

BioSANS Data Reduction With drtsans

Quick Reference for the data reduction parameters

Introduction

The various parameters required by drtsans are listed below with a brief description of their meaning, the acceptable values, and appropriate format for the information. Additional information can be obtained through your local contact. An example is shown here.

Below is the same configuration file expanded into a more readable format.

```
{"schemaStamp": "2020-04-15T21:09:52.745905",
"instrumentName": "BIOSANS",
"iptsNumber": 25816,
"dataDirectories": null,
"sample": {"runNumber": "6679",
"thickness": 0.1,
"transmission": {"runNumber": "6679", "value": null}},
"background": {"runNumber": "6649, 6659",
"transmission": {"runNumber": "6649, 6659", "value": null}},
"emptyTransmission": {"runNumber": "6641", "value": null},
"beamCenter": {"runNumber": "5896"},
"outputFileName": "test_data",

"configuration": {
"outputDir": "/SNS/users/q3n/reduce2020/etcetc",
"wavelength": 6.0,
"wavelengthSpread": 0.132,
"useTimeSlice": false,
"timeSliceInterval": 7200.0,
"useLogSlice": false,
"logSliceName": "CG3:SE:PolyScience:TempRead",
"logSliceInterval": 0.01,
"sampleOffset": null,
"sampleApertureSize": null,
"sampleDetectorDistance": null,
"sampleToSi": null,
"sourceApertureDiameter": null,
"usePixelCalibration": false,
"maskFileName": null,
"useDefaultMask": true,
"defaultMask": [{"Pixel": "1-14,242-256"}, {"Bank": "21-24,45-48"}],
"useMaskBackTubes": false,
"darkMainFileName": "CG3_5884.nxs.h5",
"darkWingFileName": "CG3_5884.nxs.h5",
"normalization": "Monitor",
"sensitivityMainFileName":
"/SNS/users/q3n/reduce2020/sensitivity487/CG3_sens_main5904sac_tdc7m.nxs",
"sensitivityWingFileName":
"/SNS/users/q3n/reduce2020/sensitivity487/CG3_sens_wing5946sac_tdc3.2d.nxs",
"useSolidAngleCorrection": true,
"blockedBeamRunNumber": null,
"useThetaDepTransCorrection": true,
"DBScalingBeamRadius": 40.0,
"mmRadiusForTransmission": null,
"absoluteScaleMethod": "standard",
"StandardAbsoluteScale": 4.71e-11,
"numMainQxQyBins": 100,
"numWingQxQyBins": 100,
```

```

"1DQbinType": "scalar",
"QbinType": "log",
"numMainQBins": null,
"numWingQBins": null,
"LogQBinsPerDecadeMain": 30,
"LogQBinsPerDecadeWing": 30,
"useLogQBinsDecadeCenter": false,
"useLogQBinsEvenDecade": true,
"WedgeMinAngles": [-45.0, 165.0],
"WedgeMaxAngles": [45.0, 190.0],
"autoWedgeQmin": 0.003,
"autoWedgeQmax": 0.04,
"autoWedgeQdelta": 0.01,
"autoWedgeAzimuthalDelta": 1.0,
"autoWedgePeakWidth": 0.25,
"autoWedgeBackgroundWidth": 1.5,
"autoWedgeSignalToNoiseMin": 2.0,
"AnnularAngleBin": 1.0,
"useErrorWeighting": false,
"smearingPixelSizeX": null,
"smearingPixelSizeY": null,
"useSubpixels": false,
"subpixelsX": null,
"subpixelsY": null,
"QminMain": 0.0067,
"QmaxMain": 0.1,
"QminWing": 0.07,
"QmaxWing": 0.6,
"overlapStitchQmin": [0.075],
"overlapStitchQmax": [0.095],
"wedge1QminMain": 0.02,
"wedge1QmaxMain": 0.09,
"wedge1QminWing": 0.08,
"wedge1QmaxWing": 0.09,
"wedge1overlapStitchQmin": 0.0825,
"wedge1overlapStitchQmax": 0.0875,
"wedge2QminMain": 0.02,
"wedge2QmaxMain": 0.125,
"wedge2QminWing": 0.06,
"wedge2QmaxWing": 1.0,
"wedge2overlapStitchQmin": 0.075,
"wedge2overlapStitchQmax": 0.095,
"wedges": [[-45.0, 45.0], [165.0, 190.0]],
"symmetric_wedges": true,
"logslice_data": {}
}

```

Parameter Descriptions

Note that all key:value pairs use quotes around both the key and value unless the value is null or a mathematical constant. Also note that the file has a hierarchical structure, where {} are used to denote groupings. The descriptions of the parameters below reflect the structure of the hierarchy.

1. "schemaStamp": "2020-04-15T21:09:52.745905"

This particular parameter is autogenerated by the scripting method for reducing data. It should not be changed if you can access it, even when hand-modifying the contents of the configuration file.

2. "instrumentName": "BIOSANS"

The instrument name is used by drtsans to know how to use some of the specified parameters. It must be consistent with the instrument used for the data collection (i.e. do not try to reduce data from BIOSANS if this parameter is set to "GPSANS"). Note that there is no dash in the name of the instrument in the drtsans parameter file.

3. "iptsNumber": "25816"

The proposal number for the experiment allows drtsans to quickly find the data to be reduced, rather than using tools to find the data based solely on the run number. It can be left blank (i.e. "").

4. "sample":

This is the first parameter that contains a set of parameters grouped using {}. The various parameters in the group follow.

a. "runNumber": "6679"

This is the run number for the sample scattering to be reduced. It can be found via OnCat. It is possible to specify a set of scattering runs for a single sample that are to be summed together into a single data set for reduction. To do so, use the following format, which uses a single pair of quotes to enclose the list.

i. "runNumber":{"run1, run2"}

b. "thickness": 0.1

This parameter specifies the sample thickness in centimeter. Note that the value is not enclosed in quotes.

c. "transmission":

This is the start of another level of the hierarchical structure. Of the two key:value pairs in this grouping, only one can have an actual value: either the run number or the value of the transmission to use for the reduction. One rarely specifies a simple value for the transmission for EQ-SANS data because the transmission is wavelength-dependent.

i. "runNumber": "6679"

This is the run number of the transmission for the sample. At Bio-SANS, we are using a semi-transparent beam stop for 6Å neutron so that the transmission is taken while measuring the scattering. The run number in this case will be the

same as the sample run number. But for other wavelengths, the run number will be different. There can only be a single run number specified here.

ii. "value": ""

This would be a numerical value for the transmission to use for the reduction, which would normally only be done for quick qualitative checks if the data needs to be viewed prior to the completion of the transmission measurement for a sample. Note that the value must be enclosed in quotes ("").

5. "background":

The set of parameters that follow specify information required to identify the background to use for the reduction. It is possible to reduce data without a background by leaving the run numbers in this set of parameters empty (i.e. "").

a. "runNumber": "6649, 6659",

The run number(s) of the background data to subtract from the sample scattering. In this case, two runs are used.

b. "transmission":

The following set of parameters are used to specify either the run number for the background's transmission measurement or to specify a value for the transmission of the background.

i. "runNumber": "6649, 6659"

ii. The run number for the background's transmission measurement. If no background is specified, then this run number should not be specified (i.e. set to "").

iii. "value": ""

iv. This would be a numerical value for the transmission to use for the reduction, which would normally only be done for quick qualitative checks if the data needs to be viewed prior to the completion of the transmission measurement for a sample. Note that the value must be enclosed in quotes ("").

6. "emptyTransmission":

This grouping of parameters is used to specify the reference measurement (usually an empty position in the sample holder), or value, used to calculate the transmission from the other

specified measurements or values. If the transmissions are specified as values, the value specified here should be "1.0".

- a. "runNumber": "6641"

The run number for the background's transmission measurement.

- b. "value": null

A value can be specified for the reference transmission. If used, it should be "1.0", if not specify it as null, as shown above.

7. "beamCenter":

The beam center is specified by providing a run number for an empty beam's transmission measurement to calculate the beam center from.

- a. "runNumber": "5896"

This is the run number of an empty beam's transmission measurement without a beam stop in front of detector. It cannot be left blank.

8. "outputFileName": " test_data "

This is the prefix used to construct all of the file names that result from the data reduction process. In this example, all of the associated files will be named "test_data*.*". The filename can be any valid string that is acceptable for filenames for a unix operating system.

9. "configuration":

A large number of parameters are specified within this hierarchical grouping, most of which directly impact the reduction process and results produced. Many of these parameters will be provided by your local contact and should not be changed without discussion with the local contact. In the jupyter notebook, some of these parameters may or may not be presented to you. If they are not presented to you in either the scripts that your local contact helps set up for you, then you do not need to provide them directly.

- a. "outputDir": "/SNS/users/q3n/reduce2020/etcetc",

The directory to write the data reduction result to is listed here. Normally, it would be the shared directory for the particular proposal, which allows other team members and the local contact to view the results. However, it is also possible to specify a location in a user's home directory. It is left to the discretion of the user.

- b. "wavelength": 6.0,

Wavelength in Angstrom, it is can be specified or leave as null, in which the meta data value in the raw data file will be used.

- c. "wavelengthSpread": 0.132

Wavelength spread in decimal, it is can be specified or leave as null, in which the meta data value in the raw data file will be used.

- d. "useTimeSlice": false

If the user wishes to parse the event stream contained in the run specified in the "sample:" parameter set, then set this value to true. If this value is true, then the parameter "useLogSlice", below, must be false.

- e. "timeSliceInterval": 7200.0

This is the interval in seconds to use for the time slicing of the event stream. The event stream will be cut into as many consecutive portions of the event stream as exist in the file, with a final bin that contains as much time as remains in the stream. In this case, the various slices are for the following intervals: $0 \leq t < 7200$ seconds, $7200 \leq t < 14400$ seconds, etc. Note that the value is not contained in quotation marks.

- f. "useLogSlice": false,

It is possible to divide an event stream into bins that derive from another parameter that is saved by EPICS in the NeXus file, such as temperature, pressure, magnetic field, or even a motor that continuously moves during data collection. If a user wishes to do so, set the value to true. Note that useLogSlice and useTimeSlice cannot both be true. Discuss the use of log slicing with your local contact.

- g. "logSliceName": "CG3:SE:PolyScience:TempRead"

This is the name of the instrument log to use for log slicing. If useLogSlice is true, change this to the name of the EPICS parameter that you wish to employ. Discuss the use of log slicing with your local contact.

- h. "logSliceInterval": 0.01

This parameter sets the interval of the instrument log specified in logSliceName to use. It must be in the units of the device, be it degrees, millimeters, Celcius, etc. Discuss the use of log slicing with your local contact. Note that the value is not enclosed in quotation marks.

- i. "sampleOffset": null

This parameter is not used by HFIR SANS instruments (Bio-SANS and GPSANS). Please ignore.

- j. "sampleApertureSize": null

This parameter specifies the diameter of the sample aperture used in millimeters. While it is possible to specify the diameter of this aperture during data acquisition, specifying a different value here allows you to over-write the incorrect value saved in the data files in case it is needed. The sampleApertureSize impacts the calculation of the resolution information for the instrument (i.e. the uncertainty in Q), which is required to accurately analyze your data. Note that the value is enclosed in quotation marks.

- k. "sampleDetectorDistance": null,

This parameter overwrites the meta data "**sample-to-detector-distance**" from the raw data in case there is an error. It is the full sample to detector distance in the unit of meter. Don't change it without consultation with your local contact.

- l. "sampleToSi": null,

This parameter overwrites the meta data the distance between the sample to Bio-SANS detector tank Si window from the raw data in case there is an error. The unit is mm. Don't change it without consultation with your local contact.

- m. "sourceApertureDiameter": null

This can be used to specify the diameter of the source aperture in millimeters used for a measurement. Normally, this parameter is pulled from data file meta data. If you feel that you need to change this value, which you would specify as a number enclosed in quotation marks, consult your instrument scientist.

- n. "usePixelCalibration": false

This parameter is using a pixel map that takes into account the center of pixel on the detector along with its corresponding width and height. This calibration takes into account the nonlinearity of the detector tubes. Please consult the local contact before changing this option.

- o. "maskFileName": null

This is the name of a hand-drawn mask. Currently it is not used at Bio-SANS since no detector bank shows abnormality.

p. "useDefaultMask": true

This is to use additional mask is applied in addition to the user-specified mask from the maskFileName parameter. If the value is set to true, any mask specified with the "defaultMask" parameter, below, will be applied.

q. "defaultMask": [{"Pixel": "1-14,242-256"}, {"Bank": "21-24,45-48"}]

This parameter is used to select certain tube banks not used. At Bio-SANS, it is usually used to mask the shadowed tubes or the edge pixels that are distorted. Don't change the value without consulting your local contact.

r. "useMaskBackTubes": false

The Bio-SANS detector, like the EQ-SANS and GP-SANS detectors, consists of an array of linear position sensitive detectors that are arranged in two planes that are offset to ensure complete coverage across the area of the detector. When this parameter is set to true, the back plane of tubes, being those furthest away from the sample, are all masked. Typically, this is only done when the detector is positioned close to the sample.

s. "darkMainFileName": "CG3_5884.nxs.h5",
"darkWingFileName": "CG3_5884.nxs.h5",

They specify the names of the files that contains the "dark current" measurement for main and wing detectors, respectively. At Bio-SANS, it is normally a measurement performed during regular calibrations with the facility running but the instrument shutter closed. It is a measure of cosmic radiation and detector electronic noise. Your local contact will provide the correct file to use.

t. "normalization": "Monitor"

The data can either be normalized by the measurement time ("Time") or the beam monitor ("Monitor"). The normal method for normalizing Bio-SANS data is "Monitor". "Time" is less accurate and reserved for the rare monitor malfunction event.

u. "sensitivityMainFileName":
"/SNS/users/q3n/reduce2020/sensitivity487/CG3_sens_main5904sac_tdc7m.nxs",
"sensitivityWingFileName":
"/SNS/users/q3n/reduce2020/sensitivity487/CG3_sens_wing5946sac_tdc3.2d.nxs",

The file names of the pre-processed relative pixel response of the detector is specified with the parameters. These calibration files are measured during instrument

commissioning each cycle and are prepared by staff for use in data reduction. Consult your local contact for the correct file to use.

- v. "useSolidAngleCorrection": true

This parameter specifies whether or not to correct the data for the solid angle subtended by each pixel, which can be a considerable effect for configurations with the detector positioned close to the sample. It is recommended to leave this parameter set to true.

- w. "blockedBeamRunNumber": null,

This is the option to use the blocked beam as dark background correction. It is not used at Bio-SANS as the instrument background is low.

- x. "useThetaDepTransCorrection": true

When set to true, the data reduction will correct the data in each pixel for the actual distance that the neutrons travel through the sample when performing the correction for the transmission. The effect increases with scattering angle and can be considerable when the detector is positioned near the sample. It is recommended to leave this parameter set to true.

- y. "DBScalingBeamRadius": 40.0,

This value is to set the beam radius that is used by empty beam scaling which is not deployed at the Bio-SANS. In the current implementation, the empty beam scaling is disabled.

- z. "mmRadiusForTransmission": null

This parameter allows the user to specify the radius in millimeters to use when integrating the attenuated direct beam measurements for calculating the transmissions. At Bio-SANS, this value is optimally determined in the drtsans, and is not required. Consult your local contact if you feel that another value may be required.

- aa. "absoluteScaleMethod": "standard"

At present, the method available for scaling data collected on Bio-SANS into absolute units of 1/cm is by using a calibrated standard. Do not change the value of this parameter. Presently, the standard is well-characterized sample of porous silica or H₂O that your local contact will provide to you during your experiment. A measurement of the standard is used to derive the absolute scale factor, which is specified with the StandardAbsoluteScale parameter, described below.

- bb. "StandardAbsoluteScale": "4.71e-11"

This is the scale factor that must be applied to the data to place it into absolute units of 1/cm. Your local contact can help you derive it from a measurement of a standard.

- cc. "numMainQxQyBins": 100,
"numWingQxQyBins": 100,

This parameter specifies the number of Q-bins in the 2D reduced data, which is always part of the output by drtsans. Note that only a single value may be provided, which implies that the 2D reduced data is on a regular, square grid that covers the Q-range in 2D measured by the detectors. The beam center is not necessarily in the center of the output data. The grid in Q-space is always linear.

- dd. "1DQbinType": "scalar"

Three options exist for the kind of 1D data that are output by drtsans. Possible values are "scalar", which is used for 1D azimuthally averaged data that most people are familiar with; "wedge" makes it possible to define wedges to perform scalar binning within, as one might do for anisotropic data and utilize the WedgeMinAngles, WedgeMaxAngles and the various autoWedge parameters described below, although automatic wedge determination is not enabled for EQ-SANS at this point in time. The "annular" binning makes it possible to visualize how data varies around the beam center within a Q-range specified by the user and requires that the parameters AnnularAngleBin, Qmin and Qmax, described below, be provided.

- ee. "QbinType": "log"

This parameter dictates whether the Q-spacing of the intensity profiles calculated when performing scalar or wedge binning is logarithmic or linear. The possible values of this parameter are "log" and "linear". The choice of binning determines how the numQBins, LogQBinsPerDecade and useLogQBinsEvenDecade parameters work.

- ff. "numMainQBins": null,
"numWingQBins": null,

This parameter must be set to an integer value if QbinType is "linear", but can also be used if it is "log". The value is the number of Q-values that are in the 1D data that is binned as "scalar" or "wedge" and their spacing is determined by the value of QbinType. This parameter must be null if LogQBinsPerDecade is set to an integer value. Note that the value is enclosed in quotation marks.

- gg. "LogQBinsPerDecadeMain": 30,
"LogQBinsPerDecadeWing": 30,

This parameter only works when QbinType is "log". The value specified here will be the number of Q-bins that are present within each decade between the minimum and

maximum Q values that the reduced data contain. For example, if the value is “30”, then there are 30 Q-bins between 0.01 Å⁻¹ and 0.10 Å⁻¹ and 30 Q-bins between 0.10 Å⁻¹ and 1.0 Å⁻¹ or any other decade in Q that are present in the reduced data. The parameter useLogQBinsEvenDecade must be set to true to enable this option and numQBins must be null.

hh. "useLogQBinsDecadeCenter": false

At present, this option is no longer enabled. The Q-values when using an even number of Q-bins per decade by setting useLogQBinsEvenDecade to true and providing a value for logQBinsPerDecade to a non-zero, positive integer always have a bin centered on 0.001 Å⁻¹, 0.010 Å⁻¹, 0.100 Å⁻¹, etc.

ii. "useLogQBinsEvenDecade": true

This parameter tells drtsans to use a fixed number of Q-bins per decade when binning the result. The logQBinsPerDecade parameter must have a non-zero integer value and numQBins must be null.

jj. "WedgeMinAngles": [-45, 165]

"WedgeMaxAngles": [45, 190]

The WedgeMinAngles and WedgeMaxAngles are only used when QbinType is set to “wedge”. The arrays provide a matched set of angles, specified in degrees and indexed from the Qx axis, within which to perform 1D Q-binning. In this particular example, 1D Q-binning will be performed in two wedges: from -45° to 45° and from 165° to 190°. The angles need not be the same size and need not be symmetric. It is also possible for the angles to overlap, should the user desire it. The only requirement is that both arrays have the same number of elements and that the minimum angle for a wedge be lower than the maximum value for that wedge.

Parameters shown in points kk through qq, zz and ccc, below, are required for the drtsans methods for automatically determining the correct wedges to use for binning reduced data into 1D. Development of these routines was driven by the Bio-SANS instrument team. At present, automatic wedge determination is not available for data collected using EQ-SANS.

kk. "autoWedgeQmin":

"autoWedgeQmax": null

"autoWedgeQdelta": null

"autoWedgeAzimuthalDelta": null

These parameters are used to convert the Qy vs Qx 2d-image into a series of curves, Intensity vs. Phi (azimuthal angle) for different fixed Q-values. The Q-range of the main

detector determines Q_{min} ('kk') and Q_{max} ('ll'). The Q bin size is determined by Q_{delta} ('mm'); an optimal setting of Q_{delta} would be to result in ~ 10 Q-bins in the range- Q_{min} to Q_{max} . The choice of Q_{delta} is a delicate balance between small Q_{delta} (weak signal to resolve the wedge angles) and large Q_{delta} (smeared anisotropy in the data). The Phi bin size is determined by 'nn'; a good estimate is between 1° to 5° .

- ll. "autoWedgePeakWidth": null
"autoWedgeBackgroundWidth": null
"autoWedgeSignalToNoiseMin": 2.0

These parameters are used to determine wedge angles by performing peak fitting to the curves produced above (kk). The angular range of the wedge(s) associated to the enhanced scattering peak is set by the peak width parameter ('oo'). This number is a ratio of the peak's full-width-half-maximum (FWHM); typical values are between 0.25 to 1.0, i.e., from $1/4^{\text{th}}$ FWHM to one FWHM. Similarly, the angular range of the wedge(s) associated to the background scattering (flat background scattering) is set by the background width parameter ('pp'); typical values are between 1.0 to 2.0. The last term is used to detect the presence of enhanced scattering peaks. If the process of detecting a peak has failed due to weak scattering signal, one option is to reduce signal-to-noise min value progressively until 1.25. Note, a value of 1.0 implies that the signal and noise are of equal magnitude, which is not recommended.

- mm. "AnnularAngleBin": 1.0,

When the 1DQbinType parameter is set to "annular" this parameter specifies the size of the bins in degrees that are to be used for binning. Annular binning takes the data in a ring of Q-values and creates a profile as a function of angle around the beam center. Annular binning also requires that Q_{min} and Q_{max} , described below, be specified.

- nn. "useErrorWeighting": false,

If weighting by the experimental uncertainty is desired when binning the reduced data and propagating the corresponding uncertainties, set the value of this parameter to true.

- oo. "smearingPixelSizeX": null,
"smearingPixelSizeY": null,

The detectors used in the SANS instruments at ORNL are gas detectors. The pixel sizes are determined from parameters supplied to the hardware that determines where a neutron is detected and can be varied by changing said parameters. In actuality, there is intrinsic uncertainty in the position of the event along the tube. Further, the arrangements of the tubes in the detector makes it possible to have a neutron in the region of overlap between a tube in the front panel and a tube in the back panel be

detected in either, which also creates uncertainty in the position in which an event is encoded. The `smearingPixelSizeX` and `smearingPixelSizeY` parameters make it possible to account for this uncertainty when calculating the uncertainty in Q . The effect is small for most Q -values, but can impact data analysis when sharp features are present. Your local contact can provide suitable values for the parameters. Note that specifying values for these two parameters does not change the calculation of the value of Q or the intensity profile that results after reduction. It only alters the uncertainty in Q (ΔQ) of the result.

pp. `"useSubpixels": null`

In cases where there are sharp features in the data, or a need to use as much data near the beam stop as possible, it is possible to divide the pixels defined on the detector into sub pixels to improve the quality of the results from the 1D binning process. Subpixels, if specified, will also be used in the 2D binning. To enable this feature, set `useSubpixels` to true and set `subpixelsX` and `subpixelsY`, described below, to positive integers.

qq. `"subpixelsX": null,`
`"subpixelsY": null,`

Set these two parameters to a non-zero, positive integer to use subpixels when binning the data. The real pixels will then be divided into subpixels for the binning in the data reduction. If `subpixelsX` is set to 2 and `subpixelsY` is set to 3, then each pixel will be divided into a 2 by 3 grid for the binning process.

rr. `"QminMain": 0.0067,`
`"QmaxMain": 0.1,`
`"QminWing": 0.07,`
`"QmaxWing": 0.6,`

When performing annular binning this is the minimum and maximum Q -values, specified in \AA^{-1} , to use during the binning. These values are used at Bio-SANS to create a clear cut-off for both main and wing detector in both scalar and annular binning.

ss. `"overlapStitchQmin": [0.075],`
`"overlapStitchQmax": [0.095],`

This pair of parameters are to set the overlap range for stitching 1D data from two instrument configurations to produce a single curve. This is in addition to the merged curve from two detectors at one single configuration. The range is usually determined during the calibration, please consult your local contact if any change is desired.

tt. `"wedge1QminMain": 0.02,`

```
"wedge1QmaxMain": 0.09,  
"wedge1QminWing": 0.08,  
"wedge1QmaxWing": 0.09,  
"wedge1overlapStitchQmin": 0.0825,  
"wedge1overlapStitchQmax": 0.0875,
```

These parameters help cleanly present the data from the main detector, wing detector and based on the overlap region defined, the stitched data for wedge1. These parameters are only enabled when wedge reduction is chosen (auto or manual).

```
uu. "wedge2QminMain": 0.02,  
"wedge2QmaxMain": 0.125,  
"wedge2QminWing": 0.06,  
"wedge2QmaxWing": 1.0,  
"wedge2overlapStitchQmin": 0.075,  
"wedge2overlapStitchQmax": 0.095,
```

These parameters help cleanly present the data from the main detector, wing detector and based on the overlap region defined, the stitched data for wedge2. These parameters are only enabled when wedge reduction is chosen (auto or manual).

```
vv. "wedges": [[-45.0, 45.0], [165.0, 190.0]],
```

There is no need to change this. This is part of some output parameters, not input for reduction. They are used in plotting. If you specify the `WedgeMinAngles` and `WedgeMaxAngles`, or if you use automatic wedge detection, this "wedges" entry will be populated to give you easier access to plot with those parameters.

```
ww. "symmetric_wedges": true,
```

This parameter is associated with the auto-wedge process. If the scattering has 2-fold symmetry ('true'), the wedges on diametrically opposite directions are set to be identical. If 4-fold symmetry ('false'), then all the four wedges are considered to have independent angular ranges. Default is 'true'.

```
xx. "logslice_data": {}
```

There is no need to change this. This is part of some output parameters, not input for reduction. This contains information about the splitting. For example, if you use temperature metadata as a function of to slice data, this will provide metadata reference to the temperature.