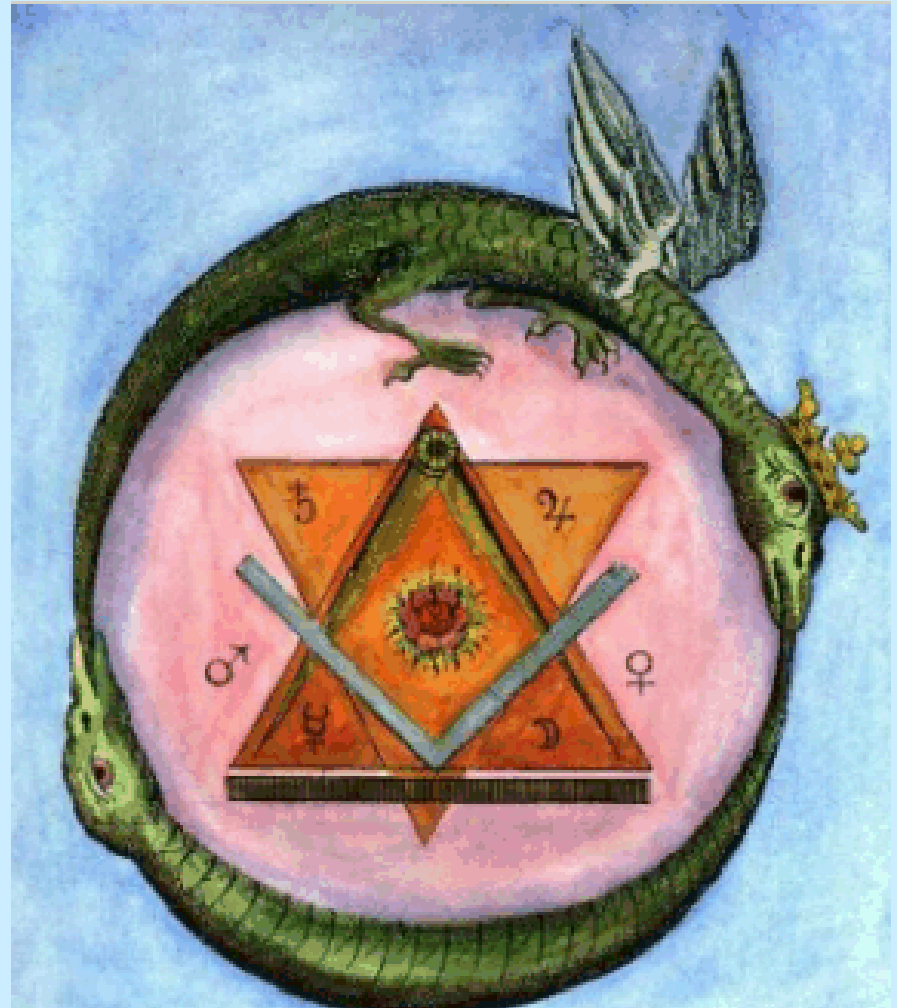


Processing of Bruker & Nonius CCD data



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Processing of Bruker & Nonius CCD data

There are two main stages of CCD data processing :

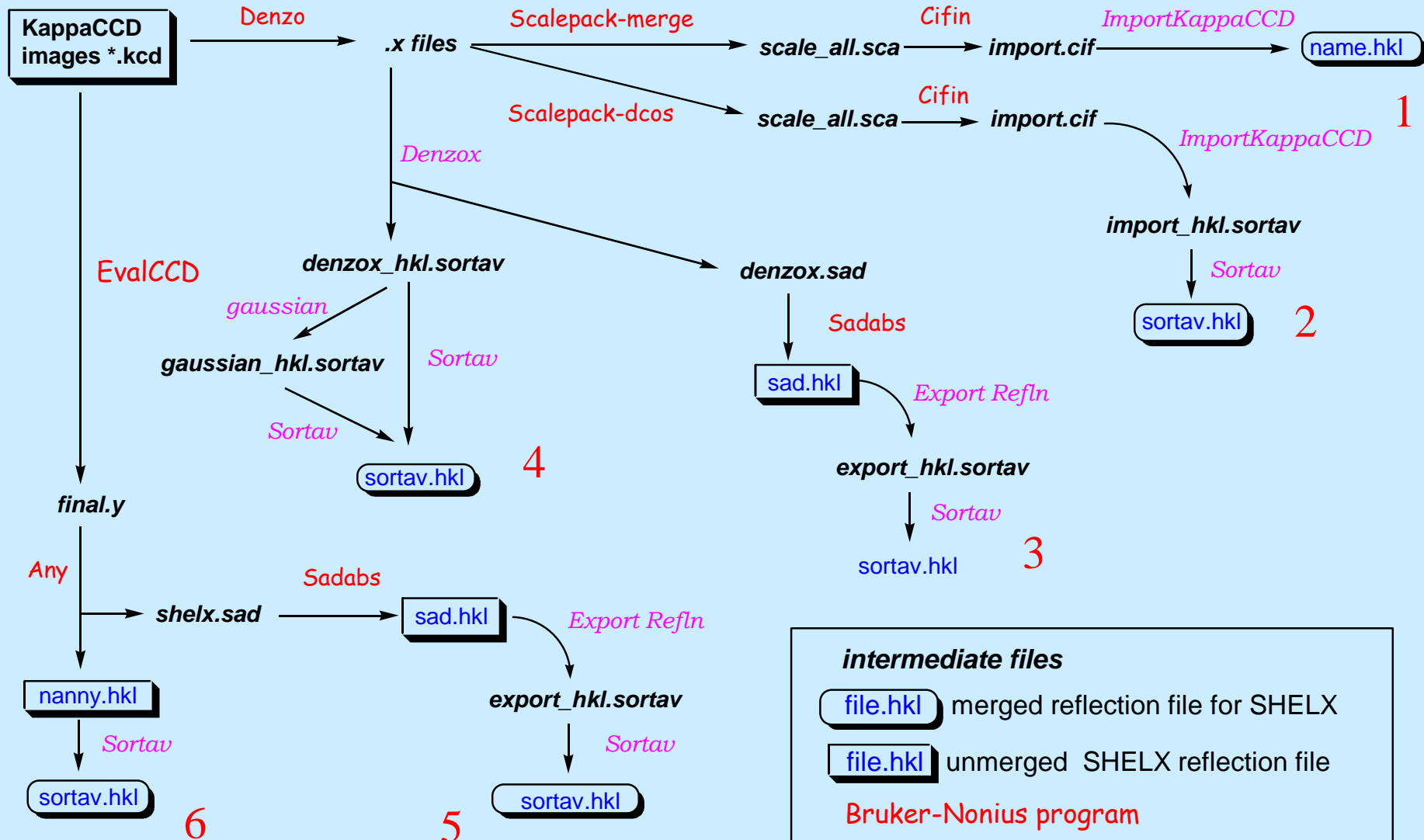
- Frame integration - extraction of intensities from images
- Post processing - error modelling, merging, abs corrections, *etc*

First procedure is specialised, involves many corrections to the raw CCD data - no facilities in WinGX for this (**Denzo**, **EvalCCD**, **SAINT**).

Second procedure is handled in **WinGX** by a variety of routes

Frame integration relies on “black box” commercial software.

Flowchart for data reduction of Bruker Nonius KappaCCD images

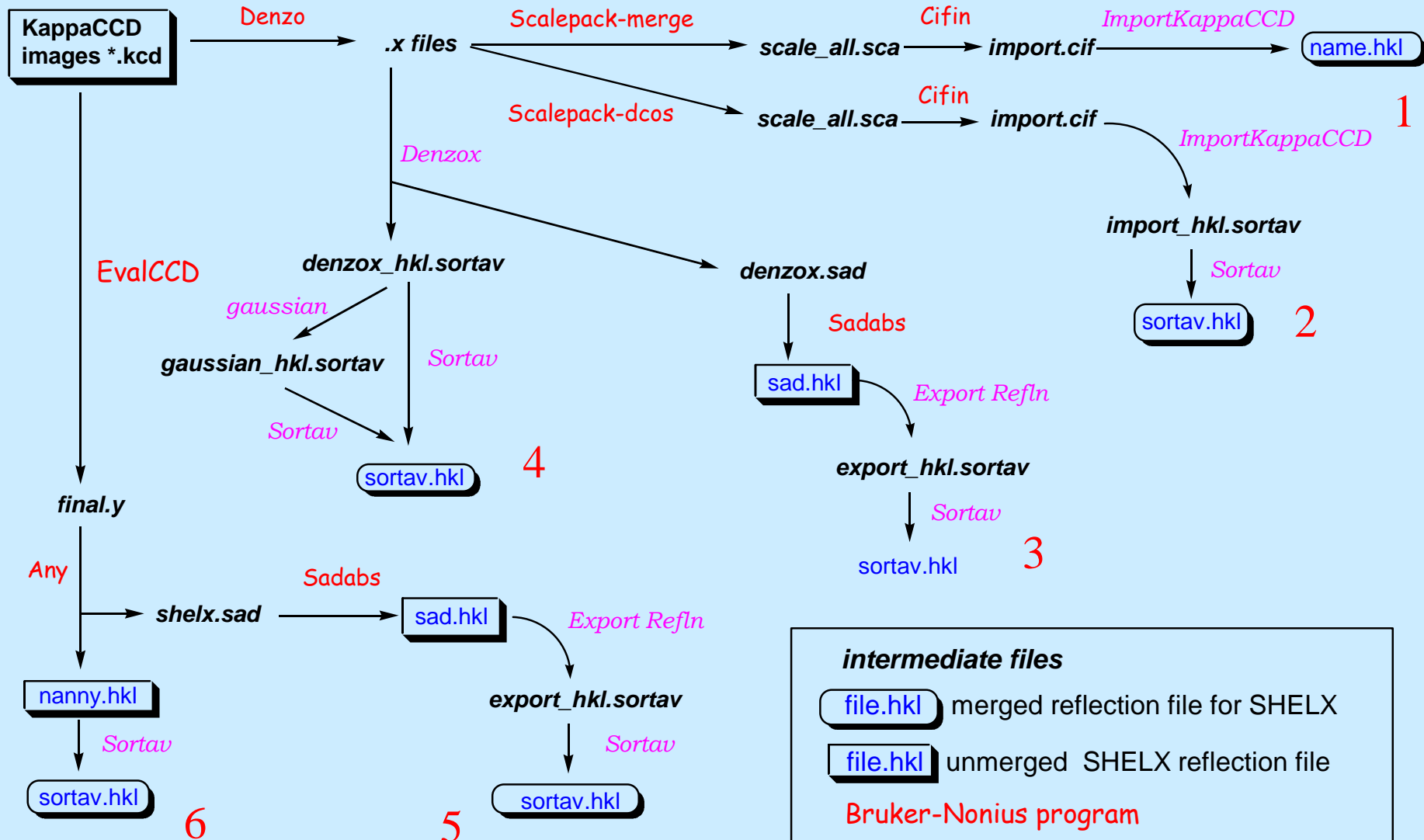


Denzox program

Denzox was written by Bob Blessing, but extensively modified in Glasgow

- Reads .x files produced by Denzo and concatenates data
- does little massaging of reflection intensities
- transfers *fulls* transparently - no change in I or $\sigma(I)$
- simple statistical summation of *partials* to provide I and $\sigma(I)$
- some rejection criteria - χ^2 of fit, partials at edge of scan set, $\sin\theta/\lambda$
- calculates direction cosines
- re-indexing for equivalent orientation matrices (NOT re-orientation !)
- various possibilities for batch number - frame, scan-set, experiment
- output file *denzox_hkl.sortav* for Sortav (or Gaussian abs correction)
- output file *denzox.sad* for Sadabs

Flowchart for data reduction of Bruker Nonius KappaCCD images

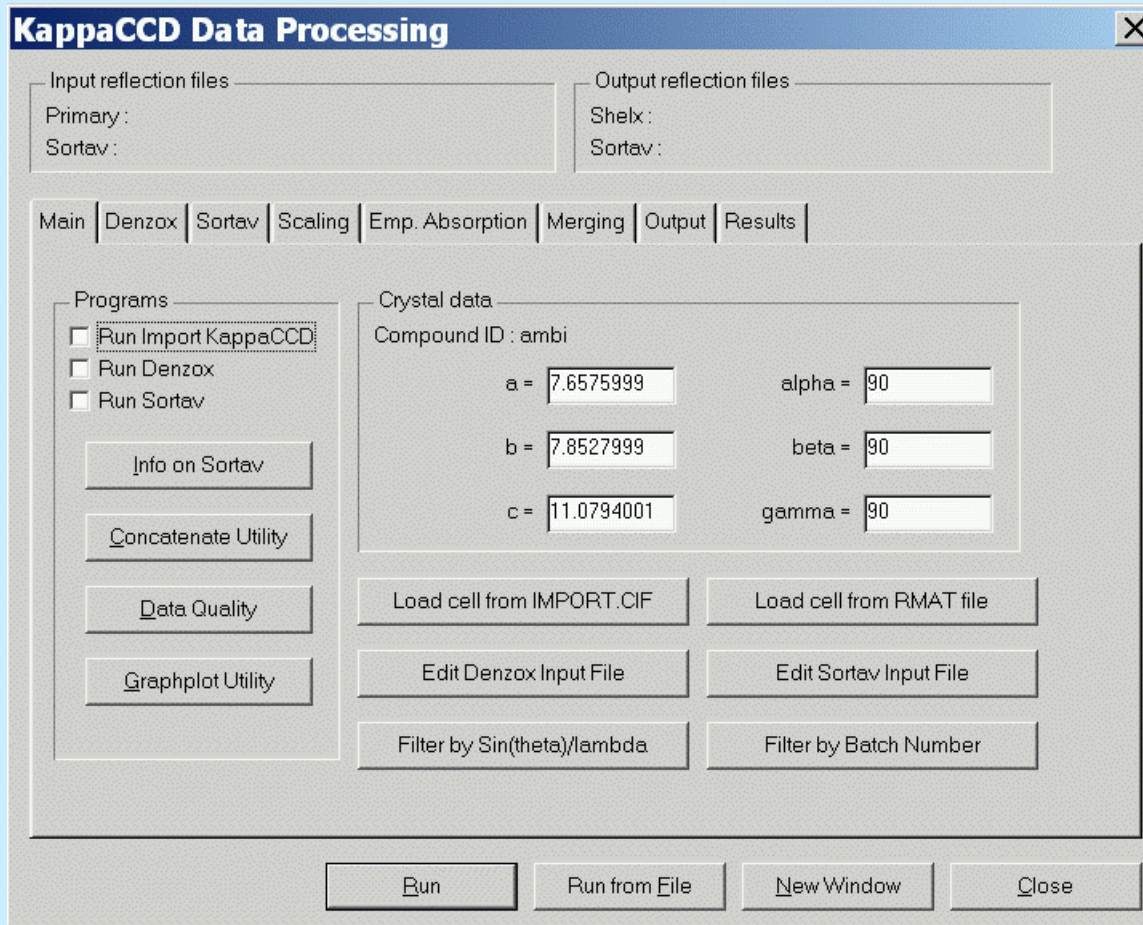


Processing of KappaCCD data

Summary of Data Reduction methods for AMBI (ammonium bitartrate)

	Denzo Scalepack-m	Denzo Scalepack	Denzo Denzox/Sadabs	Denzo Denzox/Sortav	EvalCCD Sadabs	EvalCCD Sortav
	route1	route2	route3	route4	route5	route6
Total unique	1930	1923	1931	1935	1952	1953
Observed	1641	1684	1684	1700	1523	1525
$R(\sigma)$	0.0366	0.0357	0.0316	0.0332	0.0427	0.0436
w R^2	0.810	0.0818	0.0795	0.0792	0.0813	0.0815
R_1 (obs)	0.0326	0.0336	0.0331	0.0334	0.0385	0.0385
R_1 (all data)	0.0428	0.0429	0.0426	0.0425	0.0618	0.0619
$\Delta\rho$	0.18 -0.22	0.20 -0.22	0.23 -0.20	0.23 -0.18	0.20 -0.22	0.19 -0.21

Processing of KappaCCD data



Load cell from various sources

Filter data by $\sin(\theta)\lambda$ or batch no.

Quick view of data quality by Weiss or Diederich - Karplus programs

Concatenation of input files

Plots (Sortav)

Most data reduction programs handled through KappaCCD GUI

Processing of KappaCCD data

Data Quality ✕

This utility provides a quick indication of data quality using several different statistical descriptors, i.e. the standard Rmerge (Rsym), the redundancy-independent Rmeas (Rrim), the pooled coefficient of variation (PCV) or the precision indicating R-value (Rpim). For a definition of these descriptors, see :

K. Diederichs and P.A. Karplus, Nature Struct. Biology (1997) 4, 269, and
M. S. Weiss, J. Appl. Cryst (2001), 34, 130.

15963 reflections read from BATCH1_HKL.SORTAV Diederichs/Karplus data quality analysis finished
3079 unique merged reflections for Laue class 2/m
15962 observations in merging calculations

Reflection data | R-values | Rmrg I-values

Bin	Res (Å)	Rmeas (Rsym) (%)	PCV (%)	<I-over-sigma> measured data merged data		fract multi (%)
1	1.27	4.9 (4.4)	7.8	40.0 (40.0)	105.5 (****)	13.8 6.8
2	0.90	4.3 (4.0)	7.3	32.2 (32.2)	94.6 (94.6)	17.5 8.5
3	0.76	4.8 (4.5)	8.6	24.8 (24.8)	68.3 (68.3)	15.6 7.6
4	0.68	6.0 (5.5)	10.5	20.0 (20.0)	52.6 (52.6)	14.1 6.9
5	0.63	6.6 (6.0)	10.4	15.1 (15.1)	37.9 (38.0)	12.6 6.3
6	0.59	7.9 (7.1)	12.3	12.9 (12.9)	29.1 (29.9)	9.9 5.1
7	0.56	7.6 (6.2)	10.2	12.7 (12.6)	20.6 (21.6)	5.1 2.6
8	0.53	9.5 (7.7)	13.3	9.9 (9.9)	15.5 (16.6)	4.2 2.5
9	0.51	12.9 (10.2)	18.3	7.8 (7.7)	12.0 (12.7)	4.4 2.4
10	0.49	15.4 (12.3)	23.1	7.2 (7.1)	10.1 (11.3)	2.9 2.1
Totals		5.0 (4.5)	16.4	22.4 (22.6)	45.8 (49.0)	100.0 5.2

Load cell from various sources

Filter data by $\sin(\theta)\lambda$ or batch no.

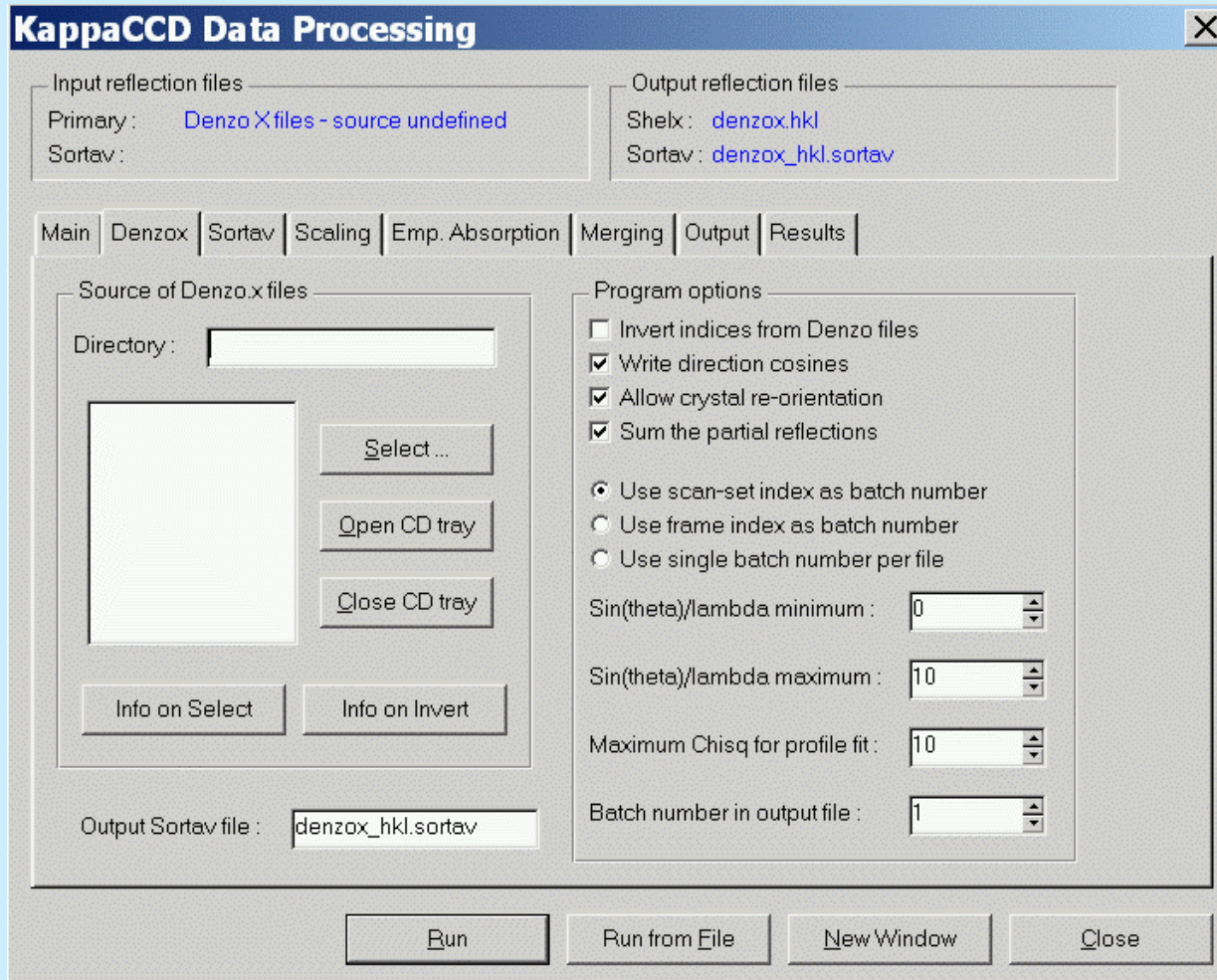
Quick view of data quality by Weiss or Diederich - Karplus programs

Concatenation of input files

Plots (Sortav)

Most data reduction programs handled through KappaCCD GUI

Denzox GUI



Denzox by R. Blessing

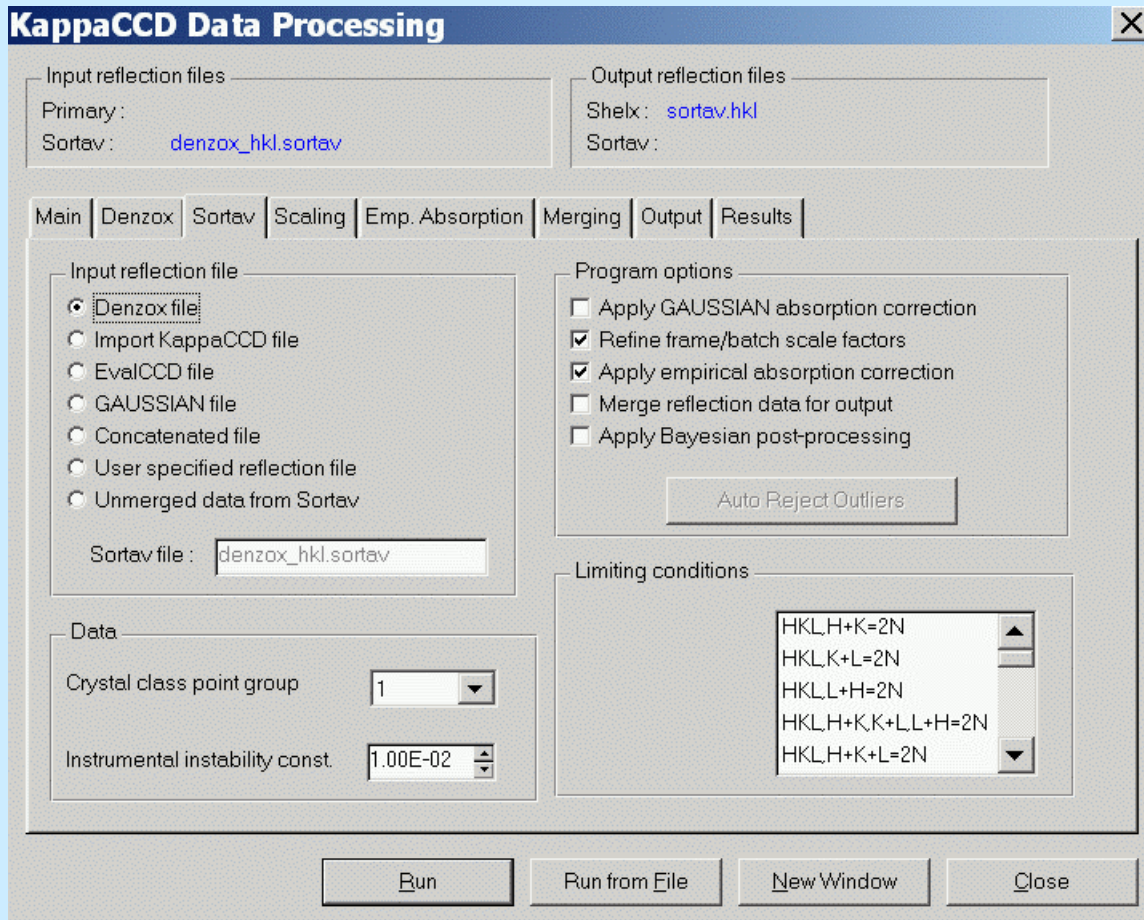
Reads .x files and
calculates direction
cosines + batch no.'s

Writes out files
denzox_hkl.sortav
denzox.sad

Reads .x files from disk
files or CD-ROM

Allows for Denzo
matrix variation

Sortav GUI



Sortav by R. Blessing

Pre-correction with
GAUSSIAN abs. cor.

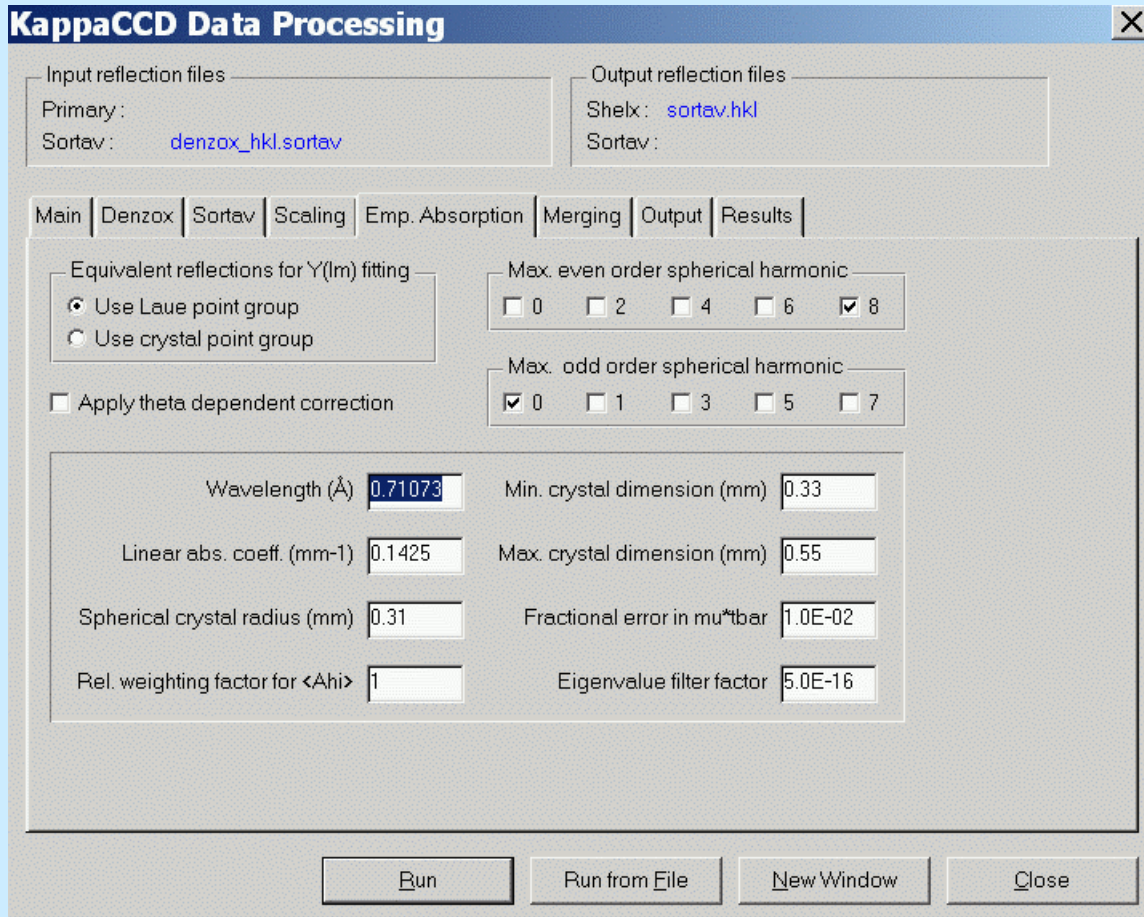
Apply frame/batch
scaling

Apply empirical
absorption correction

Data merging & reject
outliers

Check that parameters are correct !

Sortav GUI - Empirical absorption



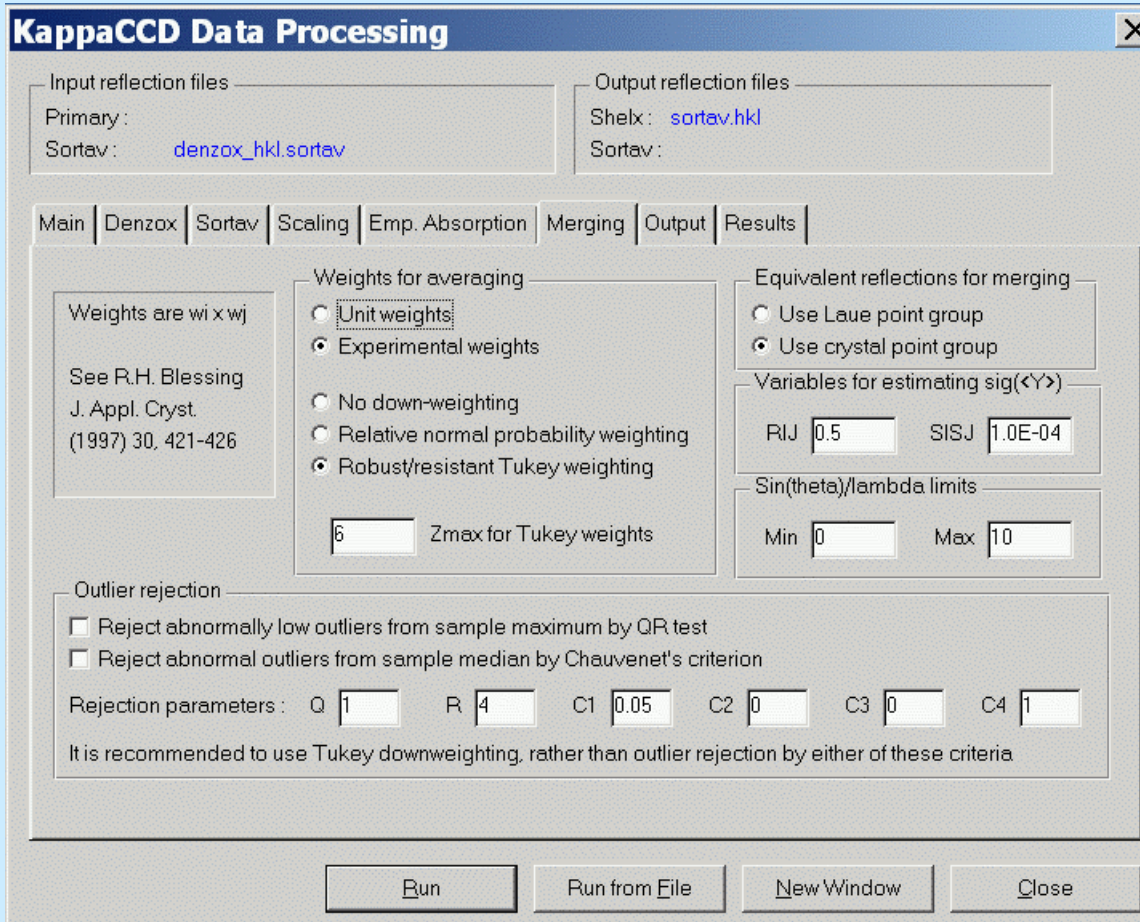
Requires sufficient data redundancy

Uses spherical harmonics to model absorption anisotropy

Odd harmonics used to model non-centrosymmetric systematic errors

θ -dependency also possible

Sortav GUI - Merging

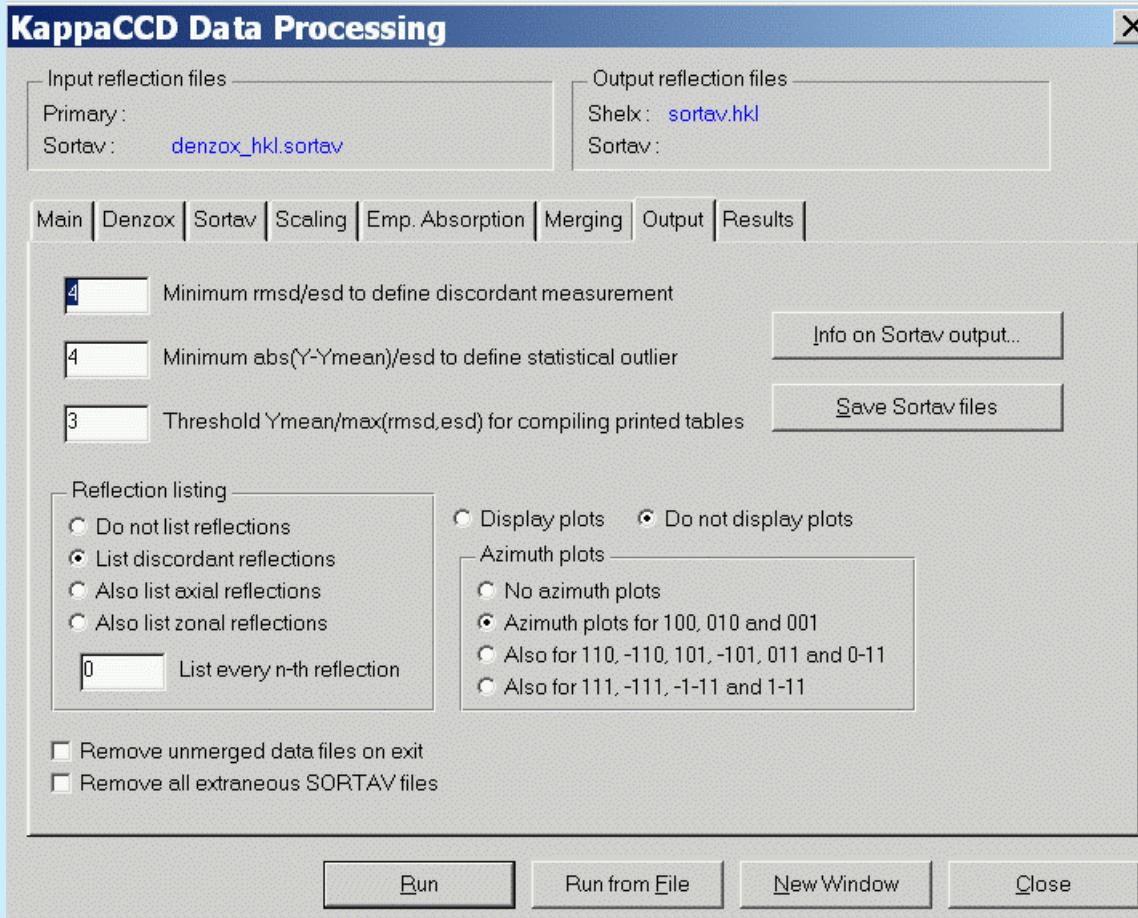


Several schemes for outlier rejection

Normally use Tukey downweighting and rejection of outliers

“Autoreject Outliers” until no further ones found

Sortav GUI - Output

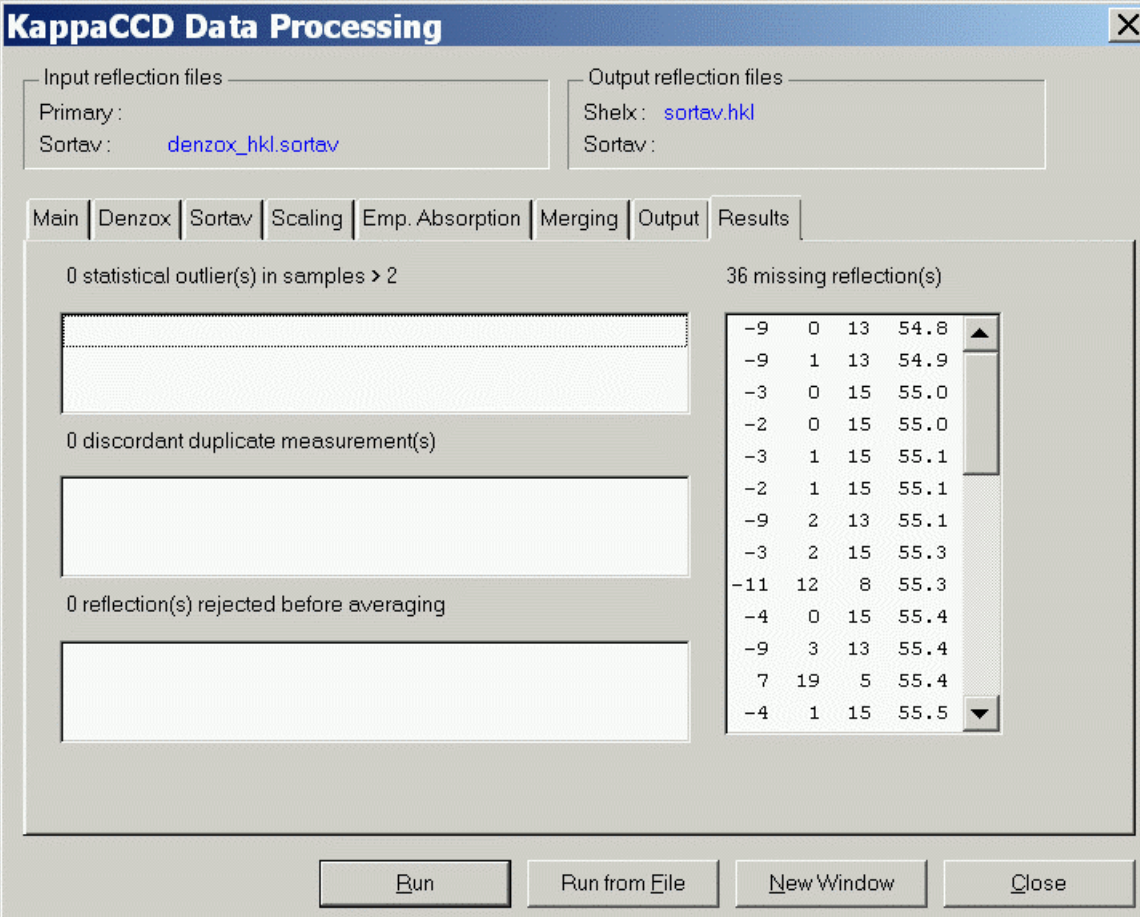


Save intermediate results here

Controls number of plots and verbosity of output.

Remove unwanted files

Sortav GUI - Results



KappaCCD Data Processing

Input reflection files: Primary: Sortav: `denzox_hkl.sortav`

Output reflection files: Shelx: `sortav.hkl` Sortav:

Main | Denzox | Sortav | Scaling | Emp. Absorption | Merging | Output | Results

0 statistical outlier(s) in samples > 2

0 discordant duplicate measurement(s)

0 reflection(s) rejected before averaging

36 missing reflection(s)

-9	0	13	54.8
-9	1	13	54.9
-3	0	15	55.0
-2	0	15	55.0
-3	1	15	55.1
-2	1	15	55.1
-9	2	13	55.1
-3	2	15	55.3
-11	12	8	55.3
-4	0	15	55.4
-9	3	13	55.4
7	19	5	55.4
-4	1	15	55.5

Run Run from File New Window Close

Shows outliers and rejected reflections

Shown missing reflections

Processing of SMART/SAINT data

SMART-SAINT RAW File(s) Summary [X]

	Intensity ranges		Exposure time (min)		Frame numbers		No. reflns
	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum	
FEPNCOA	-146.72099	58332.6992	4	596	4	597	2452
FEPNCOB	-74.964996	58147.3007	602	1200	3	600	2474
FEPNCO C	-68.375999	53412.6015	1203	1799	4	600	2504
FEPNCO D	-100.32299	41693.3984	1802	2054	3	255	1034
FEPNCO E	-62.098999	105834	2056	2354	3	600	1969
FEPNCO F	-31.742000	93237	2356	2654	3	600	1981
FEPNCO G	-32.820999	100514	2656	2953	4	598	1975
FEPNCO H	-92.516998	103624	2956	3253	4	598	1969
FEPNCO I	-42.411998	172722	1	99	3	596	989
FEPNCO J	-32.826999	148280	101	200	4	600	999
FEPNCO K	-58.915000	109070	200	299	3	600	1020
FEPNCO L	-29.718000	140085	1	100	4	598	961
FEPNCO M	-28.516000	162600	100	200	3	600	988
FEPNCO N	-55.997001	190336	200	299	5	598	963
FEPNCO O	-439.25399	551677	299	310	3	596	1031
FEPNCO P	-290.51699	533255	310	319	4	600	1043
FEPNCO Q	-107.28900	444682	319	329	3	600	1047
NFEPNCO A	-97.099998	44182.3007	4	596	4	597	2452
NFEPNCO B	-64.400001	44854	602	1200	3	600	2474
NFEPNCO C	-44.900001	49512.5	1203	1799	4	600	2504

OK Cancel

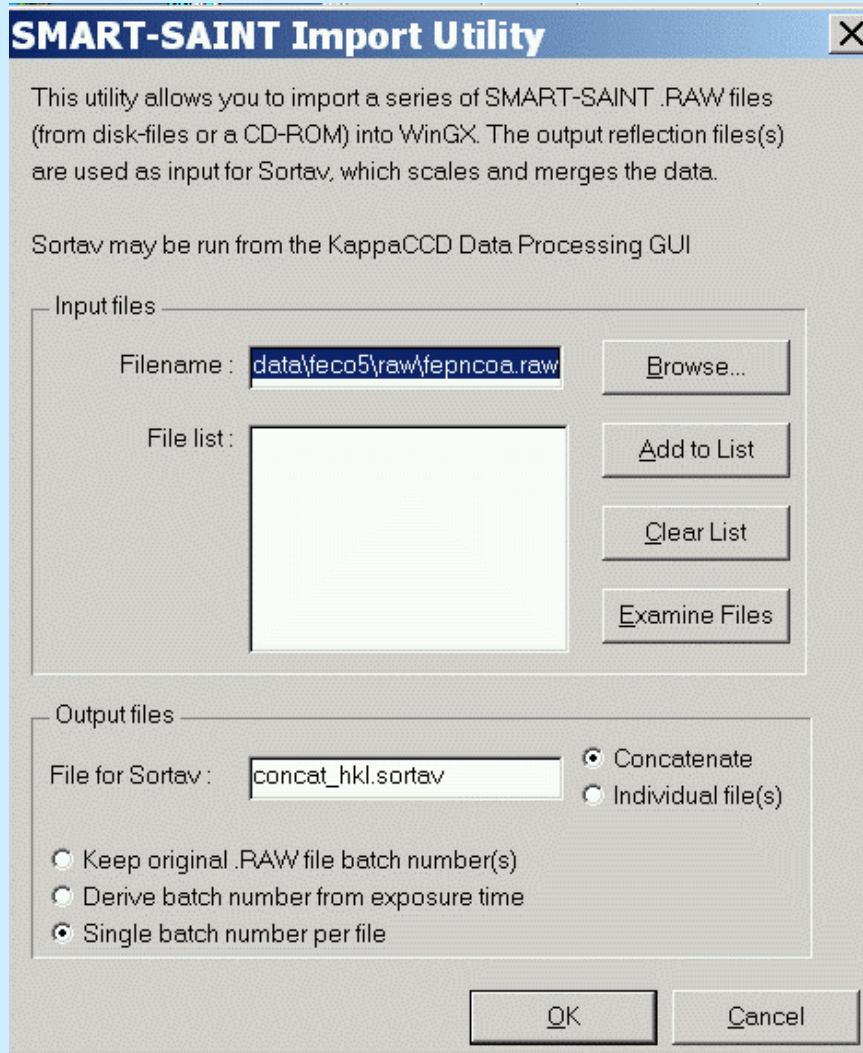
Reads in all .RAW files found in directory

Provides ranges of Intensities, exposure time, frame numbers.

Necessary to provide batch numbers for scaling.

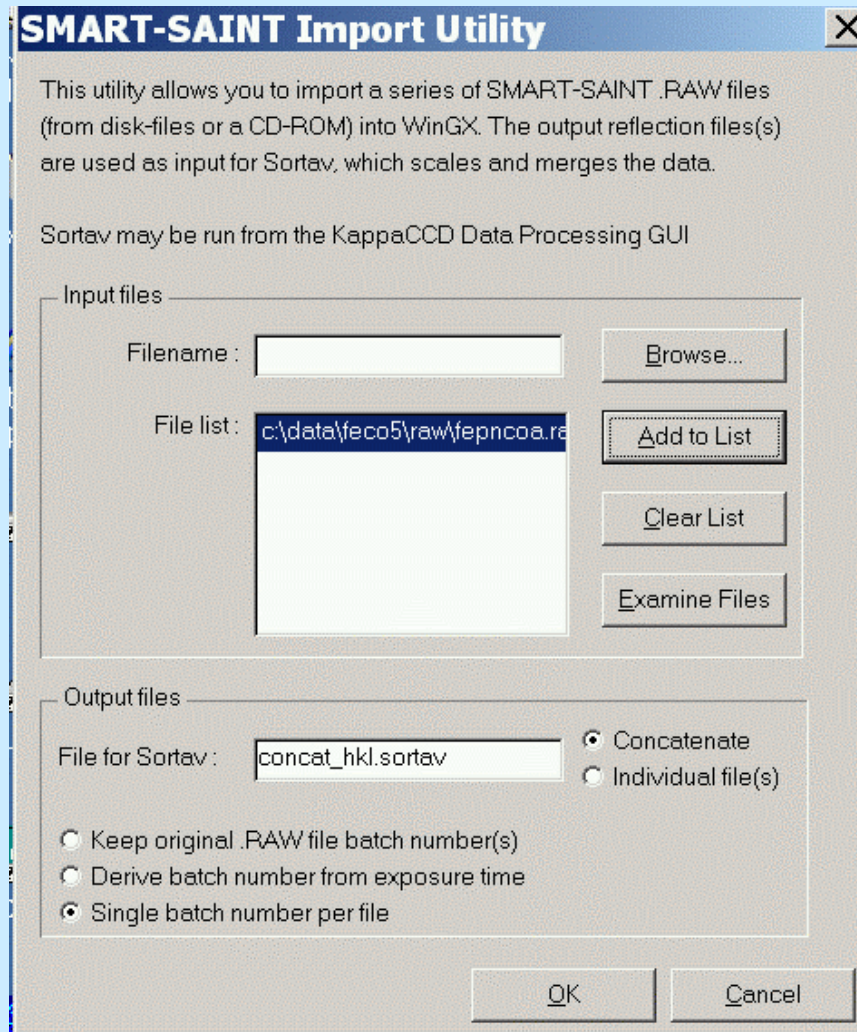
In this example, files should be processed in *four* batches

Processing of SMART/SAINT data



Choose which sets of RAW files to concatenate

Processing of SMART/SAINT data



Choose which sets of RAW files to concatenate

Decide on way to derive batch numbers for scaling

Write file *concat_hkl.sortav* which is exact translation of the data in RAW file.

Suitable for merging *etc* with Sortav