How to use ISAP for any kind of spectral data (e.g. non-ISO spectra)

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Before you begin:

Although ISAP was designed to reduce and analyse the pipeline products of the spectrometers on board ISO, it can be used for any kind of spectral data, i.e. also non-ISO spectra. All the basic ISAP functions – like rebin, average, or line fit – work just as well on simple spectra, which contain only wavelength and flux density information, as on the complicated structures that represent the ISO spectra. Even if you just want to have an easy but powerful environment to visualize your data ISAP will be a good choice. This guide is intended to give a basic description of how to use ISAP in the GUI mode to manipulate such a generic spectrum. If you are specifically interested in the processing and analysis of ISO data you'll find dedicated recipes (e.g. "How to reduce SWS AOT01 data in the ISAP GUI") on the ISAP web pages. This guide assumes that you are working with ISAP version 2.0. For a full description and alternate uses of a particular routine, consult the ISAP help. This help is accessible on the web: http://www.ipac.caltech.edu/iso/isap/isap.html or http://www.mpe.mpg.de/www_ir/ISO/observer/isap/isap.html. From within the GUI simply use the "Help!" button and select "WWW pages." The help pages contain - among other things - a beginners' GUI guide, a description of all the GUI Buttons, and links to the detailed help text of each individual ISAP routine ("Command Line Routines"). Here you'll also find the necessary information about routines that are not mentioned in this recipe. A brief description of ISAP can also be found in E. Sturm et al. 1998, ASP Conf. Ser. 145: Astronomical Data Analysis Software and Systems VII, 7, 161. Before you begin we **strongly recommend** to carefully read at least the beginners' GUI guide, which will make you familiar with the basic principles of the ISAP GUI!

Before starting ISAP (IDL in general), you should close all applications which use color (e.g., Netscape, or additional IDL sessions), as they will interfere with the ISAP color table. After ISAP has been started, you may restart these applications without affecting the ISAP session.

Finally: Whenever you have comments, suggestion or complaints about this manuscript (e.g., if you are missing some information), please let us know! Please check the web site for modifications of this document - from time to time.

1) **Data input and the interface between ISAP and other environments**

There are two major ways to start the GUI and read in data. One way is to start the GUI from your shell and then read in the data from within the GUI. If you have non-ISO data the easiest way to provide the data is to produce an ascii file with wavelength and flux. The rules for valid ascii files are described in detail on the web: at the ISAP homepage click on "GUI Buttons - Detailed Description", and then go to "input AAR data - read data - ascii" (OR: at the ISAP homepage click on "Documented headers of all ISAP Procedures", and then go to "ascii2yaaar" (this is the name of the basic input routine for ascii data)). But the most basic and simple file format would be a two column file with the wavelengths in the first column and the flux densities in the second column. Start ISAP in the GUI mode (possibly "isap" or "isap_gui" - see the readme text of your installation). Click on "Read data..." and then select "ASCII". Choose the desired file from the file selection tool which pops up (i.e. double click on the file name). If you do not provide any unit information in the ascii file, ISAP will ask you for the units of your data in a little graphical interface.

Another way to start the GUI and read in ascii data is to start from an existing IDL session. This could be an ISAP command line session. But, since ISAP is written in pure IDL it can be linked to *any* IDL session. Simply edit the file link_isap.pro in your ../ISAP/PRO/MPE directory (follow the instructions given in that file). In IDL then type "@link_isap" (you may have to specify the full path to start_isap.pro or to copy this file to you current directory). In this case you can pass in an existing IDL variable as data, provided the structure of this variable is conform to the ISAP standards: All non-standard/non-ISO data have a certain structure in ISAP which is called "YAAAR" (Yet Another AAR). For details see the Programmers Manual on the ISAP web. The easiest way to create a variable with such a structure in an IDL session is the following: suppose you have two variables x and y which contain the wavelengths and the flux densities of your spectrum. After you have linked ISAP to your session just type:
IDL> aar = conv2yaaar(x,y)
When asked, provide the units (any units may be input, but some ISAP routines will only work if the units are among the ones defined in the "change_units" routine – see the on line help for that routine). Alternatively you can specify the units in the command line, e.g.:
IDL> aar = conv2yaaar(x,y,in_units=['um','Jy'])
Then start the GUI by
IDL> start_gui,aar_in=aar

Vice versa, the GUI – on exit – passes an AAR back to the command line. To retrieve this aar type
IDL> aar_out=gui_output()
after you have exited the GUI.

2) **ISAP as a display tool**

ISAP offers many tools for an easy plotting of data. For instance you can set the plot style (e.g. line style, use of colors, plot symbols, logarithmic scale etc.) simply by clicking on buttons ("Set Plot Style"). You can zoom in by click-and-drag with the mouse, or you can read off x- and y-positions by moving the mouse across the plot window or by using the middle mouse button (see below). Another powerful tool is the oplot facility to overplot two spectra or two parts of one spectrum in different plot styles, using different scalings, etc. So, even if you just want to display your data, ISAP, in combination with the easy interface described above, could be very helpful.

To make use of the different color coding options offered by ISAP you would have to add a tag to your spectrum, either "det", "scan", "scandir" or "line". Click on "Special Fns...", then on "Data Tags", and then select "Add data tag". At this point it does not matter which of the possible tag names you choose. Only if you want to use the "shift" routine later on you should follow a few considerations about tag naming (see section).

You would also have to give different parts of your spectrum different tag values. For instance, if you have an echelle spectrum, you could choose the "line" tag and give the different orders of that spectrum different values (different line numbers). To do so, you would either have to read in the different orders from different files, or to split the spectrum into different parts (see section).

You can also include the tag information in your ascii data file (see the on line help for ascii reader), identifying different parts with different tag values directly in the ascii file.

Now click on "Select Plot Style" and set the color coding preference according to the tag you have provided. Note, that **plotting** of large data sets in plot modes **other than the default** "dot cloud" mode can take a **long time**. If you want to interrupt a plotting process, and you are running UNIX, type "Ctrl-C" in the command line of your IDL window, and then type "return". You should now be able to reset the plot style and to plot again.

If you want to know the flux and wavelength values of a certain point, simply click on it (or near it) with the middle mouse button. The text field at the bottom of the GUI will show these values.

You can also overplot two spectra: Make one of the spectra the reference spectrum (click on "Stored data sets", select the file and select "use as reference"). Make the other spectrum the prime spectrum ("Stored data sets" →"Make prime"). Now catch the part of interest in that spectrum (e.g. all of it) with the right mouse button and select "oplot data to ref" in the tool box that pops up. The overplot tool offers different plot stytle options for primary and reference data, as well as scaling and offset options.

3) **Line fitting**

One of the most obvious reasons to use ISAP for non-ISO spectra is its' powerful line fit tool. Simply plot the line, catch it (together with some continuum around it) with the right mouse button and select "line fit" in the tool box that pops up. The units of your spectrum are supposed to be 'um' (microns) for wavelength and either 'Jy' or 'W/cm^ 2/um' for fluxes. If not you must use the unit conversion tool first (which you'll find under "Special Fns..."). Within the line fit tool you can fit and subtract the continuum (polynomials of different degrees), you can fit one or several lines and measure the line flux (gauss profile, lorentz profile, or simply integrating under the line). You'll also get other information like the line center or standard deviation of the measurement. ISAP will also suggest a line identification to you, based on a built in line list, if the line is in the 2 to 200 micron range. For this purpose you can specify a redshift.

4) **Rebin**

Another very useful ISAP function is REBIN. You can use it, e.g., before you co-add several spectra, or before you subtract a background spectrum from an on-source spectrum (both operations can be done with ARITHM2REF). You can rebin to the wavelength grid of another spectrum (REBIN2REF) or specify the new grid yourself (REBIN) through different combinations of start point, end point, resolution , step width etc. If you have data tags (like "line") with different values of that tag across your spectrum you can either rebin these different parts separately or all together.

5) **Smooth**

This function reduces the noise in the flux values of a spectrum (either in unique parts, such as detectors, or all together) by convolution with a selected function: Boxcar, Gaussian, Lorentzian, Median, Hanning, or Sinc. If you are interested in line profiles you should, however, be very careful when choosing the function width (in other words: don't smooth too much!). Stay well below the FWHM of your lines (or try using the boxcar or median filter).

6) **Removal of bad data**

To remove "bad data" from you spectrum you can choose between "Tippex", "Mask" and "Zap" (invoked via the tool box which pops up if you select some data with the right mouse button). With TIPPEX a single point is replaced by a linear interpolation between the two corresponding neighbouring points. This is done as unique as possible, i.e. the two points choosen as basis for the linear interpolation are of the same detector, scan and scan direction, if any of this information is available. MASK simply masks out the selected data, i.e. they will not be taken into account for the computation of correction functions in the subsequent processing steps (e.g. in AVERAGE they won't contribute to the average). But the masked data stay in the data set, and shift, for instance, shifts masked points as well (without using them for the computation of the correction). Note, that MASK makes use of the flag word in the YAAAR structure. So if you later on process the data with a non-ISAP tool which does not consider this flag you will process (e.g. plot) all masked points as well.

With ZAP you really get rid of the data, they are thrown away.

If you have to zap (mask/tippex/etc.) a lot you can make use of the "Preselect" button: Click on it and choose "Zap". From now on ISAP will automatically zap whenever you catch data points with the right mouse button. Don't forget to switch preselect off when you are done with zapping. (If you do forget, the "undo" button in the upper right corner of the GUI might come in handy...).

An alternative to zapping "by hand" is automatic "Clipping" (see section).

If you just want to reduce noise you can use the routines SMOOTH or REBIN.

Don't forget to STORE!

7) **Average and Clip**

For a detailed description of the average tool please read the web pages (see "GUI Buttons"). The bin size should correspond to the spectral resolution. To preserve oversampling the bin size should be smaller than the actual resolution element.

The plot style for the "before" window should be the default style (unconnected, white, dots). The plotstyle options in combination with the possibility to zoom in (with the left mouse button), e.g. into a small range around a line, and to freeze the plot range in both windows to identical values, should help you to judge the result. To adjust the plot ranges in both windows use "Replot Max" in the left window, then use "Copied Range" in the right window.

If the oplot button is checked, ISAP overplots the result directly in the left hand side plot window. To check if your bin size is appropriate you could perform a few spot checks prior to the actual averaging.

In oplot mode you will also see the points that have been clipped by the clipping routine (in red). Note, that the small bin sizes can be too small for a significant clipping. In this case try to lower the sigma value (e.g. 2 or 1). Alternatively, there are two stand alone clipping routines available. A very basic one is available under the "arithm" button (in the tool box). It performs a kappa x sigma clipping on the basis of all selected data (i.e. the bin size is the entire selected wavelength range). Kappa can be specified by the user (e.g. 2.5). Outliers more than kappa x sigma off will be masked. You can then use the plot option "show masked data" to view the result. If you like it: "zap masked", if not: "unmask". A more advanced clipping tool is available under "Clipping". This routine allows you to adjust a bin size.

You can choose between different methods of averaging (see the description on the web). Try all of them to find the best method for your data set.

Don't forget to STORE!

8) **Flatfielding (shift)**

SHIFT is a tool to normalise different parts of a spectrum either to a reference spectrum or to a common level, preserving their mean value. It was developed with the characteristics of the two ISO spectrometers in mind. But it can be useful for non-ISO spectra, too, if you follow a few simple considerations: First you must edit the EOHAAOTN keyword in the header. The header editor can be invoked via the button "Header" in the top row of the GUI. Click on the line with this keyword, edit the value in the top row of the editor, i.e. set the value to 'S01', and click on “overwrite”. Then exit (and store if you wish). SHIFT identifies the different parts it is supposed to normalise by their intrument tags, i.e. DET, SCAN, or LINE. So you must add one of these tags to your spectrum, with different values for the different parts of interest. If you choose DET, SHIFT will compute the common average for the overlap region of the different “detectors” only. In this case you have a choice between “preserve mean” and normalise to a “good detector” as reference. For instance, if you have 10 “detectors” you can either adjust all 10 detectors to the mean level or adjust 9 detectors to the level of a 10th, “good” detector. For SCAN or LINE SHIFT will work on the full wavelength range that your data span. Here you have only the “preserve mean” option. In other words: When you shift two “detectors” the result will have a common average in the overlap region of these two detectors (if you have more than two dets, shift will start with the first one – or the “good” one – and ripple through the entire spectrum). If you shift “lines” or “scans”, each line or scan will be shifted such that it – as a whole – has the same average than all the other ones.

Here is an example: suppose you have an Echelle spectrum where the different overlapping orders have not yet been normalised to each other, i.e. have not been “glued” together. In this case you could assign a detector tag to the different orders (see section), and then use SHIFT in the “preserve mean” and (presumably) “gain” mode (see below) to produce a normalised version. Subsequently you could use AVERAGE to average across detectors, producing one single contiguous spectrum.

Shifting can be done in “offset” (additive) or “gain” (multiplicative) mode. For instance, if the differences between the spectra can be attributed to uncertainties in the dark current subtraction the “offset” mode should be choosen. If the dark current can be neglected and differences are due to gain effects, i.e. multiplicative effects, “scaling” would be the right option. No general rules can be given here to decide which of the modes is the best. An example for a problematic case is the combination of a strong line on a weak continuum: the continuum may be better corrected in “offset” mode, whereas the line itself might need a “gain” correction. If the continuum flux is around zero, both modes may fail, however. In this case you could try the following: mask out either the line or the continuum (depending on what you are interested in most) and shift in offset or gain mode. Then unmask again. (Note: shift will not use the masked data for the computation of the correction, but it will apply the correction to the masked data as well).

The result of the shifting should in any case be examined critically. Two other tools for normalisations are NORM2REF and NORM2CONST.

9) **subsetting and merging**

Sometimes it is necessary to divide a spectrum into several sub-spectra, to work on these sub-spectra separately, and finally to merge back these parts to a single spectrum again. For instance, if you have a single Echelle spectrum with different orders you might want to give each order a different detector tag value. To do so you first have to “add tag” (under “Special Fns....”). Then you have to select each order (part) of the spectrum with the right mouse button, and make this part a “new aar” (button named “Make

AAR"). You will be asked for a name for this new sub-spectrum. Then use "Special Fns..." →Data Tags →"Increment data tag" to assign a value to the tag, and STORE the result. Loop through all the different parts. Finally, you can merge all parts back to one single spectrum by using the "merge group of AARs" routine under "Special Fns...".

10) **Further functions**

Black body fit: The purpose of this routine is to enable the user to fit one, two, or three summed blackbody components to a data set. See the on-line documentation for more details.

Photometry: This routine provides photometric measurements of ISO SWS and LWS spectra or other spectra introduced into the ISAP environment. The routine will either integrate or average a source energy distribution (SED) over a specified range, and will do so while weighting the distribution with a "filter" function. With the appropriate filter function, the user may make flux comparisons with measurements from ISOPHOT, IRAS, KAO instruments, ground-based telescope instruments, or theoretical predictions. See the on-line documentation for more details.

Arithm may be helpful for all kinds of arithmetic operations (e.g. to subtract or add two spectra or to add a constant, etc.). See the on-line documentation for more details.

The **unit conversion** tool (accessible under "Special Fns...") may also be of interest for you. See the on-line documentation for more details.

Zodiacal can be used to subtract the dominant foreground at ISO-SWS wavelengths. It has implement a model for zodiacal light, including the effect of varying solar elongation (to be computed from ra,dec,ut). You will have to add seven keywords to the header, providing the intrument coordinates (ra and dec in degrees), date, ut, telescope, and instrument information. The header editor can be invoked via the button "Header" in the top row of the GUI. Add the two keywords RA and DEC with ra and dec, the two keywords TELESCOP and INSTRUME with telescope and instrument names, DATE (CCYY-MM-DD), UT (HH:MM:SS.SS), and EPOCH (2000). Example:

RA	148.96124
DEC	69.6790
DATE	1998-05-28
UT	12:24:13.00
TELESCOP	VLT
INSTRUME	ECHELLE13
EPOCH	2000

See the on-line documentation for more details.

Dered (available in the command line mode only) allows to deredden the spectrum according to a given extinction law. See the on-line documentation for more details.

Defringe (sws) See the on-line documentation for more details.

Again: when you exit the GUI you will be in ISAP's command line mode. By typing *aar=gui_output()* you'll get the aar which was prime on exit of the GUI. You can then work on your aar just like in a normal IDL command line environment. You can go back to a GUI session any time by typing *start_gui* or *start_gui,aar_in=aar*. The latter command passes an aar from your command line session directly into the GUI (see the information on the ISAP web page under "IDL-ISAP interface").

If you need more help, you should contact (or consider to schedule a visit to) IPAC, MPE, VILSPA or one of the other national ISO data centers. Informations about IPAC, MPE or the VILSPA IDC can be found on the web:
http://www.ipac.caltech.edu/iso/
http://www.mpe-garching.mpg.de/iso/
http://isowww.estec.esa.nl/
You can also email us any kind of problems with ISAP and any suggestions you have:
isap_dev@ipac.caltech.edu. (Within the GUI just click on "Send Mail")
The author of this recipe can be contacted via: sturm@mpe.mpg.de

If you are going to publish results which are based on a data reduction and/or analysis with ISAP we would very much appreciate the following acknowledgement:
"The ISAP Spectral Analysis Package (ISAP) is a joint development by the LWS and SWS Instrument Teams and Data Centres. Contributing institutes are CESR, IAS, IPAC, MPE, RAL and SRON."

And now: Good luck with the reduction and analysis of your data!