_cnt = mtd['data_Q'].getExperimentInfo(0).run().getProperty('monitor_count').value
159 time_array = mtd['data_Q'].getExperimentInfo(0).run().getProperty('duration').value
160 flux = monitor_cnt / time_array
161 flux_err = np.std(flux)*6/np.mean(flux) # +/- 3 std fluctuation with respect to average flux
162
163 for no in range(mtd['bragg'].getNumberPeaks()):
164     p = mtd['bragg'].getPeak(no)
165     pI, perr = p.getIntensity(), p.getSigmaIntensity()
166     perr_new = np.sqrt( (pI*flux_err)**2 + perr**2 )
167     p.setSigmaIntensity( perr_new )
168
169 SaveReflections(mtd['bragg'], Format = "Fullprof", Filename = peaklist_outdir + 'method_1_peaks.int')
170

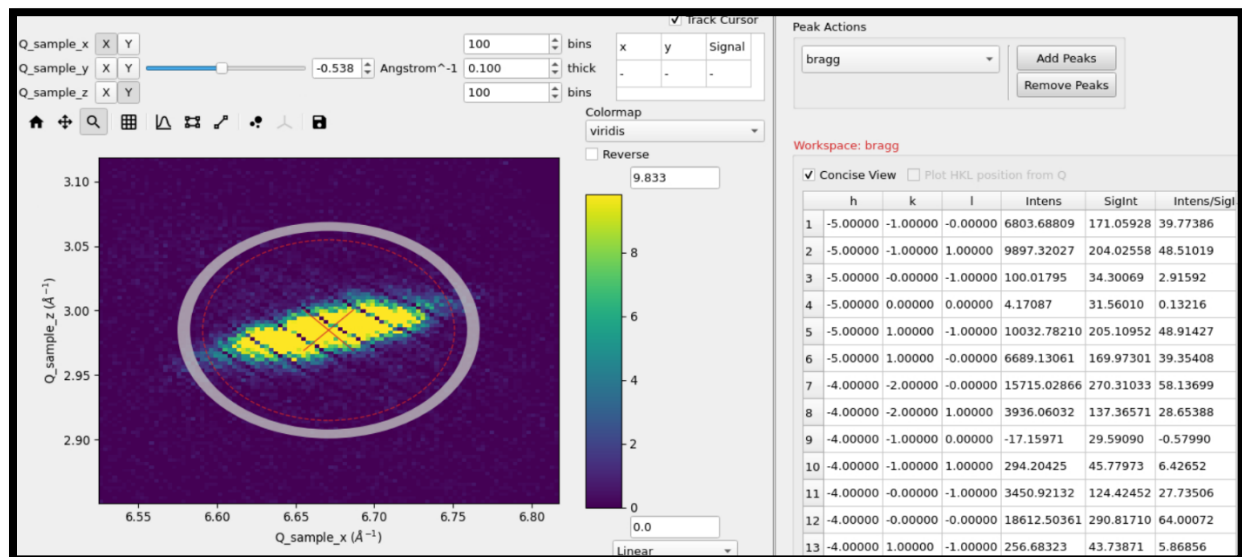
```

Note:

- A percentage uncertainty coming from neutron beam fluctuation is propagated into the estimation of peak intensity error. The percentage uncertainty is included in Method 2 as well.

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- **SaveReflections** saves the peak workspace into a readable peak file for later refinement. Available formats:
 - “Fullprof”
 - “GSAS”
 - “Jana”
 - “SHELX”
- Details of **IntegratedPeaksMD** can be found on <https://docs.mantidproject.org/nightly/algorithms/IntegratePeaksMD-v2.html>.
- After execution, open **data_Q** in the slice viewer.
 - Add peak overlays as we do in the “Inspect peaks in Slice Viewer” section.
 - Click on any peak to check integration statistics. The integration ellipsoid will be visualized on the left-hand side, shown below.
 - The **red cross** is the peak center.
 - The **red dash ellipse** is the 3D ellipsoid range.
 - The **grey ring** is the region of background estimation, determined by **BackgroundInner/OuterRadius**.
- The error (**SigInt** shown in the table below) of the integrated peak intensity obtained from **IntegratedPeaksMD** is highly dependent on **BackgroundInner/OuterRadius** (try different settings to see the dependence). The percentage uncertainty is additionally propagated to the intensity error to alleviate the problem.



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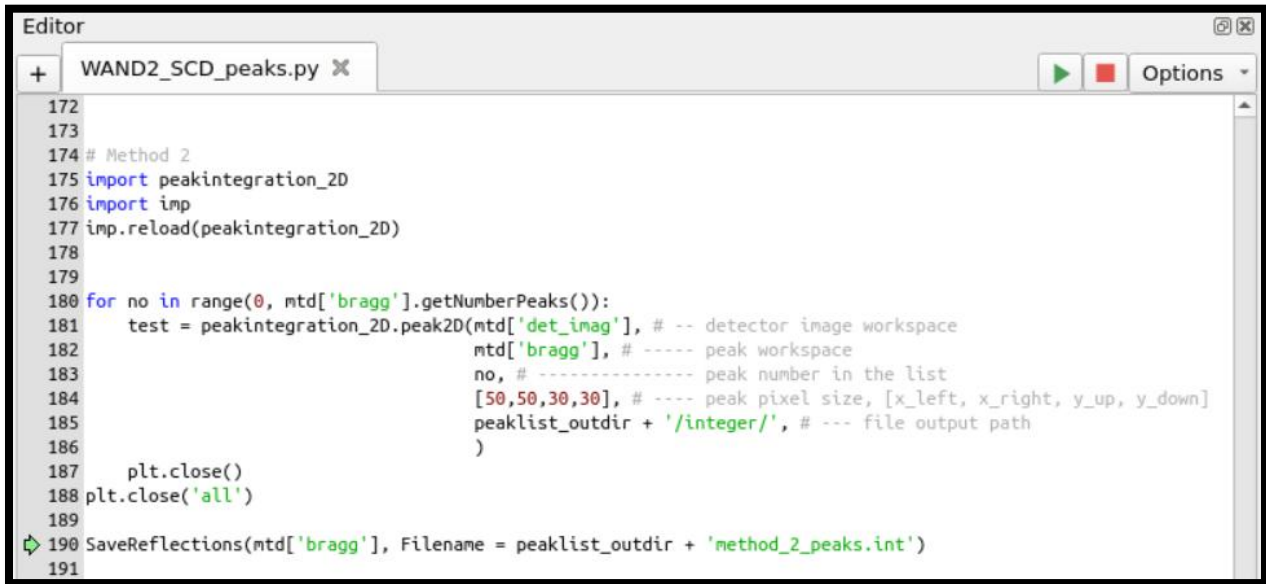
(ii) Method 2: Detector image integration

(1) Follow the path “/data/HFIR/shared/WANDscripts/” and locate the script

peakintegration_2D.py

(2) Copy and paste this python file into your working directory.

(3) Highlight command lines (line 175 to 190) shown below and hit the **Run** button (green triangle).

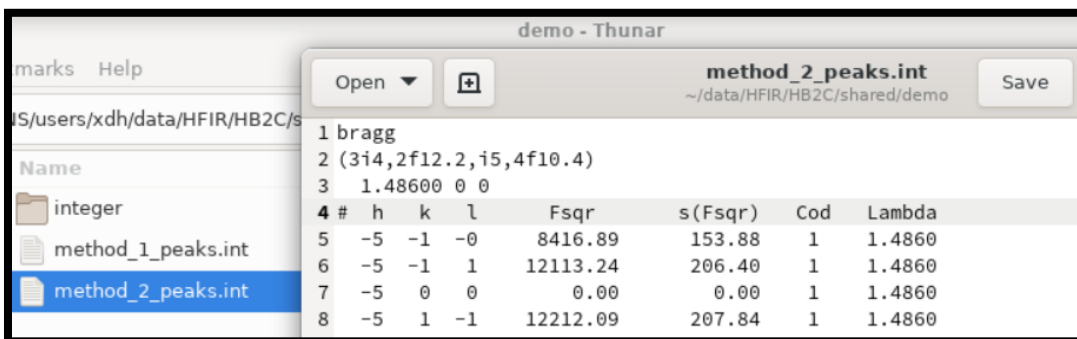


```

172
173
174 # Method 2
175 import peakintegration_2D
176 import imp
177 imp.reload(peakintegration_2D)
178
179
180 for no in range(0, mtd['bragg'].getNumberPeaks()):
181     test = peakintegration_2D.peak2D(mtd['det_imag'], # -- detector image workspace
182                                     mtd['bragg'], # ---- peak workspace
183                                     no, # ----- peak number in the list
184                                     [50,50,30,30], # ---- peak pixel size, [x_left, x_right, y_up, y_down]
185                                     peaklist_outdir + '/integer/', # --- file output path
186                                     )
187     plt.close()
188 plt.close('all')
189
190 SaveReflections(mtd['bragg'], Filename = peaklist_outdir + 'method_2_peaks.int')
191

```

(4) In the output directory, a corresponding folder containing png files of peak statistics and a peak list file (.int) are generated.



4 #	h	k	l	Fsqr	s(Fsqr)	Cod	Lambda
5	-5	-1	-0	8416.89	153.88	1	1.4860
6	-5	-1	1	12113.24	206.40	1	1.4860
7	-5	0	0	0.00	0.00	1	1.4860
8	-5	1	-1	12212.09	207.84	1	1.4860

Note:

- Parameter setting and explanation details can be found in the [Appendix](#).
- To integrate satellite peaks, replace **bragg** strings with **satellite** strings, and replace the directory path and output file name with other distinguishable names as needed.
- In rare cases, if the integration fails for some peak(s), think about using **IntegratePeaksMD** (Method 1) to deal with it(them) specifically.

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Appendix

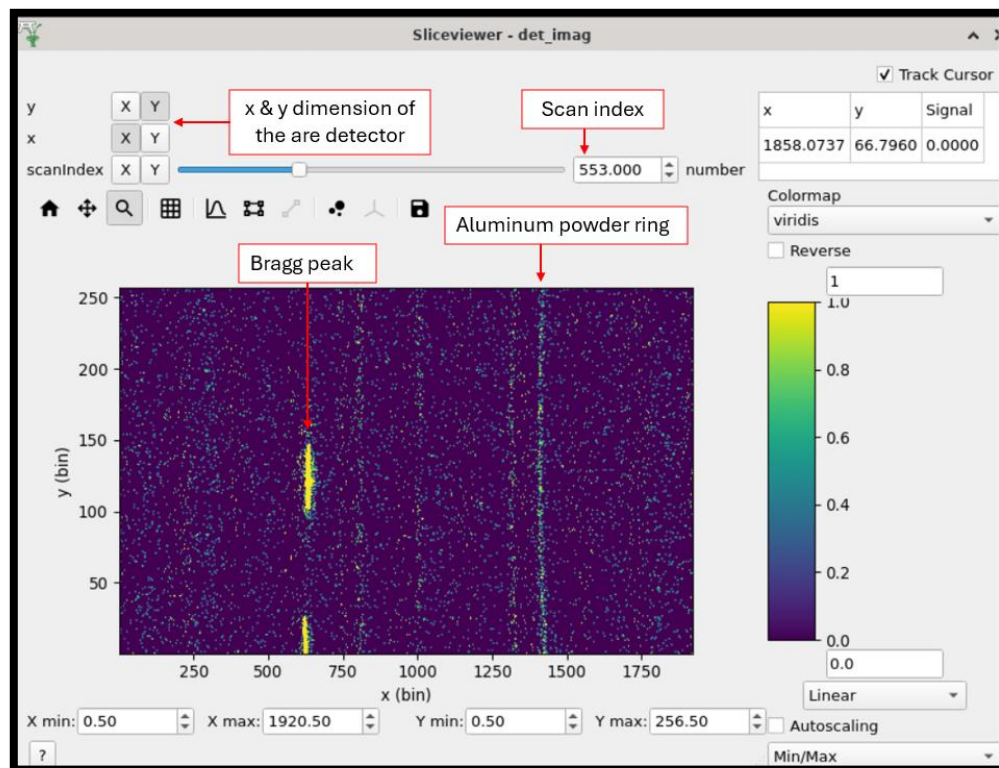
(a) Peak integration algorithm details (Method 2)

(1) Data

We first look at the data we use for peak integration --- detector image workspace.

Right-click **det_imag** workspace and select **Show Slice Viewer**. A window containing the detector images will pop up (shown below).

- **scanIndex** is the number of the scan, which corresponds to an s1 motor angle value. If the measurement is a 180-degree rotation scan with a step size of 0.1 degree, there will be in total $180/0.1 = 1800$ scans, and **scanIndex** will be 1~1800.
- **x & y** (or xbin & ybin) are dimensions of the area detector. There are in total $3840 \times 512 = 1966080$ detector pixels in the area detector, xbin = 1~3840, ybin = 1~512. Here we chose grouping = '2x2', so the regrouped xbin = 1~1920, ybin = 1~256.
- Bright spot in the 2D contour plot is a Bragg peak. Due to instrument resolution, the spot is elongated along the vertical direction (ybin). Aluminum powder ring can be seen as well.



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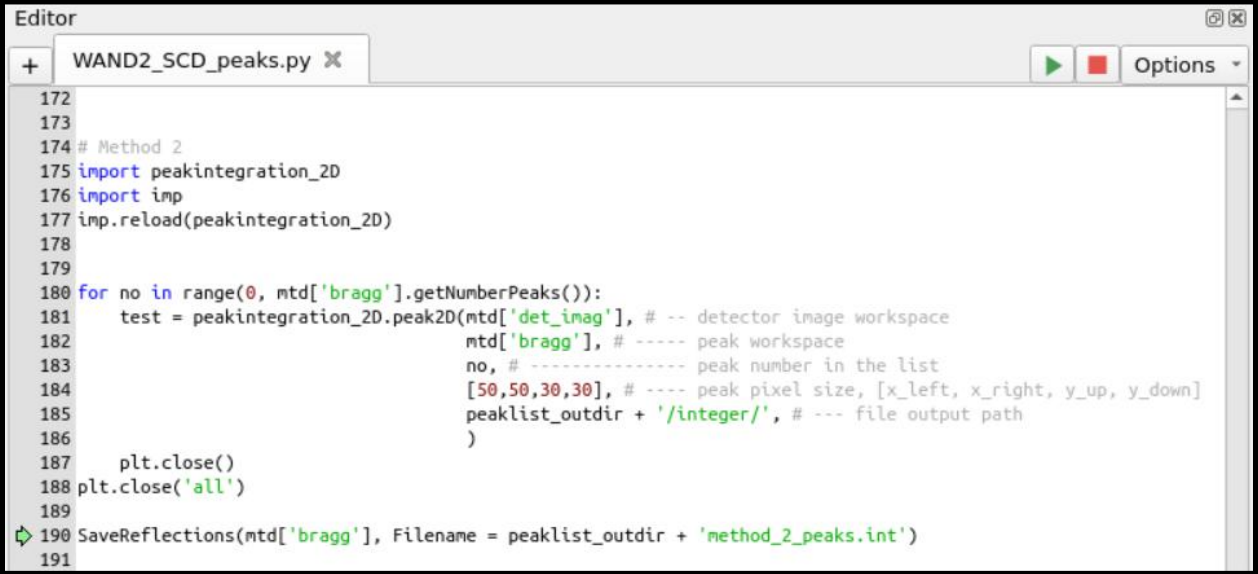
(2) Algorithm input parameters

As shown below, the algorithm calls for: (workspace names are free to change)

- **det_imag** ----- detector image workspace, generated during data loading
- **bragg** ----- target peak workspace
- **no** ----- peak number in the peak workspace, start from 0 (python gauge)
- **[x_left, x_right, y_up, y_down]** ----- 4-number array. It is the peak ROI size for integration (explained in “Algorithm output 2” later)
- **file output path** ----- a string describing the output directory path
- In **SaveReflections**, a file name is needed to store output peak information

Note:

- “mtd” is a built-in function in Mantid. It assigns a handle to the workspace.
- “test” in line 181 means nothing, just a handle to execute algorithm.



```

172
173
174 # Method 2
175 import peakintegration_2D
176 import imp
177 imp.reload(peakintegration_2D)
178
179
180 for no in range(0, mtd['bragg'].getNumberPeaks()):
181     test = peakintegration_2D.peak2D(mtd['det_imag'], # -- detector image workspace
182                                     mtd['bragg'], # ---- peak workspace
183                                     no, # ----- peak number in the list
184                                     [50,50,30,30], # ---- peak pixel size, [x_left, x_right, y_up, y_down]
185                                     peaklist_outdir + '/integer/', # --- file output path
186                                     )
187     plt.close()
188 plt.close('all')
189
190 SaveReflections(mtd['bragg'], Filename = peaklist_outdir + 'method_2_peaks.int')
191

```

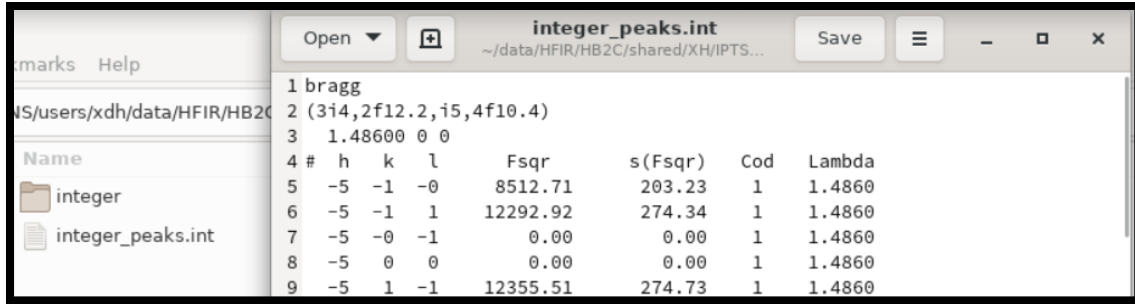
(3) Algorithm output 1 --- peak list .int file

SaveReflections (line 190) will save the target peak workspace into a peak list .int file in the output directory. The output file contains peak information, such as peak indices, intensity, and error for refinement (snapshot shown next for FullProf format).

Note:

Peak intensity = 0 means the peak is rejected. Remove it from the refinement.

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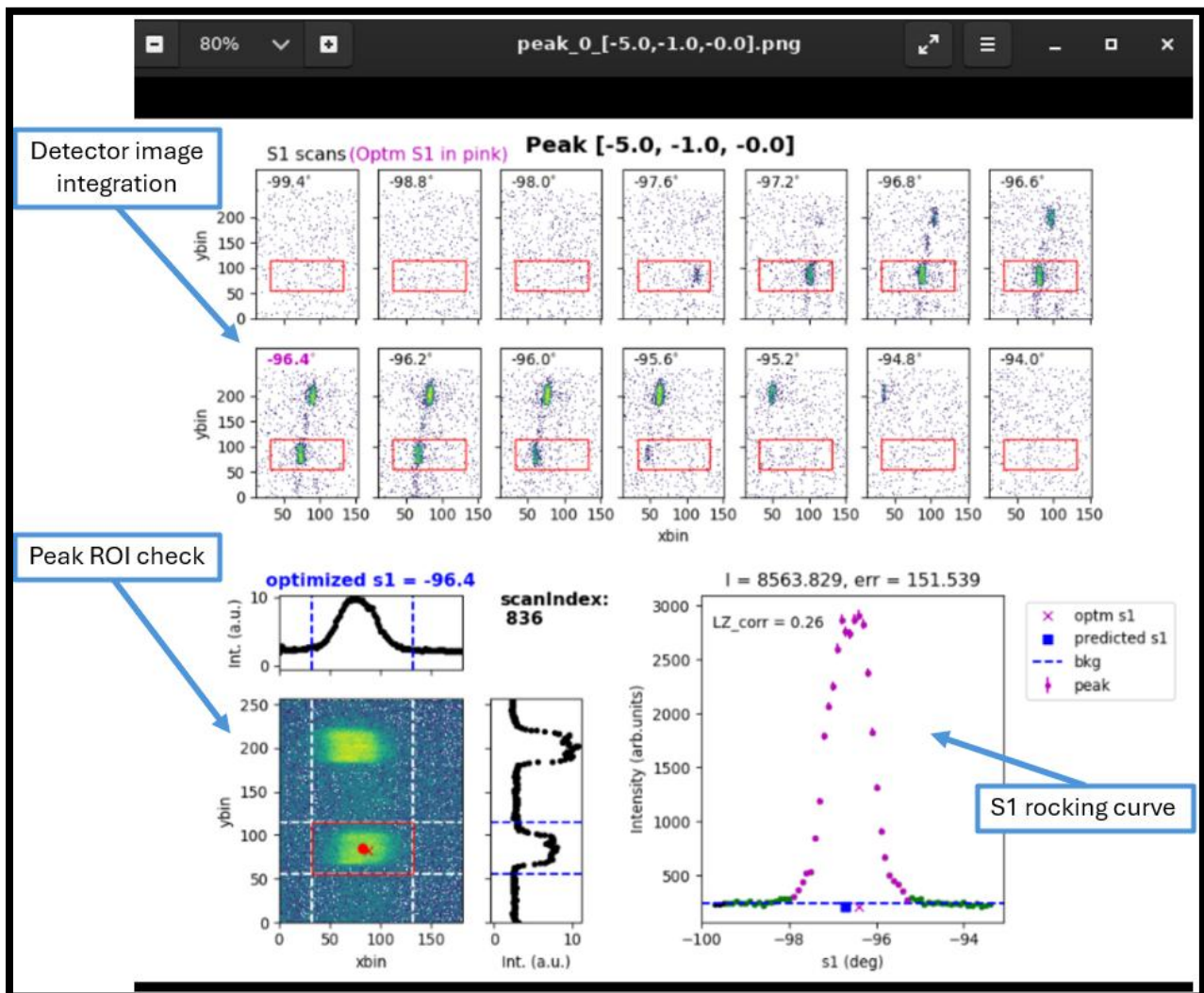


(4) Algorithm output 2 --- png files summarizing peak statistics

The algorithm will also generate a folder containing a series of png files, as shown above.

Each png file contains integration information of each peak.

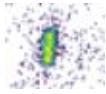
Below is a png file summarizing the Bragg peak $(-5, 1, 0)$.



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In this png file, the title shows the target peak (with index), and 3 sections are summarized:


- **Detector image integration:**

- In the upper half of the png file, a series of detector images are listed. Each image corresponds to an s1 motor value (the numerical value shown in each image).
- In each detector image, one colored spot, something like this , corresponds to one peak in the logarithmic color scale. A peak will gradually appear in the detector image and then fade away as s1 motor rotates, as observed in the example above for peak (-5, -1, 0). The image with **bold magenta** s1 value refers to where peak intensity collected in the detector image reaches its maximum as s1 motor rotates.
- The **red box** in each image highlights the integration region. **As long as the peak intensity is covered by the red box, the integration is legit.** The size of the **red box** is determined by the input 4-number array (see in “Peak ROI check” next).
- **If multiple peaks appear in the red box of the same detector image, be careful. It could be due to twin domains, or impurity, or very close satellite peaks. Think about dealing with it using IntegratePeaksMD (Method 1) if necessary.**

- **Peak ROI (region-of-interest) check:**

- This panel shows the part of detector image around the target peak. The **red cross** is the predicted peak center. The **red dot** is the optimized peak center. **If they differ from each other substantially (e.g., half of the red box size), consider optimizing the peak prediction, and redo the integration.**

```
gg'].getNumberPeaks():
2D.peak2D(mtd['det_imag'], # -- detector image workspace
          mtd['bragg'], # ---- peak workspace
          no, # ----- peak number in the list
          [50,50,30,30], # ---- peak pixel size, [x_left, x_right, y_up, y_down]
          peaklist_outdir + '/integer/', # --- file output path
          )
```



- The size of the **red box** in this contour plot is determined by the input 4-number array (shown above). **x_left** and **x_right** determine the box size

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along xbin direction with respect to the optimized peak center (**red dot**).

y_up and **y_down** determine the size along ybin direction. If the target peak falls outside the **red box**, modify this 4-number array accordingly.

- This **red box** is the same **red box** shown in the upper series of detector images.
- The panels on top and right-hand side of the contour plot are ybin-averaged and xbin-averaged cuts of the contour plot, respectively. The **blue dash lines** align with the **red box** boundary in the contour plot. They help users decide whether the **red box** size is proper to cover the target peak.
- **S1 rocking curve:**
 - The data in the **red box** of each detector image (shown in the upper half of the png file) are integrated. The integrated intensities are plotted as a function of the s1 motor value, shown in this panel.
 - **Blue dashed line** is the Gaussian-fitted background level.
 - **Purple dots** are the integrated peak range.
 - The integrated peak intensity is calculated by integrating the **purple dots** and subtracting the background level.
 - **LZ_corr** refers to a correction coefficient --- Lorentzian correction, calculated using peak positions. Information of Lorentzian correction can be found at <https://single-crystal.ornl.gov/more/integration/index.html>.
 - Final integrated peak intensity and its error are shown in the panel title.

Note:

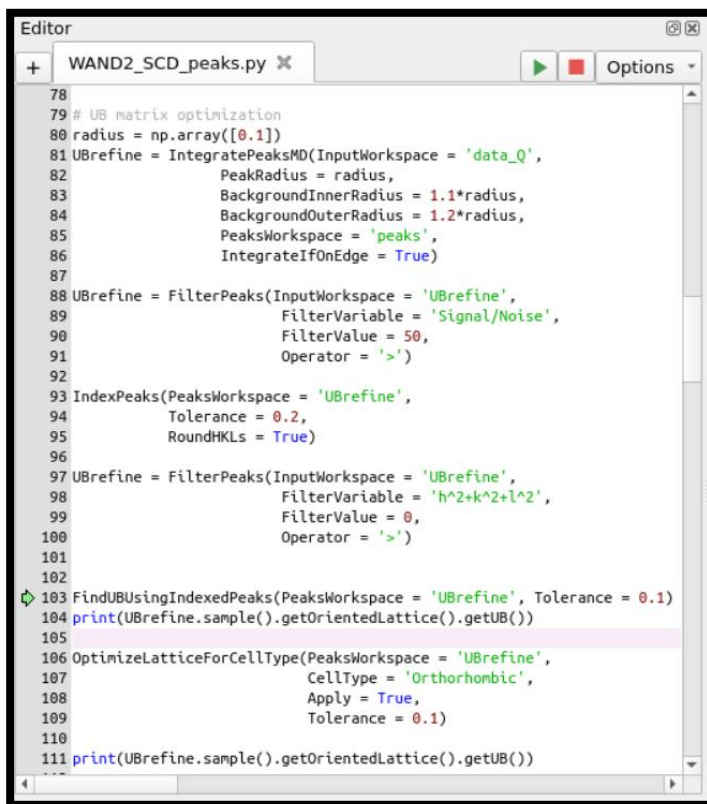
- *The **red box** (ROI) can help distinguish the target peak from other adjacent peaks.*
- *If the target peak intensity is fully contained in the **red box** (ROI), the peak profile (shape) will not affect the integration.*
- *When the target peak is close to or sits on top of the aluminum powder ring, the powder ring signal would be contained in the **red box**. This contained part of powder ring signal can be approximated to be constant as s1 changes within the range of +/- 2~3 degrees. Thus, the powder ring signal will be part of the background level in the s1 rocking curve and hence be filtered out from the final integrated peak intensity.*

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(b) UB matrix optimization

In certain situations, we want to optimize the UB matrix. A straightforward way is to refine UB matrix using strong Bragg peaks (integer-HKL peaks). To do so, after the peak prediction, we add/use and execute command lines shown below:

- (1) Set **radius** for peak filtering. We use **IntegratedPeaksMD** to integrate peaks with assigned spherical radius → we get a peak workspace **UBrefine**.
- (2) Filter peaks based on **Signal/Noise** ratio. Here we set the threshold = 50. Larger threshold value gives us stronger peaks remaining. Modify it accordingly.
- (3) **IndexPeaks** will index peaks in **UBrefine**.
- (4) **FilterPeaks** will filter out peaks that cannot be indexed (HKL = (0,0,0)).
- (5) Two options for optimizing the UB matrix:
 - **FindUBUsingIndexedPeaks** uses peak information (e.g., Q-positions) from **UBrefine** to calculate an optimized UB matrix within assigned tolerance.
 - **OptimizeLatticeForCellType** calculates an optimized UB matrix with the constraint of “**CellType**”. Available choices for cell type: “Cubic”, “Tetragonal”, “Orthorhombic”, “Hexagonal”, Rhombohedral”, “Monoclinic”, “Triclinic”.



```

78
79 # UB matrix optimization
80 radius = np.array([0.1])
81 UBrefine = IntegratePeaksMD(InputWorkspace = 'data_Q',
82                             PeakRadius = radius,
83                             BackgroundInnerRadius = 1.1*radius,
84                             BackgroundOuterRadius = 1.2*radius,
85                             PeaksWorkspace = 'peaks',
86                             IntegrateIfOnEdge = True)
87
88 UBrefine = FilterPeaks(InputWorkspace = 'UBrefine',
89                        FilterVariable = 'Signal/Noise',
90                        FilterValue = 50,
91                        Operator = '>')
92
93 IndexPeaks(PeaksWorkspace = 'UBrefine',
94            Tolerance = 0.2,
95            RoundHKLs = True)
96
97 UBrefine = FilterPeaks(InputWorkspace = 'UBrefine',
98                        FilterVariable = 'h^2+k^2+l^2',
99                        FilterValue = 0,
100                        Operator = '>')
101
102
103 FindUBUsingIndexedPeaks(PeaksWorkspace = 'UBrefine', Tolerance = 0.1)
104 print(UBrefine.sample().getOrientedLattice().getUB())
105
106 OptimizeLatticeForCellType(PeaksWorkspace = 'UBrefine',
107                            CellType = 'Orthorhombic',
108                            Apply = True,
109                            Tolerance = 0.1)
110
111 print(UBrefine.sample().getOrientedLattice().getUB())

```

Note:

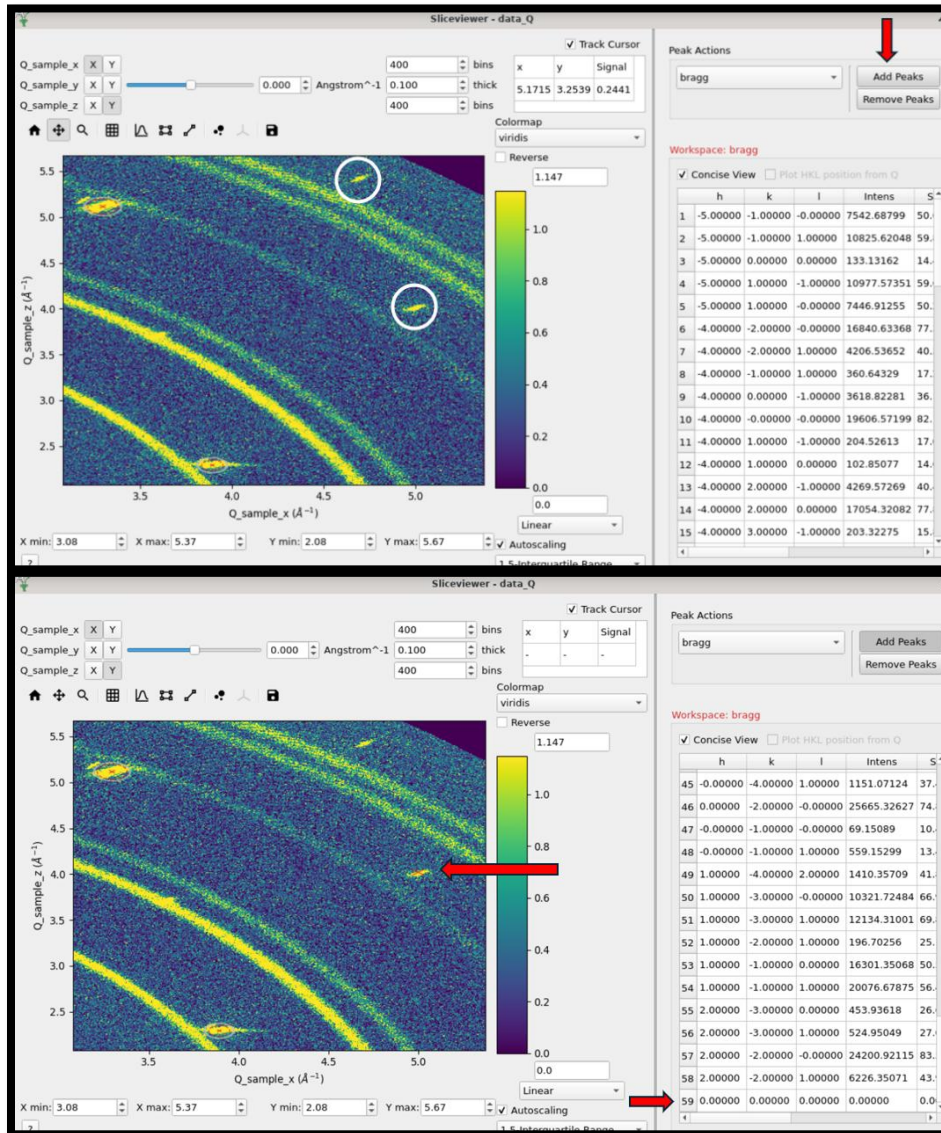
- Both methods will update the UB matrix stored in the peak workspace **UBrefine**.
- The command line **print(UBrefine.sample().getOrientedLattice().getUB())** will print the UB matrix in the “Message” window on the right-hand side of the interface.
- Use **SetUB** algorithm to update the UB matrix of data workspace if needed
https://docs.mantidproject.org/nightly/algorithm_s/SetUB-v1.html

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(c) Add, remove, adjust peaks for peak analysis

(i) Add peaks

In some rare situations, some of the observed peaks are not included in the peak workspace. For example, in the slice viewer shown below, each peak in the **bragg** workspace will have a **red cross** assigned at its peak position. However, we see that there are two peaks not included in the **bragg** workspace (highlighted by white circles).



To add these two peaks to the peak workspace,
(1) Click on **Add Peaks** button on the upper right corner.

(2) Move the mouse to the peak position and click. A **red cross** will appear at the peak position, and the new peak will be included at the end of the workspace table (right-hand side) with a (0,0,0) index.

(3) Run peak indexing command lines again.

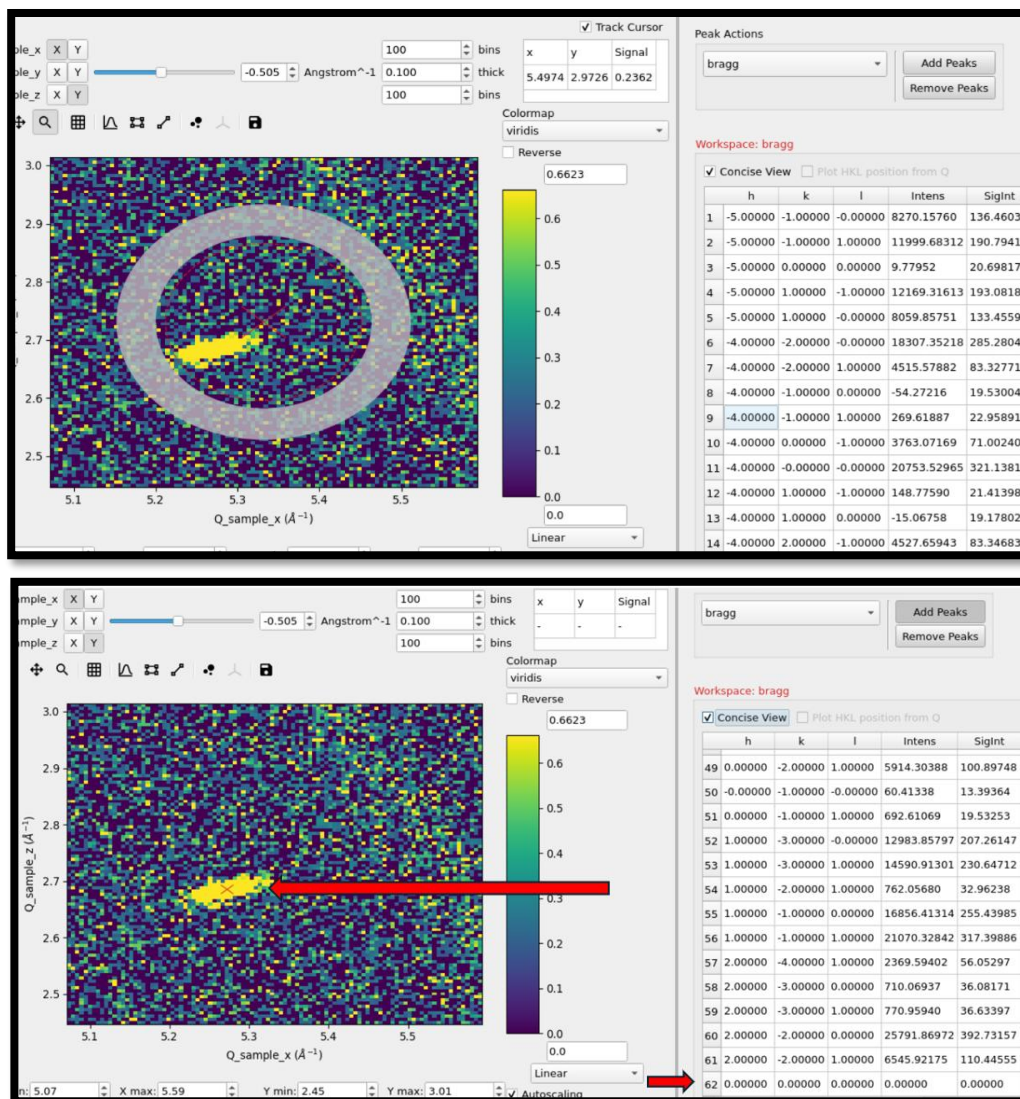
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(i) Remove/Adjust peaks

In more common situations, some of the peaks are not well predicted, as shown below. For peak (-4, -1, 1), its predicted peak position (**red cross**) clearly deviates from the peak intensity spot. To adjust the prediction, follow the path:

- Click “Remove Peaks” on the upper right → Click on the **red cross** in the color plot (this will remove the predicted peak from the peak workspace) → Click “Add Peaks” on the upper right → Click at the expected peak intensity spot (a new **red cross** appears at the expected position, shown below).

This operation will include the target peak in the peak workspace with a (0,0,0) index with the revised peak position, shown in the second snapshot. **Run peak indexing command lines again** to revise the peak workspace.



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