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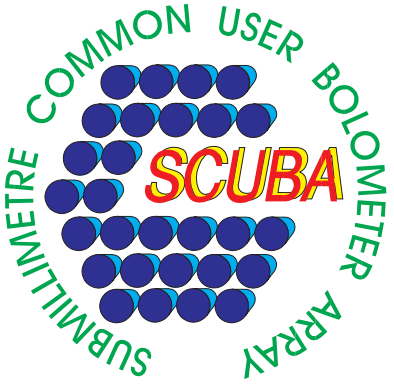
SURF – SCUBA User Reduction Facility
1.6
User's manual



Abstract

SURF is a set of ADAM tasks necessary for reducing demodulated Submillimetre Common-User Bolometer Array (SCUBA) data obtained from the James Clerk Maxwell Telescope. The tasks allows one to completely re-reduce your SCUBA data.

This document describes how to reduce SCUBA data and includes detailed descriptions of each task.

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1 Introduction

The Submillimetre Common-User Bolometer Array (SCUBA) [1, 2] is a continuum instrument on the James Clerk Maxwell Telescope[1], Mauna Kea, Hawaii. SCUBA has two arrays and can observe simultaneously at two wavelengths (three wavelengths when using the photometry pixels) – the layout of the SCUBA arrays is shown in Fig. 1.

The on-line system produces data in the Starlink NDF format [3]. Both the raw demodulated data (signified by '_dem_' in the file name) and a reduced image ('RO' file) can be stored. This package is designed to take the demodulated data (stored in the `[.dem]` directory on-line) and remove SCUBA dependent effects. In the case of MAP data, a rectangular-gridded image is produced, for PHOTOM observations a set of photometry data. Packages such as GAIA[4] or KAPPA[5] display, for MAP, and KAPPA linplot and drawsig, for PHOTOM, can be used for further processing. Calibration via planet observations can be determined using the FLUXES[6] package. The CONVERT[7] package can also be used to export the data into your favoured data format.

The RO file (signified by '_red_' in the file name) contains the reduced data (image, skydip result, photometry result) calculated by the on-line system. These data can be examined either by using hdstrace[8] or, for images, a Starlink-compatible image display package (note that nested NDFs are used - see Appendix E).

[1] http://www.eaboservatory.org/jcmt

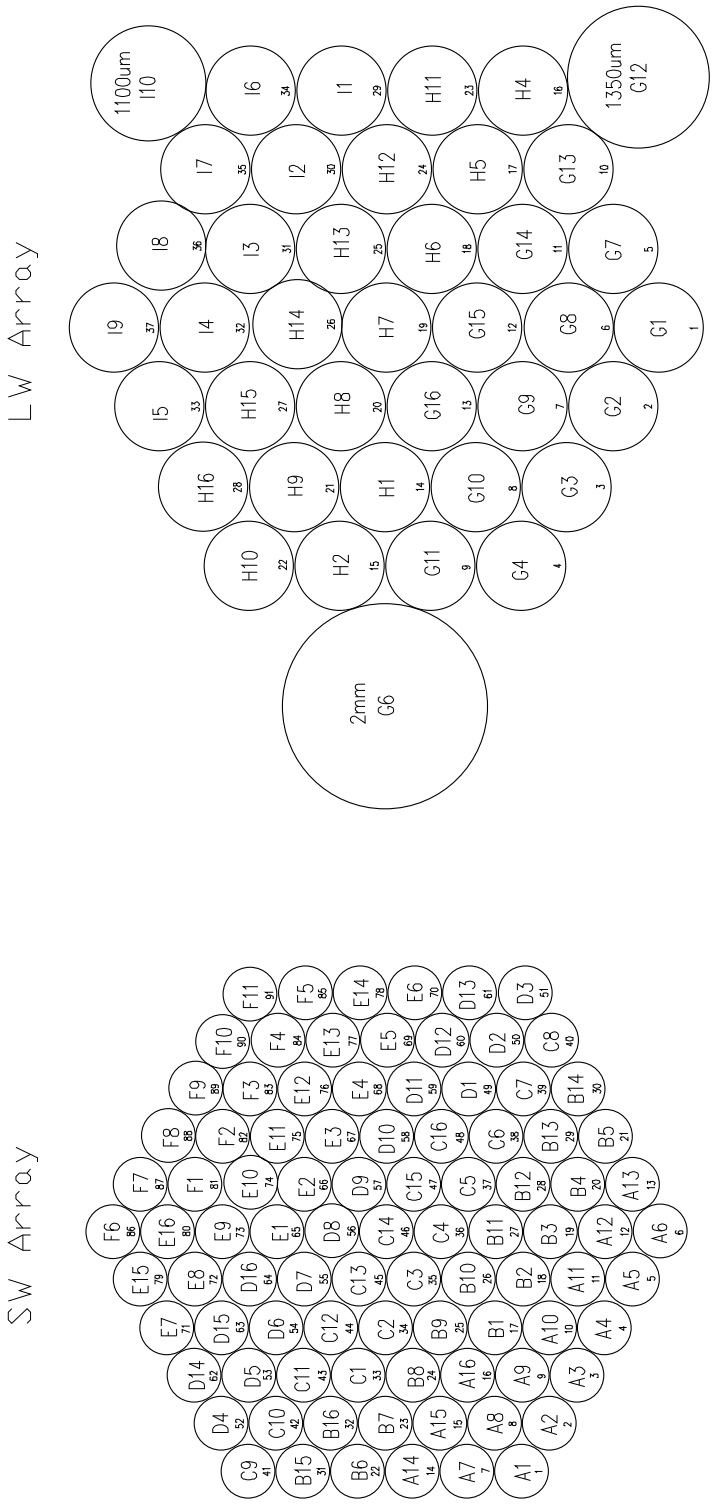

Figure 1: The SCUBA arrays

2 Starting up SURF

The SURF environment can be initialised from the C-shell using the `surf` command.

```
% surf

   SURF - SCUBA User Reduction Facility
     Commands are now available -- (Version 1.6-0)

     Type scuhelp for help on SURF commands.
     Type "showme sun216" to browse the hypertext documentation.
```

Note that the % represents the C-shell prompt and shouldn't be typed. SURF is also available from the ICL command language.

2.1 Getting help

Help is available in two forms; from the command-line and via a hypertext version of this document. The command-line version is available with

```
% scuhelp
```

and the hypertext version can be obtained with

```
% findme surf
```

or

```
% showme sun216
```

A WWW browser will be started up if necessary.

It is possible to start the help system when responding to an ADAM prompt. Supplying a '?' will give more information on the parameter being requested and supplying '??' will start the interactive help system.

There are also two cookbooks available; one dealing with the reduction of photometry data [9] and the other dealing with the reduction of map data [10].

Alternatively, you can contact JCMT staff for advice via the World-Wide-Web[2].

[2]http://www.eaobservatory.org/jcmt/help

3 What data do I have?

Journal software is available to aid with book-keeping of observation files.[3] If you are reducing your data at the Joint Astronomy Centre you may need to read Appendix D to find where the data are stored.

sculog will give a summary of all NDF files in a directory (the directory is the current working directory and, if set, the directory specified by the DATADIR environment variable (§7)).

```
% sculog

 Enter starting observation number [0] 94
 Enter final observation number [last] 95
-Log for directory: /jcmt_sw/scuba/sun216
                    /scuba/observe/apr25/dem
94      JUPITER             PHOTOM        1997:4:25     17:43:39.99893
   RA: 21 26  1.54 Dec: -15 42 52.0 (J2000) Observed centre: PLANET
   Mean airmass: 1.2310825  Bolometers:   H7                Filter: 450N:850
   Throw:    60 arcsec  AZ  Integrations: 4      Measurements: 1
   Accept: not used         DATA_KPT: DEMOD              Gain: 1
   Observation file: jupiter_h7.obs             Data file: apr25_dem_0094

---------

95                 SKYDIP        1997:4:25     17:46:26.99799
   Bolometers:   SHORT_DC,LONG_DC                Filter: 450N:850
   Max EL: 80   Min EL: 15  Integrations: 20     Measurements: 10
   Accept: NO               DATA_KPT: DEMOD              Gain: 1
   Observation file: scuba_skydip.obs           Data file: apr25_dem_0095
---------
```

In most cases sculog provides far too much information and a one line summary is more desirable. obssum[4] is provided for this purpose:

```
% obssum -demod

 Enter starting observation number [0] 92
 Enter final observation number [last] 98
-Log for directory: /jcmt_sw/scuba/sun216
                    /scuba/observe/apr25/dem

 #    HST    Obsmode   Source   Meas/Int Airmass  Filter  Bolometers
---- -----   --------- -------  -------- ------- -------- ----------
92   07:33   PHOTOM    JUPITER     1/4   1.229 450N:850N G4
93   07:36   PHOTOM    JUPITER     1/4   1.229 450N:850N G3
94   07:43   PHOTOM    JUPITER     1/4   1.231 450N:850N H7
95   07:46   SKYDIP    SKY        10/20        450N:850N SHORT_DC,LONG_DC
96   07:54   POINTING  uranus      1/2   1.337 450N:850N LONG
97   07:57   MAP       uranus      1/1   1.407 450N:850N SHORT,LONG
98   08:45   POINTING  uranus      1/2   1.488 450N:850N LONG
```

[3] only available if `ndfperl` is installed on your system (see Appendix K)

[4] obssum is simply an alias for sculog `-summary`.

In this example a summary listing has been requested for observations 92 through 98 from the $DATADIR directory (there were no demodulated data files in my current directory). The '–demod' flag indicated that I am only interested in raw demodulated data (i.e. files containing '_dem_' in their names). sculog (and obssum) supports many more options and these are detailed in §C.

Alternatively, listings of certain observations can be obtained by using the more specialized listing programs photsum, mapsum, pointsum and skysum. pointsum lists pointing observations, photsum lists photometry observations (and, in fact, skydip observations), mapsum lists map observations and skysum lists skydip observations. Using photsum instead of sculog on the data used above gives:

```
% photsum --begin=92 --end=98
 #    HST    Source   Meas/Int  Am   Filter  SubInst Signal   S/N   Tau  Seeing
---  -----   -------  -------- ---- -------- ------- ------  -----  ---  ------
92   07:33   JUPITER     1/4   1.23 450N:850 LONG   7.85e+00 2841.  0.074 0.161
93   07:36   JUPITER     1/4   1.23 450N:850 LONG   6.34e+00 1257.  0.074 0.161
94   07:43   JUPITER     1/4   1.23 450N:850 LONG   5.97e+00 936.4  0.074 0.423
                                               SHORT  9.26e-01 164.
**************
95   07:46   SKYDIP     10/20       450N:850 SHORT:  1.756          0.074 0.423
                                               LONG    0.310
```

In this case I specify the range of observations on the command line and the format of the listing has changed from that returned by sculog. Note that the signal and signal-to-noise are now provided[5] – this is only the case if RO files are catalogued since the demodulated data files do not contain results (the column is left blank if no reduced data is found).

On the other hand, mapsum gives this output:

```
% mapsum --begin=92 --end=100
 #    HST    Source   Meas/Int  Am   Filter    Mode    Thr Crd  PA   Tau  Seeing
---  -----   -------  -------- ---- -------- -------- --- --- ----  ---  ------
**************
95   07:46   SKYDIP     10/20       450N:850 SHORT:  1.756          0.074 0.423
                                               LONG    0.310
--------------
97   07:57   uranus      1/1   1.41 450N:850 RASTER   40  SC     0  0.074 0.423
```

pointsum can be used to list pointing data:

```
% pointsum --begin=50 --end=98
 #    LST    Source  Meas/Int Az  El  Filter  Inst   Uaz  Uel   Tau  Seeing Hum
---  -----   ------- -------- --- -- -------  ----   ---  ---   ---  ------ ---
51   19:32   jupiter    1/1   140 45 450N:850 LONG  -1.6 -9.5  0.074 0.344  14%
62   20:06   jupiter    1/1   150 49 450N:850 LONG  -2.1 -10.  0.074 0.351  14%
83   20:56   jupiter    1/1   168 53 450N:850 LONG  -1.8 -11.  0.074 0.242  15%
96   21:47   uranus     1/2   203 48 450N:850 LONG  -2.7 -11.  0.074 0.423  14%
98   22:38   uranus     1/2   218 42 450N:850 LONG  -3.0 -9.6  0.074 0.984  20%
```

[5]Note that HDS creates temporary files when mapping the reduced data. If the files are in a directory in which you do not have write permission, this operation will fail and photsum will return an error message. This can be overcome by forcing HDS to write temporary files to another directory by setting the HDS_SCRATCH environment variable to a writeable directory (e.g. `% setenv HDS_SCRATCH /tmp`)

Note that UAZ and UEL indicate the offsets before the pointing observation and that the time is now quoted as LST instead of HST since this is the format expected by change_pointing.

In all cases the output can be stored in a file using standard unix redirection so long as the search path is fully specified (either with the '-all' flag or with '-begin=' and '-end=') so that the programs are not waiting for input. e.g.:

```
% obssum -all > summary.txt
```

4 Supported Observing Modes

The SURF package supports the following SCUBA observing modes:

- **ALIGN**

  This is the mode used for setting the X and Y alignment of the secondary mirror. This mode usually consists of 5 measurements, one for each secondary mirror position. Currently the standard observing mode uses a single pixel to calculate the best secondary mirror position since it is the most efficient method for determining the alignment – this is similar to the heterodyne X and Y focus observations – and this mode is not supported by SURF. Alternatively it is possible to ALIGN using the entire array and, since these data are simply 5 JIGGLE/MAPS, this mode can be reduced with SURF. Care must be taken to make sure that each measurement is rebinned independently (switch off the measurements that are not required by using change_quality) otherwise you will end up with the average of all the measurements at all secondary mirror positions (the unfocussed images will dominate). Note that no special processing is perfomed on these data and SURF does not provide a way of calculating the secondary mirror offset.

- **FOCUS**

  This is the mode used for focussing the Z axis of telescope. This mode is similar to ALIGN in that five measurements are taken and that the single pixel mode is not supported. The same care must be taken when reducing the unfocussed images since each measurement will be from a different secondary mirror position.

- **JIGGLE/MAP**

  This is the main imaging mode for sources which are smaller than the array (i.e. less than about 2 arcmin). All JIGGLE/MAP observations (including ALIGN, FOCUS and POINTING) are reduced in the same way using rebin to make the final image. [info on how a JIGGLE/MAP is taken - reference exposures and switches]

- **NOISE**

  This is the mode used to measure the noise behaviour of the array. Data are reduced using reduce_noise. Noise data can be inspected with scunoise.

- **PHOTOM**

  This mode is used to measure the flux of a point source. In its simplest guise the observation involves pointing a single bolometer at the source, measuring the signal, chopping and

nodding to reduce the effect of sky emission, and integrating to build up the signal-to-noise. SCUBA also allows for 2 or 3 bolometer photometry (chopping on the array), simultaneous photometry using the long and short wave arrays, and jiggling on source to reduce the effects of seeing. The scuphot task is used to reduce photometry observations to a simpler form (one data point per integration) for further analysis.

- **POINTING**

  This mode is used to check the pointing of the telescope by observing a bright source with a known position. A single-pixel observing mode is available and is not supported by SURF. The JIGGLE/MAP implementation can be processed as a standard JIGGLE/MAP. The pointing offset can be checked by using, say, the KAPPA centroid task.

- **POLPHOT/POLMAP**

  These are PHOTOM or MAP observations observed in polarimetry mode. For these observations a measurement is taken (usually consisting of one integration) for different positions of a half-wave plate. SURF can be used to reduce these measurements so they can be processed by a specialized polarimetry data reduction package such as POLPACK.

- **SCAN/MAP**

  In SCAN/MAP mode (also known as 'on-the-fly' mapping) the telescope is continuously scanned across the sky (usually at a Nasmyth position angle of 18 degrees so that the image is fully-sampled on a single pass) whilst using the secondary mirror to chop so that atmospheric contributions can be minimized. Scan rates of up to 24 arcseconds per second are possible in this mode and it is the most efficient SCUBA mapping mode. One problem with this mode is that the data is taken in dual-beam mode; each data point is the difference between the left and the right chop positions. This means that sources appear twice in data, separated by the chop throw: a positive beam and a negative beam – this dual beam response must be taken out in software. Two forms of data taking are implemented: one involves chopping along the scan direction [11] whilst the other involves chopping in a fixed direction on the sky but combining data from many chop configurations [12, 13].

- **SKYDIP**

  This mode measures the sky brightness temperature at a range of elevations and uses that data to calculate the zenith sky opacity. In most cases the values found in the RO file should be sufficient and skydip data should not need to be reanalysed. The skydip task can be used to re-reduce the data if necessary (see also sdip). A summary of the skydip observations in a given directory can be produced with the skysum command.

5 Message filtering

All of the tasks print messages to standard output. On some occasions it is desirable for more or less information to be displayed to the user. For this reason the verbosity of all the tasks can be modified by use of the MSG_FILTER parameter. This parameter controls the messaging level of the tasks and can take values of NORM (normal messaging level), VERB (verbose) or QUIET [18]. Note that warning messages (such as forgetting to flatfield) are always displayed whereas the general messages can be turned off by using QUIET mode.

Specifier	Definition
{	Begins a SCUBA section
}	Ends a SCUBA section
b	indicates that the following numbers
	describe bolometer numbers (ie X axis)
p	indicates data position (ie Y axis).
	Can not be used in conjunction with s, e, i or m
s	switches
e	exposures
i	integrations
m	measurements
;	Separates components
,	Separates numbers
:	indicates a range of values
−	negates the section when placed after the last curly bracket

Table 1: Special characters used to describe SCUBA sections

6 SCUBA sections

Since all the tasks rely on information in the NDF extensions that must correspond to data in the main DATA_ARRAY none of the SURF tasks can accept NDF sections [3]. On many occassions it is desirable to work on a subset of the observation (e.g. data from a specific exposure, integration or measurement) and the SURF package supports this via the concept of a 'SCUBA section.'

A SCUBA section is indicated by using curly brackets after the file name (c.f. round brackets for NDF sections). The brackets then contain a specification that selects a certain part of the input data using the format shown in table 1.

Note that SCUBA data is organised with bolometer number along the X axis and time (eg jiggle) along the Y axis so that the 'b' specifier simply selects out bolometer data but the p, s, e, i and m specifiers select data by time.

Here are some example SCUBA sections:

test{}
: select all points (good for resetting change_quality mask)

test{i3}
: means select all bolometers in integration 3 for all measurements

test{b3:5}
select bolometers 3 to 5 for all points

test{e3}–
select everything except the 3rd exposure in each integration

test{e3;i4}
select the third exposure in integration 4

test{b5;p500:600}
select points 500 to 600 for bolometer 5

test{b5:7,19}
select bolometers 5 through 7 and bolometer 19

test{i1:4,7}{b3}
select integrations 1,2,3,4 and 7 and all data for bolometer 3.

test{b2}{i3}
select bolometer 2 and integration 3. Note that this is different to {b2;i3} which would only select the second bolometer from integration 3.

test{p50:100}{b32}–
select samples 1 through 49 and 101 through to the end, and all bolometers except number 32.

The tasks rebin, bolrebin, intrebin, change_data, change_quality and extract_data understand the concept of SCUBA sections.

7 Environment variables

The behaviour of SURF can be modified by the use of environment variables.

7.1 SURF environment variables

This section describes environment variables that are spcific to SURF. SURF has variables for determining the location of the data (DATADIR and SCUBA_PREFIX)[6] and the behaviour of the automatic filenaming system (SCUBA_SUFFIX).

7.1.1 DATADIR

DATADIR can be used to specify an alternative location for the raw data. This means that users do not need to make multiple copies of the demodulated data files (for example, at the JAC support scientists access the data archive directly and never take their own copies) and saves disk space.

As an example, at the JAC, to access demodulated data taken on the 30th October 1997 all that is needed is

[6]These variables are directly comparable with the SPECX [14] use of the DATADIR environment variable and the `set-gsd-filename` command.

```
% setenv DATADIR /scuba/observe/19971030/dem
```

$DATADIR is supported by all routines that access demodulated data (reduce_switch, sdip, skydip, sculog etc.) but is not recognised by routines that deal with partly processed data.

Note that use of DATADIR is equivalent to setting a unix-style path of: `.:$DATADIR` (i.e. the current working directory is always chosen in preference to DATADIR).

7.1.2 SCUBA_PREFIX

In general, the initial stages of data reduction involve data taken on the same night. Typing in the full name of demodulated data files every time an observation is to be analysed is somewhat tedious and it would be much simpler if only the observation number was required.

Two pieces of information are required to spcify the file associated with a particular observation:

(1) The observation number

(2) The constant prefix of the data file

The SCUBA_PREFIX environment variable can be used to inform SURF of the form of the fixed prefix. Data files of the form `prefix_dem_`*nnnn* can be accessed by observation number (*nnnn*) so long as SCUBA_PREFIX is set to `prefix` (the `_dem_` is added automatically).

Also, if the full path name is specified for SCUBA_PREFIX, DATADIR is not required. As an example, data in `/scuba/observe/19971015/dem` can be accessed by number either by setting

```
% setenv DATADIR /scuba/observe/19971015/dem
% setenv SCUBA_PREFIX 19971015
```

or by just setting SCUBA_PREFIX:

```
% setenv SCUBA_PREFIX /scuba/observe/19971015/dem/19971015
```

Note that the current directory is not searched in the second case (since the software adds the prefix before trying to load the file). The scusetenv command can be used to set this variable (this command is especially useful when reducing data at the Joint Astronomy Centre as DATADIR is also set correctly).

7.1.3 SCUBA_SUFFIX

Most SURF tasks automatically constructs a default output filename based on the input filename (rebin bases the output filename on the object name). In this way it is possible for the filename to reflect the data reduction history.[7] The SCUBA_SUFFIX environment variable can be used to select the preferred method to use for constructing the output name.

Three modes are available:

[7] The KAPPA command hislist provides an explicit data reduction history for a file.

Table 2: Output file suffices for each task.

Task	Suffix	
	SHORT	LONG/VERBOSE
reduce_switch	o*nn*[a]	o*nn*
flatfield	f	_flat
restore	r	_res
extinction	_???_x[b]	_???_ext
remip	i	_ip
remsky	s	_sky
despike	d	_dsp
despike2	d	_des
scuclip	c	_clip
scan_rlb	b	_rlb
scuphot	p	_pht
change_data	a	_cdata
add_dbm	2_*thr_pa*[c]	_dbm_*thr_pa*

[a] *nn* = observation number
[b] ??? = first three letters of the selected sub-instrument (e.g. *lon, sho, p20, p11, p13*)
[c] These include the throw and position angle of the chop to be added to the data.

SHORT

In this mode, the output filename is constructed by appending the short suffix related to the current task to the input filename.

LONG

In this mode, the output filename is constructed as follows:

(1) Remove everything from the last underscore to the end of the input string.

(2) Append the long task suffix

For example, for scuclip an input string of `o15_lon_ext` would become an output string of `o15_lon_clip` (i.e. the trailing `_ext` has been replaced with `_clip`. This method ensures that the length of the filename does not grow out of control during the data reduction. Additionally, if the suggested output filename would be the same as the input (e.g. by running scuclip successively), a '-' is appended to the string so that the two can be distinguished.

This is the default method (and is used by scuquick).

VERBOSE

In this mode, the output filename is constructed by appending the long suffix related to the current task to the input filename. This means that the filename becomes longer and longer as the reduction proceeds.

The method of choice can be selected by setting SCUBA_SUFFIX to one of the above values (case independent) e.g.:

```
% setenv SCUBA_SUFFIX verbose
```

The suffix strings related to each task and mode are detailed in table 2 and typical examples from a data reduction are shown in table 3. Currently modes LONG and VERBOSE share the same suffices but use them in different ways.

7.2 Other useful environment variables

Three non-SURF environment variables can be used to affect the behaviour of SURF.

HDS_SCRATCH

As described in (SUN/92), this variable defines the directory in which HDS will create temporary files. This variable must sometimes be set when you are accessing data from directories in which you do not have write permission.

Usually, this variable should be set to a local scratch disk:

```
% setenv HDS_SCRATCH /tmp
```

This has the additional advantage that NFS traffic can be reduced when accessing data on remote disks as the scratch files can be written locally.

ADAM_ABBRV

Another useful environment variable is ADAM_ABBRV. If this envrionment variable is set, parameter abbreviation is turned on (e.g., PIXSIZE_OUT can be referenced as PIX).

Table 3: Filenames generated from a typical data reduction. Each row demonstrates how the filename is constructed from the previous row. An observation number of 15 is used in this example.

Task	Short	Long	Verbose
reduce_switch	o15	o15	o15
flatfield	o15f	o15_flat	o15_flat
extinction	o15f_lon_x	o15_lon_ext	o15_flat_lon_ext
scuclip	o15f_lon_xc	o15_lon_clip	o15_flat_lon_ext_clip
remsky	o15f_lon_xcs	o15_lon_sky	o15_flat_lon_ext_clip_sky
despike	o15f_lon_xcsd	o15_lon_dsp	o15_flat_lon_ext_clip_sky_dsp
despike	o15f_lon_xcsdd	o15_lon_dsp-	o15_flat_lon_ext_clip_sky_dsp_dsp
rebin	3c279	3c279	3c279

ADAM_EXIT

If this environment variable is set when an ADAM task terminates, the calling process will exit with system status set to 1 if the ADAM status was set, or 0 if the ADAM status was okay. This is useful when writing shell scripts.

All the ADAM environment variables are listed in SUN/144 [15].

8 Basic outline of SCUBA data reduction

The SCUBA transputers take data at a rate of 128 Hz but data are only kept every second (until the high speed data link is installed). Each second of data therefore is the mean of 128 measurements and the standard deviation gives the error. The transputers also detect fast transient spikes which are removed from the calculation of the mean. The number of spikes detected in each measurement is stored for use by the off-line system. Note that the effects of cosmic rays may last significantly longer than 1/128 second and the transputers would probably not detect a spike.

As the SCUBA arrays are not fully-sampled and not on a rectangular grid, images can not be taken in the same way as for an optical CCD array. At least 16 individual secondary mirror, or 'jiggle', positions (each of 1 second) are required to make a fully sampled image (64 jiggles are required if both the long and short wave arrays are being used simultaneously). The SURF data reduction package must take these data, combine them and regrid them onto a rectangular grid.

The data-file produced by the on-line system contains all the information necessary to reduce the observations. As well as the raw data, the file contains information on the jiggle pattern,

the coordinates of the bolometers relative to the central pixel, flatfield information, internal calibrator signal and general observation parameters.

All SCUBA data reduction must include the following stages (see Figs. 2, 3 and 4 for flow diagrams):

(1) **Nod compensation**

The task reduce_switch takes the raw beam switched data and subtracts the off-position from the on-position ('nods'). If required, this task also divides the data with the internal calibrator signal (this is stored in the demodulated data file as well as the switch information) and sets the level at which spikes detected by the transputers become significant.

(2) **Flatfielding**

The flatfield task takes the output of reduce_switch and flatfields the array by multiplying each bolometer by the volume flatfield value (these are the volumes relative to a reference pixel – the reference bolometers are usually from the array centres: H7 and C14).

The flatfield file itself is actually stored in the demodulated data file. In order to apply a different flatfield, the internal file must be changed with the change_flat task before running flatfield. The change_flat task changes the bolometer positions as well as the volumes. To move flatfield information between files a combination of extract_flat and change_flat should be used.

It is not necessary to flatfield PHOTOM data unless sky removal is to be used or, in some cases, multiple bolometers are to be analysed together.

(3) **Extinction correction**

The extinction task takes the flatfielded data and applies an extinction correction to each pixel one jiggle at a time. The zenith sky opacity (tau) should have been obtained from skydips or estimated from photometry. The optical depth is linearly interpolated as a function of time to find the correction that should be applied to each jiggle.

Since the extinction correction is different for each array, it is at this point that the two arrays must be dealt with independently – the output of this task will contain data for one sub-instrument.

(4) **Single-beam restoration**

The dual-beam SCAN/MAP data must be restored to a single-beam map at some stage. For data taken whilst chopping along the scan, this is achieved by using the EKH algorithm [11] as implemented in the restore task. In this case the restoration must occur before regridding.

For data taken whilst chopping in a fixed direction on the sky (the so-called "Emerson-II" technique [12]), individual chop configurations must be rebinned independently and then combined using the remdbm task.

In future it is hoped that a maximum entropy algorithm can be implemented [16] for both chopping techniques.

At this stage the data reduction path diverges depending on the observation type. Map data must be regridded onto a rectangular grid using the rebin task (followed by remdbm for SCAN/MAP data if necessary) whereas photometry data must be processed using the scuphot task.

The data reduction process can be automated to a certain extent by using the scuquick script. This script can take as arguments any parameter that is expected by the SURF tasks.

A number of optional tasks are also available:

- **Changing header parameters**

  Tasks are available to change header parameters such as flatfield information (change_flat), applying pointing corrections (change_pointing) or setting pixels (bolometers) and integrations to bad values (change_quality).

- **Changing data values**

  Data can be changed using the change_data task. This task can be used to change Data, Variance or Quality arrays and should be used with care.

- **Sky noise removal**

  Instrumental variations and sky-noise can be removed either by using the task remsky (when sky bolometers can be identified) or by using calcsky in combination with remsky (for more complicated sources and scan map data).

- **Despiking**

  Occasionally, spikes get through the transputers and into the demodulated data. Tasks are provided for despiking jiggle/map data (despike), scan/map data (despike2) and photometry data (scuclip[8]).

- **IP Correction**

  Polarimetry observations need to be corrected for instrumental polarisation. The remip task can be used for this.

- **Array overlay**

  If the rebinned images are displayed using a program that writes to the AGI graphics database [17], such as KAPPA display, the array can be overlaid on the image using the task scuover. This is very useful for identifying noisy bolometers or bad pixels.

- **Display data values**

  The task extract_data is similar to the rebin tasks except that the X, Y and data values are written to an ASCII text file instead of being regridded into a final output image. This is useful for examining the data before regridding (or passing it to an external program for further processing). Obviously this task should not be used to simply examine the data, KAPPA tasks such as display and linplot can do that; this task gives you the position of each bolometer in addition to the data value. Additionally, the scuba2mem task can be used for finding the chop positions (although it would then be necessary to use the CONVERT ndf2ascii task to generate a text file).

[8] scuclip can also be used for despiking jiggle/map data as long as sources are weak

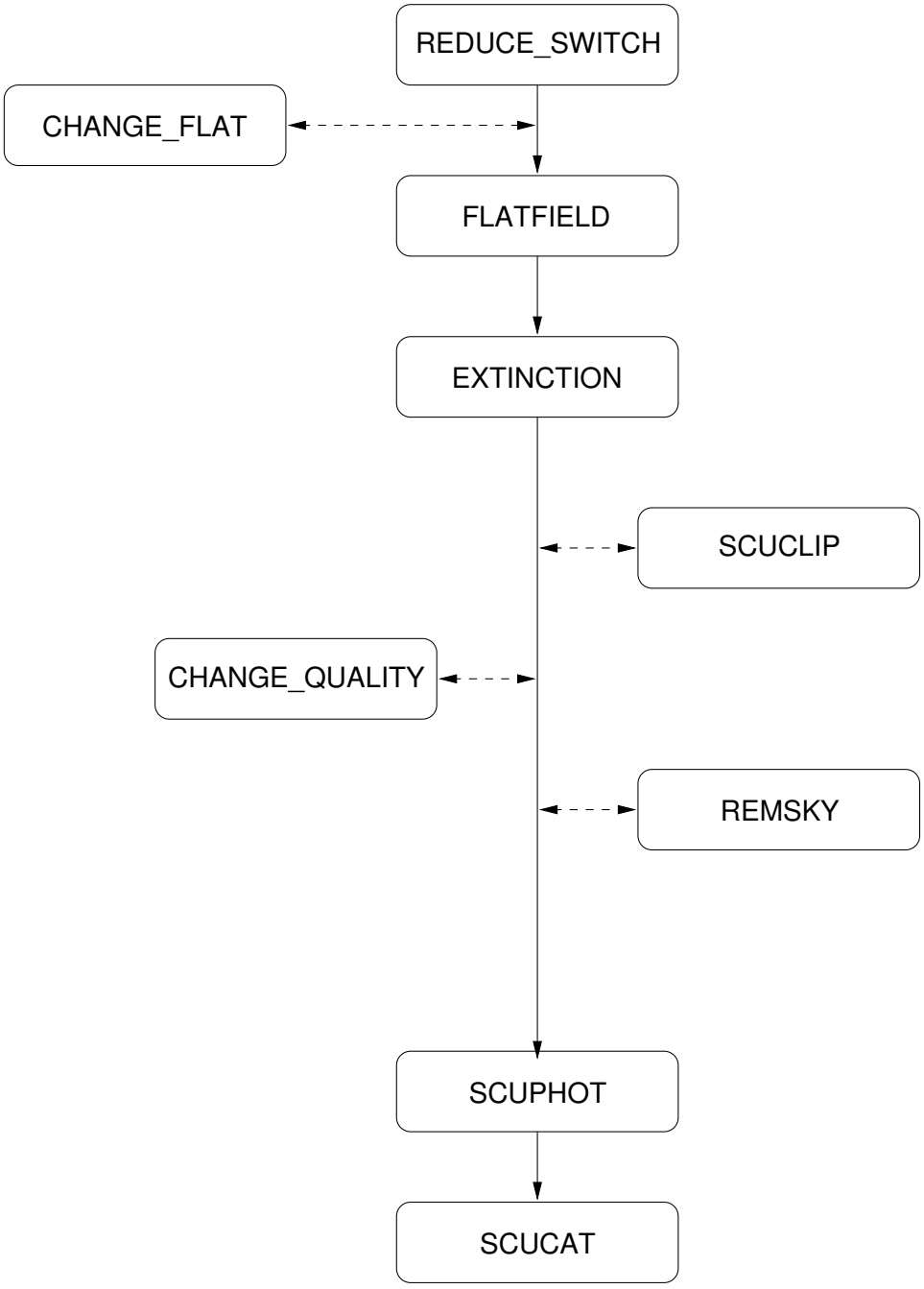

Figure 2: The SURF data reduction flow diagram for PHOTOM data. Optional tasks are indicated by dashed lines. Note that map data can follow the photometry path and photometry data can follow the map path if necessary.

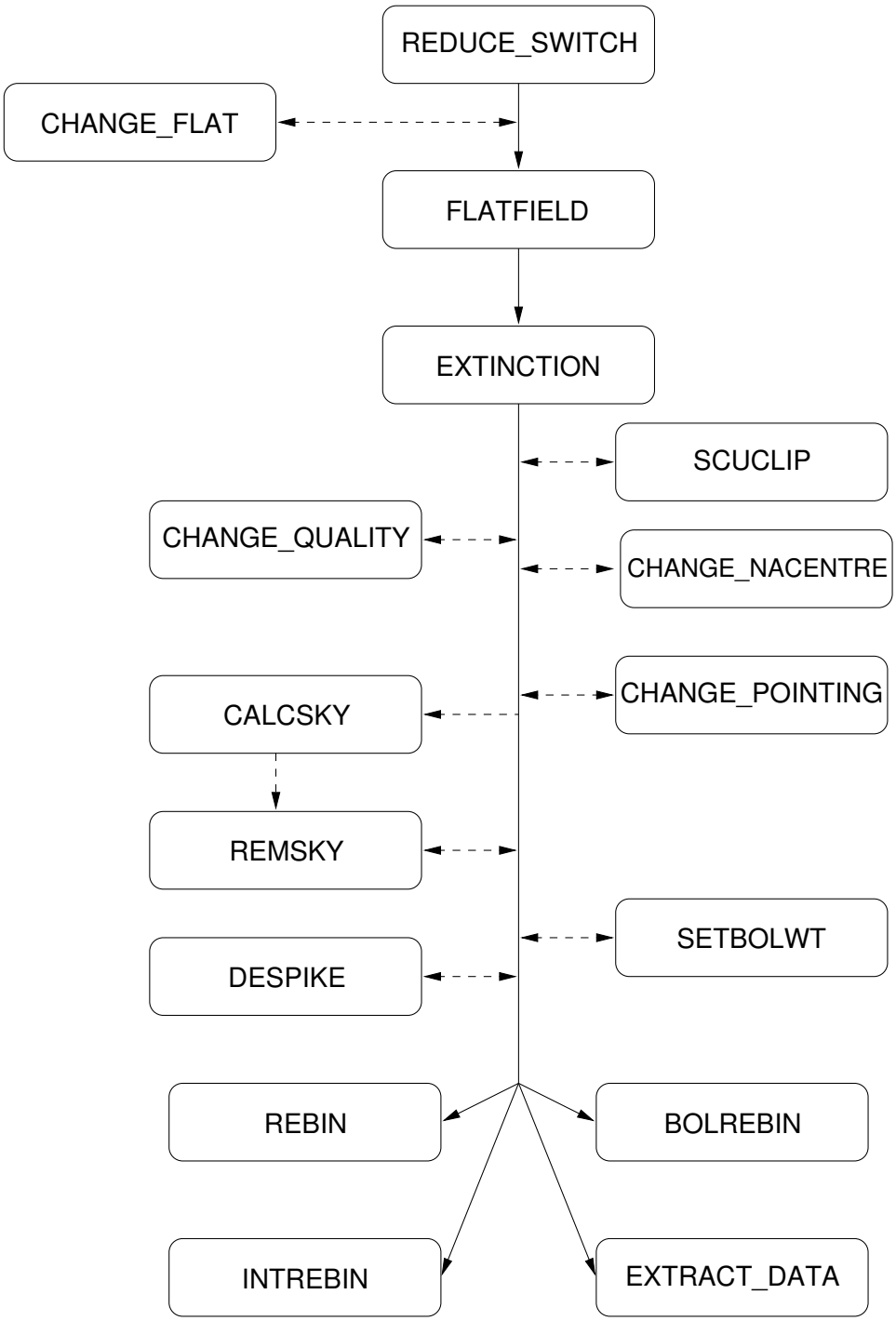

Figure 3: The SURF data reduction flow diagram for Jiggle/map data. Optional tasks are indicated by dashed lines. Note that map data can follow the photometry path and photometry data can follow the map path if necessary.

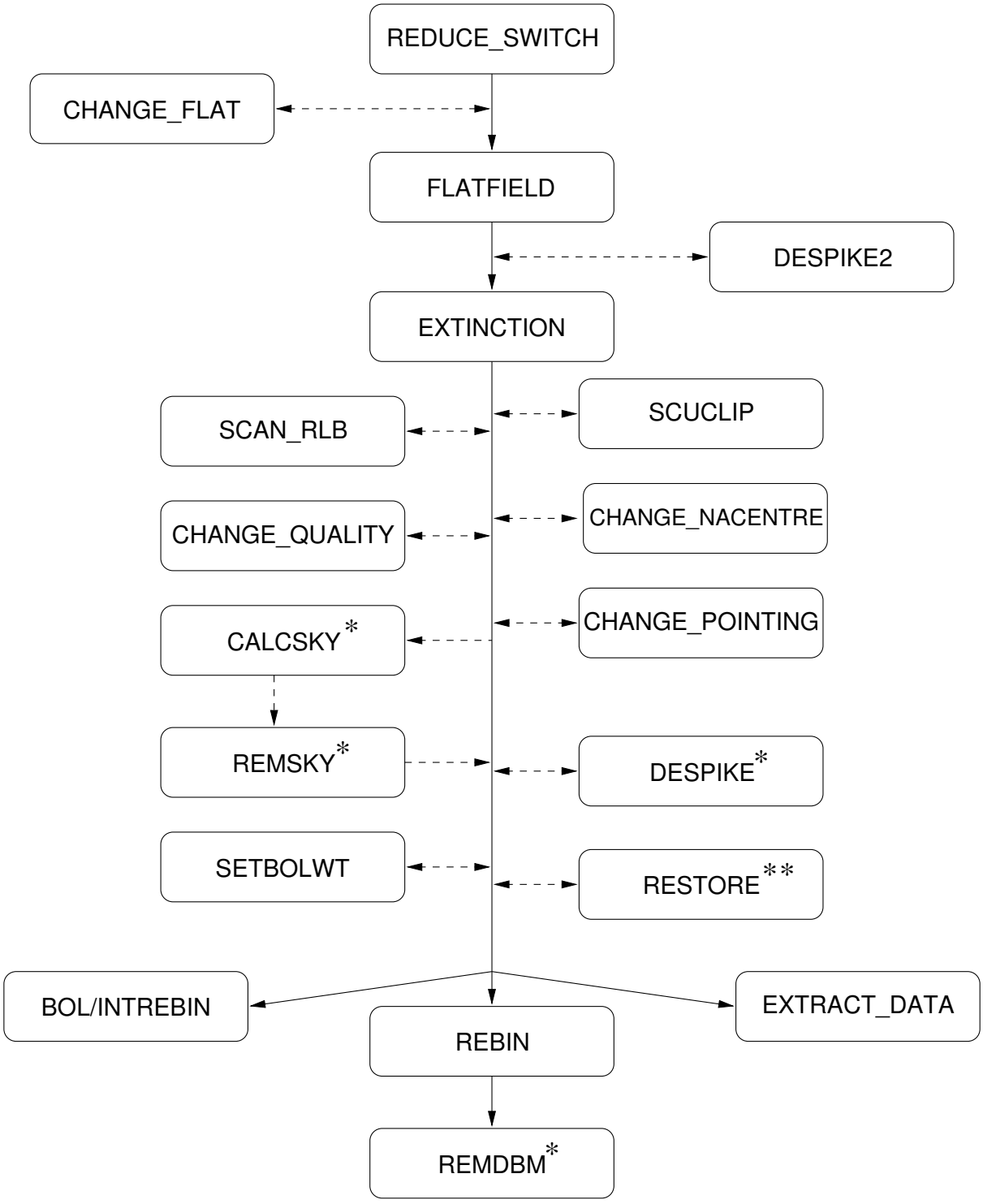

Figure 4: The SURF data reduction flow diagram for Scan/map data. Optional tasks are indicated by dashed lines. Tasks annotated with a single asterisk can not process EKH scan data (ie chopping along the scan direction). Conversely, tasks annotated with a double asterisk can not process "Emerson II" data (chopping in a fixed direction).

9 The data reduction process

This section will describe the steps needed to process SCUBA data. For more detailed examples please consult the two cookbooks [9, 10]. For this example I will use map and photometry observation of 3C279 from a commissioning night[9].

9.1 Preliminaries

The data is not in the work directory so DATADIR should be set:

```
% setenv DATADIR /scuba/observe/apr8/dem
```

assuming a C-shell type environment. I can now make a log of a subset of the nights data to find out which observations should be processed:

```
% sculog -summary --begin=54 --end=63
-Log for directory: /home/timj/scuba/maps/sun216
                    /scuba/observe/apr8/dem

 #    HST    Obsmode   Source   Meas/Int Airmass  Filter  Bolometers
---- -----   --------- -------  -------- ------- -------- ----------
54   23:02   SKYDIP    SKY        10/20          450N:850 SHORT_DC,LONG_DC
55   23:13   POINTING  3c279       1/2   1.14464 450N:850 LONG
56   23:17   PHOTOM    3c279       1/10  1.13858 450N:850 H7
57   23:22   PHOTOM    3c279       1/10  1.13217 450N:850 H7
58   23:28   PHOTOM    3c279       1/10  1.12641 450N:850 H7
59   23:35   MAP       3c279       1/3   1.12019 450N:850 SHORT,LONG
60   23:44   MAP       3c279       1/3   1.11481 450N:850 SHORT,LONG
61   23:53   MAP       3c279       1/3   1.11101 450N:850 SHORT,LONG
62   00:02   MAP       3c279       1/3   1.10965 450N:850 SHORT,LONG
63   00:03   POINTING  3c273       1/4   1.05483 450N:850 SHORT
 :                                  :                :
 :                                  :                :
98   03:18   SKYDIP    SKY        10/20          450N:850 SHORT_DC,LONG_DC
```

In order to save time typing in the filename every time we wish to access demodulated data, we also set the SCUBA_PREFIX environment variable:

```
% setenv SCUBA_PREFIX apr8
```

This variable allows demodulated data to be referenced by observation number. It is also possible to set the style for the default output filename provided by the individual tasks. In this example, we will use the default convention ('LONG'). More information on the SURF environment variables can be found in §7.

[9]Note that the naming convention has now changed to YYYYMMDD instead of MMMDD as used at the time the data were taken

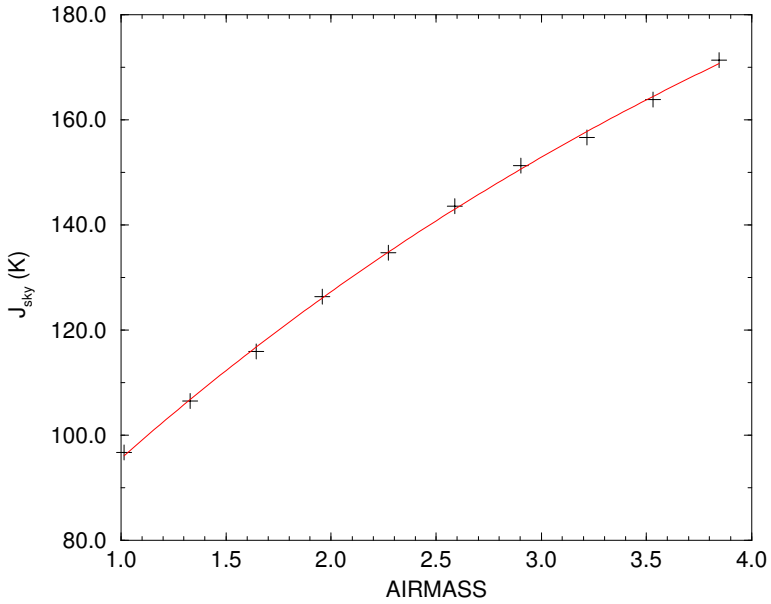

Figure 5: The Skydip result for scan 54. The crosses are the measured sky temperatures and the line is the fitted model.

9.2 Skydips

From the listing in the previous section we can see that Skydip data was taken at scans 54 and 98. From the RO (either by using mapsum or photsum on the ro data or by using hdstrace) file we can see that the fitted taus were 1.140 (short) and 0.220 (long) for scan 54 and 1.042 (short) and 0.187 (long).

In most cases these numbers will be sufficient for use by extinction but it is possible to recalculate the tau by using the skydip task. As an example here is the result of skydip on scan 54:

```
% skydip 54
SURF: Opening apr8_dem_0054 in /scuba/observe/apr8/dem
SURF: run 54 was a SKYDIP observation
SURF: observation started at sidereal time 11 47 24 and ended at 11 54 07
SURF: file contains data for the following sub-instrument(s)
 - SHORT with filter 450
 - LONG with filter 850
SUB_INSTRUMENT - Name of sub-instrument to be analysed /'SHORT'/ > l
SURF: file contains data for 20 integration(s) in 10 measurement(s)
T_HOT - Temperature of hot load (K) /278/ >
T_COLD - Temperature of cold load for LONG_DC /73.6/ >
ETA_TEL - Telescope efficiency /0.91/ >
B_VAL - B parameter /-1/ >
SCULIB: fit for filter 850 and sub-instrument LONG_DC
 eta =  0.91 +/-  0.00  b =  0.86 +/-  0.00  tau =   0.220 +/- 0.002
 Standard Deviation of fit residual =   0.74 K (X=     1.0 N=    9)
```

The results of the fit are displayed in figure 5. Points worth noting are that the local sidereal time of the observation is printed (this is useful later when running extinction), a fixed η_{tel} and

a floating value of B (the default value for η_{tel} is read from the file header) were used and the tau agrees with the on-line system (which is not surprising since the same code is used on-line as in SURF). The errors derived for the fit can sometimes be suspect since the parameters are not completely independent. The standard deviation of the fit residual gives a measure of the scatter in the points about the model fit. Note also that the 'X' indicates the reduced χ^2 of the fit (forced to be approximately 1.0 by the program when it determines the errors) and the 'N' indicates the number of iterations required to converge on the fit.

Occasionally, it is necessary to remove some points from the fit. This can be achieved by using reduce_switch and change_quality before running skydip. An example of this can be found in §I.2.

The sdip script can be used to automate the procedure of running skydip and displaying the results with KAPPA's linplot. More information on skydipping can be found in Appendix I.

9.3 Noise measurements

Noise observations are reduced on-line and written to an ASCII text file. In some cases this text file is not available and the reduce_noise task can be used to recreate it (as well as generating an NDF file containing the results) from the raw demodulated data file.

```
% reduce_noise 19981113_dem_0001
SURF: Opening 19981113_dem_0001 in /scuba/observe/19981113/dem
SURF: run 1 was a NOISE observation
OUT - Name of container file to hold map and time-sequence data /'o1'/ >
FILE - Name of ASCII file to contain results summary /'noise_981113_1.dat'/ >
```

9.4 Common data reduction

Now the data processing can begin. We will start by running reduce_switch in order to subtract the off from the on and to split the data array of the raw data into separate components.

```
% reduce_switch 59
SURF: Opening apr8_dem_0059 in /scuba/observe/apr8/dem
SURF: run 59 was a MAP observation of object 3c279
SURF: file contains data for 2 switch(es) in 4 exposure(s) in 3 integration(s)
in 1 measurement(s)
OUT - Name of output file to contain reduced switch data /'o59'/ >
```

or with the full file specification:

```
% reduce_switch apr8_dem_0059
SURF: Opening apr8_dem_0059 in /scuba/observe/apr8/dem
SURF: run 59 was a MAP observation of object 3c279
SURF: file contains data for 2 switch(es) in 4 exposure(s) in 3 integration(s)
in 1 measurement(s)
OUT - Name of output file to contain reduced switch data /'o59'/ >
```

In this example the calibrator signal has not been used and any datum from which more than 5 spikes were removed by the transputers is marked bad (these are the default settings). The processed data are then written to file o59.sdf.

In this case we need to change the flatfield file (since the flatfield was updated after the data were taken) using change_flat:

```
% change_flat
IN - Name of input file containing demodulated map data /@o59/ >
SURF: run 59 was a MAP observation of 3c279
NEW_FLAT - The name of the file containing the new flat-field > photflat1.dat
```

The next task is to flatfield the data:

```
% flatfield o59 o59_flat
SURF: run 59 was a MAP observation of 3c279
SURF: applying flatfield from photflat1.dat
```

If the input and output files are not specified on the command line they will be requested.

The data can now be corrected for airmass (elevation) and sky opacity by using extinction. According to the skydip observation taken prior to the map, the tau at 850 μm is 0.220 and a skydip taken after the map shows it was 0.187. If extinction is given two τ values from different times then the actual τ for each jiggle will be calculated by linear interpolation – obviously this assumes that the τ varied linearly with time. For this example we will assume the τ variations are correct in order to demonstrate the principle:

```
% extinction
IN - Name of NDF containing demodulated data /@o59_flat/ >
SURF: run 59 was a MAP observation with JIGGLE sampling of object 3c279
SURF: file contains data for 4 exposure(s) in 3 integration(s) in 1
measurement(s)
SURF: observation started at sidereal time 12 19 59 and ended at 12 28 40
SURF: file contains data for the following sub-instrument(s)
 - SHORT with filter 450
 - LONG with filter 850
SUB_INSTRUMENT - Name of sub-instrument to be extinction corrected /'SHORT'/ > l
FIRST_TAU - First zenith sky opacity measured /0/ > 0.22
FIRST_LST - Sidereal time of first opacity measurement; hh mm ss.ss /'0.0'/ > 11 54
SECOND_TAU - Second zenith sky opacity measured /0.22/ > 0.187
SECOND_LST - Sidereal time of second opacity measurement; hh mm ss.ss /'11 54'/ > 16 10
OUT - Name of output NDF /'o59_lon_ext'/ >
```

The arrays are separated at this point (since the extinction correction would be different). In this case the LONG-wave array was selected; extinction would have to be re-run to select the SHORT-wave array (the question is not asked if only one sub-instrument is present).

Some comment is probably required for the use of LST for the tau measurements – this is not as bad as it sounds. The skydip task prints the LST of the skydip and extinction prints the LST of the observation; in many cases it is known that the tau value was taken a certain time before or after the observation so this value can simply be added. In addition, most of the time a constant tau value is used and for the case of a constant tau the LST is irrelevant.

If desired, sky noise can now be removed. Sky signal can be identified in two ways: firstly using bolometers that are known to be looking at sky (implemented in remsky) and secondly, using a model of the source structure to enable the sky signal to be calculated with the source subtracted from the data (implemented in calcsky). In this section we will examine the first method since this is the simplest and can be used for jiggle observations. The more complex approach will be dealt with in §9.8.2 where sky removal from scan map data is discussed. remsky works in a very simplistic way: Sky bolometers are specified, each jiggle is then analysed in turn, the average value for the sky bolometers (either MEDIAN or MEAN) is then removed from the entire array. At present it is not possible to specify sky regions, only sky bolometers can be specified. This may cause problems with extended sources (rebin the map in NA coordinates initially to find the sky bolometers). remsky should normally be run after rebin in order to choose sky bolometers that are really looking at sky, for this example we will skip that step. remsky is sufficient for the mapping of compact sources in jiggle mode and for photometry; if the source structure is complex then calcsky should be considered (§9.8.2).

```
% remsky
IN - Name of input file containing demodulated map data /@w48_newrebin/ > o59_lon_ext
SURF: run 59 was a MAP observation with JIGGLE sampling of object 3c279
OUT - Name of output file /'o59_lon_sky'/ >
BOLOMETERS - The Sky bolometers, [a1,a2] for an array /['all','-h7']/ >
SURF: Using 36 sky bolometers
MODE - Sky removal mode /'median'/ >
Adding mean background level onto data (value=1.5316721E-6)
```

In this example we have used all the bolometers except for the central pixel (H7) and then used median sky removal for each jiggle. The average background level has also been added back onto the data.

The output of extinction or remsky can be displayed using, say, KAPPA display to see whether some integrations or bolometers should be marked bad.[10] Sometimes bad bolometers can only be identified after a rebin/scuover phase. The output so far can be seen in figure 6 – the axes are labeled with bolometer number along the X-axis and integration number up the Y-axis.

Now that the data have been extinction corrected and, optionally, processed with remsky, the data reduction path diverges according to the type of observation. Map making[11] (jiggle and scan) and photometry will be dealt with separately. Note that scuquick can be used to automate some of the more repetitive tasks during this stage of the data reduction process.

Before diverging though, we should first take a diversion into the question of despiking.

9.5 Despiking

This section describes the different techniques available for despiking SCUBA data.

9.5.1 Manual despiking

Manual despiking simply involves examining the data with linplot and display, identifying bad regions by eye and then running change_quality to turn off the bad points. In general this is very

[10] Note that PHOTOM data array is 3-dimensional; use the NDF section („2) with display in order to examine these data.

[11] It is possible to rebin photometry data although, obviously, the image will not be fully-sampled

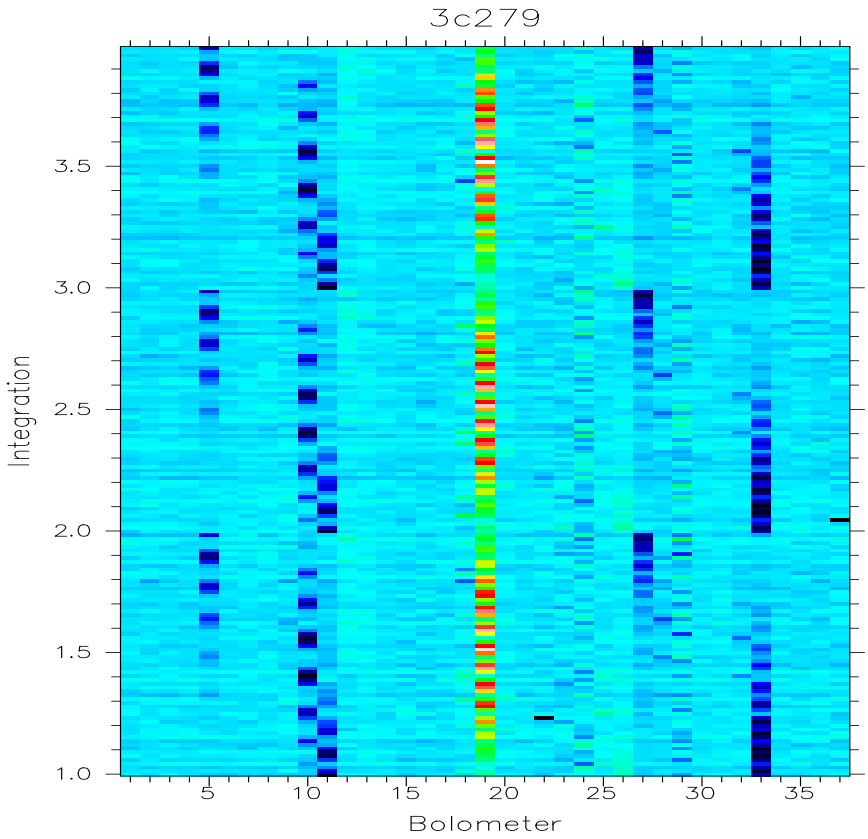

Figure 6: The 3C279 data after processing through extinction and remsky. The next stage is to regrid the data using rebin. The source can clearly be seen in bolometer 19 (H7). The negative stripes are indicating that the chop throw was smaller than the array.

time consuming (especially working out the pixel number of a spike so that change_quality can be told the exact location) so two interactive techniques are available:

(1) dspbol

This script automates the linplot-change_quality cycle – bolometers can be plotted in turn, with spikes identified and removed, all within a few seconds.

(2) FIGARO sclean

The sclean task allows users to simply click on bad points to remove them. This routine has been designed for SCUBA despiking and therefore understands SCUBA quality. sclean provides an integrated despiking environment showing the 2-D image and a 1-D slice, allowing points to be marked bad (or good) in either window. More information can be found in the FIGARO documentation.

Additionally, the rlinplot command, a wrapper for the KAPPA mlinplot command, and the pltbol command, a wrapper for the KAPPA linplot command, can be used to identify spikes and noisy bolometers rapidly without having knowledge of NDF sections or the specifics of each command.

9.5.2 Automatic despiking

At first sight, the automatic despiking of SCUBA data may seem somewhat daunting since there are 4 different tasks provided for this: despike, despike2, scuclip and sigclip. Detailed information on these can be found in the appendix (§C) but a direct comparison of the four is provided below:

sigclip

Originally intended for the final clipping of photometry data, this task finds the statistics of the entire data file and clips any point lying more than SIGMA from the mean. This task knows nothing about SCUBA data.

Disadvantages: Should not be used where bolometers see differing signals (i.e. most of the time) since the clipping is then invalid.

Advantages: Will clip any data file. Can be used on reduced photometry data (output of scucat) for clipping since only data for a single bolometer will be present.

scuclip

This task processes each bolometer in turn, finding the mean and removing any points lying more than NSIGMA from the mean for the current bolometer. An iterative clip is used so that the mean is recalculated each time a point lies NSIGMA from the mean until no points are removed. No knowledge of SCUBA is required by this task (except that it knows which quality bit to use for the despiking).

Disadvantages: For JIGGLE/MAPS, on-source bolometers jiggle on and off the source and therefore have a large change in signal (if the source signal is well above the noise level) – the mean and standard deviation calculations therefore have a tendency to remove peak signals from the data. (this can be partly overcome by setting the source bolometer bad, clipping the remaining bolometers and then setting the source bolometer to good.)

Advantages: Can be used for PHOTOM data and weak signals since each bolometers always sees approximately the same signal. Can be used for detecting large spikes on strong sources if a sufficiently large value is chosen for NSIGMA.

despike

This task places each point into a grid cell corresponding to the actual position of the datum on the sky. Each cell is then analysed in turn, any point further than NSIGMA from the mean for a given cell is then treated as a spike[12]. All modes are supported with the caveat that SCAN/MAP data should not have been restored (spikes must be removed before the single-beam restoration phase – also EKH data can not strictly be processed in this way beacause the chop angle is not fixed on the sky).

Disadvantages: For small data sets the number of points per bin is not sufficient to perform accurate statistics calculations.

Advantages: Small spikes can be detected in the presence of strong sources since the actual location on the sky is used for the calculation.

despike2

This task is designed specifically for SCAN/MAP data. Each scan for each bolometer is analysed in turn and spikes are detected using a running mean calculation.

Advantages: Finds the large spikes in SCAN/MAP data.

Disadvantages: Care must be taken when despiking bright sources (e.g. planets).

In summary, each mode should probably use different despiking techniques:

photom

scuclip can be used before scuphot and remsky. sigclip should be used after scuphot (or scucat).

scan/maps

despike2 should be used initially. For "Emerson II" data it is also possible to use despike since the chop angle is fixed on the sky (only despike data that were taken with the same chop configuration).

Jiggle maps of strong sources

Initially scuclip can be used with a large NSIGMA to remove the obvious spikes. Then despike should be used for the smaller spikes (i.e. those comparable with the source signal).

Jiggle maps of weak sources

Can probably run scuclip as for PHOTOM observations. Here 'weak source' means data where the source is not far above the noise level.

[12]More details on despike can be found in appendix G.

9.6 Map making

All that is required now is that the data be rebinned onto a rectangular grid with the rebin task. If necessary it is possible to enter Az/El pointing corrections by using change_pointing:

```
% change_pointing n59_sky_lon
SURF: run 59 was a MAP observation of 3c279
SURF: observation started at LST 12 19 59 and ended at 12 28 40
SURF: no pointing corrections found
CHANGE_POINT - Do you want to change the pointing correction data > y
POINT_LST - The sidereal time of the pointing offset (hh mm ss.ss) /!/ > 12 00
POINT_DAZ - The azimuth pointing correction to be added (arcsec) > 0
POINT_DEL - The elevation pointing correction to be added (arcsec) > 0
POINT_LST - The sidereal time of the pointing offset (hh mm ss.ss) /!/ > 12 50
POINT_DAZ - The azimuth pointing correction to be added (arcsec) > 1.1
POINT_DEL - The elevation pointing correction to be added (arcsec) > -0.9
POINT_LST - The sidereal time of the pointing offset (hh mm ss.ss) /!/ >
```

The time for the pointing corrections must be in LST (they also must be entered in chronological order). The pointing offset is assumed to vary linearly with time. Here I have assumed good pointing at an LST of 12h (the pointing observation before the map) and a small shift 50 minutes later when another pointing observation was taken (the shift can be found by using pointsum). It is probably best that the pointing offset is measured directly from the image by first regridding the data in Az/El coordinates and then using, for example, the KAPPA centroid task to find any offset.

A number of questions need to be asked before regridding the data :-

What rebin method should be used?

Currently, three methods are available. The data can be regridded with a weighting function, interpolated using spline fitting or by calculating the median data value in each cell of the output grid.

Bessel, Gaussian and linear weighting functions are available; in theory the Bessel function interpolation should give the best results but in practice the Gaussian or linear functions should be used (they are much faster and less affected by edge effects). The Gaussian function should be used if you are interested in beam shape (since it is easier to work out what is going on when you convolve a JCMT beam with a Gaussian than when you convolve it with a cone).

The MEDIAN regridding technique can be used if many data points are available (since for small output grids at least one input data point [preferably many more] must be available in each cell in the output to avoid bad pixels). If fewer points are available (only a few integrations) consider using larger cells or use the KAPPA routines fillbad or glitch to interpolate over the holes.

The spline fitting algorithms are experimental and have not been thoroughly tested – please use with care.

What coordinate system should be used?

The data can be rebinned in the following coordinate systems:

NA Nasmyth (SCUBA) coordinate frame

AZ Azimuth-Elevation offsets

PL Moving source (e.g. planet)

RB RA/Dec B1950

RJ RA/Dec J2000

RD RA/Dec epoch of observation

GA Galactic coordinates (J2000)

The first two coordinate systems are fixed on the telescope so that the source rotates during long observations. They are most useful for taking beam maps (AZ) or examining the properties of the SCUBA bolometers (NA). Obviously AZ and NA contain no astrometry information. The PL coordinate system should be used for moving sources (e.g. planets or comets) where the RA and Dec of the source is changing with time; offsets from this moving centre are calculated and no astrometry information is stored. The remaining coordinate systems correct for source rotation and do have associated FITS World-Coordinate-Systems (WCS) astrometry information [19, 20].

Map centre

The default map centre will be the map centre of the first map entered into rebin modified to the epoch of the output map if necessary. coordinates used as the map centre of the This question is not asked if a NA, AZ or PL coordinate system is being used.

Pixel size

The regridded image can be in any pixel size. The main point is that account is taken of the beam sizes: approximately 7 arcsec at 450 microns and 14 arcsec at 850 microns. The on-line system regrids with 3 arcsec pixels. Obviously the regridding takes longer the smaller the pixel size that is requested but only becomes a real problem if BESSEL regridding is used. Linear interpolation should be fast (less than 10 seconds) for most reasonable pixel sizes.

The map can now be made with rebin (in this case using linear interpolation, J2000 coordinates, 1 arcsec pixels and default map centre, looping is turned off since I am only regridding one map):

```
% rebin noloop
REBIN_METHOD - Rebinning method to be used /'LINEAR'/ >
SURF: Initialising LINEAR weighting functions
OUT_COORDS - Coordinate sys of output map; PL,AZ,NA,RB,RJ,RD or GA /'RJ'/ >
SURF: output coordinates are FK5 J2000.0
REF - Name of first data file to be rebinned /'n59_sky_lon'/ >
SURF: run 59 was a MAP observation of 3c279 with JIGGLE sampling
SURF: file contains data for 4 exposure(s) in 3 integrations(s) in 1
measurement(s)

WEIGHT - Weight to be assigned to input dataset /1/ >
SHIFT_DX - X shift to be applied to input dataset on output map (arcsec) /0/ >
SHIFT_DY - Y shift to be applied to input dataset on output map (arcsec) /0/ >
SURF Input data: (name, weight, dx, dy)
```

```
   -- 1: n59_sky_lon (1, 0, 0)

LONG_OUT - Longitude of output map centre in hh (or dd) mm ss.ss format /'+12
 56 11.17'/ >
LAT_OUT - Latitude of output map centre in dd mm ss.ss format /'- 05 47 22.1'/ >
OUT_OBJECT - Object name for output map /'3c279'/ >
PIXSIZE_OUT - Size of pixels in output map (arcsec) /3/ > 1
OUT - Name of file to contain rebinned map > n59_reb_lon
WTFN_REGRID: Entering second rebin phase (T = 0.9061 seconds)
WTFN_REGRID: Entering third rebin phase (T = 3.682912 seconds)
WTFN_REGRID: Regrid complete. Elapsed time = 4.055644 seconds.
```

If more than one map is available the extinction corrected data (with or without sky removal) can all be added into a single map at this stage. The parameter IN can be supplied with one new map at a time or via a text file (§9.6.1). Each input data set can be shifted by setting SHIFT_DX and SHIFT_DY (this shift is in arcseconds on the output grid cf. pointing corrections which are in Az/El offsets) and assigned a relative weight with the WEIGHT parameter. rebin does understand SCUBA sections (§6) so it is possible to select part of an observation for regridding at this time.

In addition to rebin there are three closely related tasks (in fact they all use the same code): bolrebin will regrid each bolometer individually, intrebin will regrid each integration into a separate file and extract_data will write the data to a text file before regridding. Note that the output file for bolrebin and intrebin is an HDS container [21] rather than a simple NDF. For example, if the OUT file is test.sdf the images will be accessible as NDFs via test.h7, test.h8 etc (or test.i1, test.i2 for intrebin).

At this point the map can be displayed with, say, KAPPA display. Fig. 7 shows the 850 micron image of 3C279 rebinned in RJ coordinates with the long wave bolometer array overlaid (note that scuover displays the array at zero jiggle offset). Fig. 7 was made as follows (note that this requires psmerge [22] in addition to KAPPA's display):

```
% display n59_reb_lon axes lut=$KAPPA_DIR/bgyrw_lut device=epsfcol_p
MODE - Method to define the scaling limits /'SCALE'/ >
LOW - Low value for display /-0.01095889788121/ >
HIGH - High value for display /0.022901531308889/ >

% scuover prompt
MSG_FILTER - Messaging level /'NORM'/ >
DEVICE - Name of graphics device /@xwindows/ > epsfcol_p
Current picture has name: DATA, comment: KAPPA_DISPLAY.
Using /scuba/maps/sun217/n59_reb_lon as the input NDF.
EXT - Name of (extinction corrected) demodulated data file /'n59_sky_lon'/ >
SURF: file contains data for 4 exposure(s) in 3 integration(s) in 1
measurement(s)
INTEGRATION - Integration number /1/ >
EXPOSURE - Exposure number /1/ >
COL - Colour of annotation /'red'/ > white
NAME - Display bolometer name (else number)? /TRUE/ >


% psmerge -e gks74.ps gks74.ps.1 > 3c279.eps
```

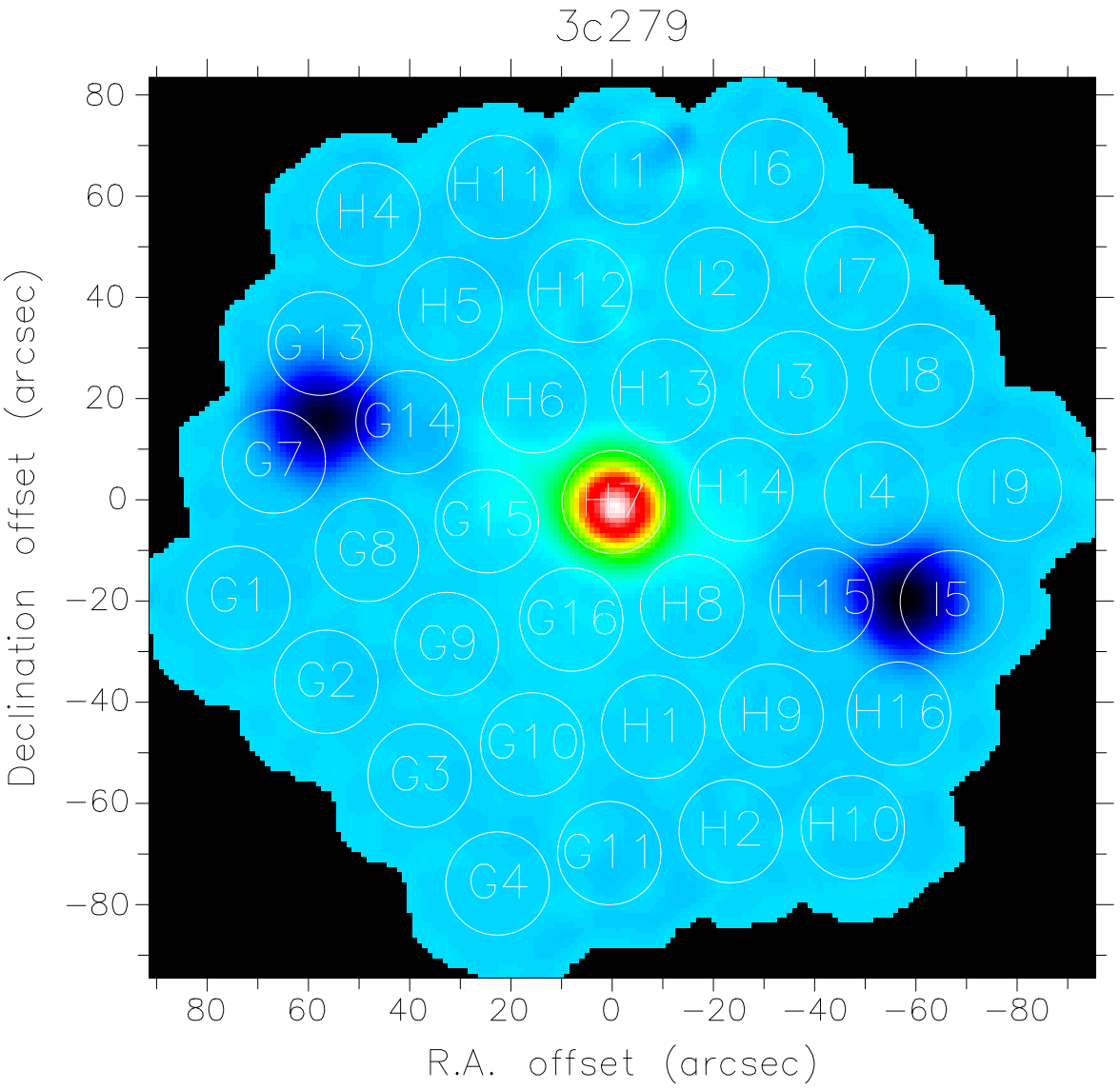

Figure 7: A 850 micron image of 3C279 rebinned in RJ coordinates with the long wave array overlaid. The two negative sources indicate the nodding and chopping that are part of a SCUBA jiggle/map.

In general, for faint sources it would now be necessary to go back to the extinction corrected (or sky-removed) data so that any bad bolometers and integrations can be turned off (using change_quality and SCUBA sections – rebin can be used to test a section before committing the change), different sky bolometers chosen or new pointing corrections added. Once complete the data can be calibrated – planet fluxes can be obtained using the FLUXES package and work is progressing on a list of secondary calibrators (see e.g. [24]).

9.6.1 Rebinning multiple datasets

On many occasions it is necessary to combine multiple observations into one regridded image to attain the desired signal-to-noise for a source map. One way of doing this is to enter into rebin (or related task) each map in turn along with the WEIGHT, SHIFT_DX and SHIFT_DY. For a small number of input sets this approach is fine but for large numbers (n $>$ 2) this approach becomes tedious and error prone. In order to overcome this problem the rebin tasks can accept an ASCII text file as input as well as an NDF.

This text file contains information on one input set per line. This line must contain either a space separated list of with the NDF, weight, shift_dx and shift_dy, or the name of another text file:

```
# Regrid text file for 3c279

# Format of text file should be
#  NDF     WEIGHT     SHIFT_DX    SHIFT_DY

n59_reb_lon  1.0   0.0   0.0    # Map 59
n60_reb_lon  1.0   1.0   0.0    # Shift 1.0 relative to n59

n61_reb_lon{i2} 1.02            # Only want the second integration from
                                # this -- shifts will be requested when
                                # the text file is included
n62_reb_lon   0.98 1.0   2.0

3c279_old.bat                   # Include previous 3c279 data via a text file.
```

From this example we can see that blank line are ignored and a '#' indicates the start of a comment; all text on the line after the '#' is ignored. Not all the parameters need to be specified on the input line; if they are missing the software will simply ask for the values from the user. The order of these parameters is important so it is not possible to specify map shifts without specifying a weight – similarly SHIFT_DY can not be given without SHIFT_DX. Also note that the NDF name can include SCUBA sections. Even though text files can include other text files a recursion depth of 5 has been hard-wired into the code to prevent abuse – it was felt that this should be sufficient in most cases.

With the default messaging level, rebin tasks always show a summary of all the input data before proceeding to the final regridding – this can be used to check that the correct files (and associated parameters) have been read in.

9.6.2 Output coordinate frames

The output map generated by rebin will contain at least 3 output coordinate frames. They are the GRID, PIXEL and AXIS coordinate frames. For maps regridded in RJ/RB/GA or RD coordinates there will be an additional SKY coordinate frame.

They can be listed with the ndftrace command:

```
lapaki[M82/short]>ndftrace m82 fullwcs

   NDF structure ..../m82:
      Title:  SURF:remdbm
      Label:  Extinction corrected

   Shape:
      No. of dimensions:  2
      Dimension size(s):  256 x 256
      Pixel bounds     :  -127:128, -127:128
      Total pixels     :  65536

   Axes:
      Axis 1:
         Label : R.A. offset
         Units : arcsec
         Extent: 127.5 to -128.5

      Axis 2:
         Label : Declination offset
         Units : arcsec
         Extent: -127.5 to 128.5

   Data Component:
      Type        :  _REAL
      Storage form:  SIMPLE
      Bad pixels may be present

   Quality Component:
      Storage form :  SIMPLE
      Bad-bits mask:  3 (binary 00000011)

   World Coordinate Systems:
      Number of coordinate Frames      : 4
      Index of current coordinate Frame: 4

      Frame index: 1
        Title               : "Data grid indices; first pixel at (1,1)"
        Domain              : GRID

      Frame index: 2
        Title               : "Pixel coordinates; first pixel at (-127.5,-1..."
        Domain              : PIXEL

      Frame index: 3
        Title               : "Axis coordinates; first pixel at (127,-127)"
        Domain              : AXIS

      Frame index: 4
        Title               : "FK5 equatorial coordinates; mean equinox J20..."
        Domain              : SKY
```

```
Extensions:
   FITS             <_CHAR*80>
   REDS             <SURF_EXT>


History Component:
   Created    :  1999 Feb 07 17:34:41
   No. records:  9
   Last update:  1999 Jun 16 17:00:07 (MATHS          (KAPPA 0.13-6))
   Update mode:  NORMAL
```

In the above example, the SKY frame is the current frame (this will be used by KAPPA display) and is set to FK5 J2000. The AXIS frame contains arcsecond offsets from the regrid centre. The PIXEL frame uses pixel indices and rebin ensures that the regrid centre is always at pixel coordinate 0,0 unlike the GRID frame where the pixel origin is always at the bottom left hand corner. The PIXEL frame is used by all KAPPA commands that combine images and also the makemos command in CCDPACK.

For more information on coordinate frames please see *Using World Coordinate Systems* in SUN/95.

9.6.3 Exporting maps

After the data have been regridded with rebin the image can then be analysed with an image-analysis tool. Obviously KAPPA, FIGARO [25] or GAIA can be used immediately since they support the NDF standard.

In order to use packages such as IRAF, AIPS or MIRIAD the data must first be converted to FITS format by using either the CONVERT task ndf2fits or the FIGARO task wdfits. The ndf2fits task is recommended since it can understand FITS tables, floating-point FITS, and the new AST extension [20][13]

For images rebinned with an older version of SURF (pre-1.3) or if using wdfits or a version of CONVERT that does not understand AST (pre-1.1) it is necessary to remove the AXIS components from the NDF before converting since the axis information (arcsec offsets from the map centre) takes priority. In order to propagate WCS astrometry information from the NDF FITS array into the FITS file the axis information must first be removed by using FIGARO's delobj or KAPPA's setaxis. For example, if the image is stored in file scuba_image.sdf and we wish to convert this to an integer FITS file scuba_image.fits, with KAPPA/CONVERT we would do:

```
% kappa
% convert
% setaxis scuba_image mode=delete
% ndf2fits bitpix=32 profits scuba_image scuba_image.fits
```

The PROFITS parameter is there to ensure that all the FITS information in the NDF is propagated to the FITS file. With FIGARO we would do:

```
% figaro
% delobj scuba_image.axis
% wdfits scuba_image scuba_image.fits
```

[13] As of release v1.3 it is no longer necessary to remove the .AXIS extension before processing with ndf2fits because rebin now writes WCS information using the AST library.

Note that wdfits always writes integer FITS whereas ndf2fits would by default write REAL FITS (bitpix=−32). ndf2fits also writes the Variance and Quality arrays to FITS tables in the output file (this can be turned off by specifying just the data component with COMP=D).

From KAPPA V0.13 the WCS information stored in the header is used when manipulating the NDF. As of SURF version 1.4, the astrometry information is no longer stored in IRAS90 or FITS extensions; all astrometry information can be found in the AST/WCS component which is understood by KAPPA, GAIA and ndf2fits.

9.7 Photometry

For photometry data all that is required after extinction/remsky is that the jiggle pattern be processed to determine the signal for each integration and bolometer. It is possible to derive the signal by taking the AVERAGE of the jiggle data or by fitting a PARABOLA to the data. Parabola fitting probably should not be used unless the sky was exceptionally stable – the individual jiggle maps rarely look like they can be fitted by a parabola.

For this example I will use photometry data on 3C279 taken just before the example used for mapping. The data have been processed in the same way as scan 59.

```
% scuphot n56_sky_lon
SURF: run 56 was a PHOTOM observation of 3c279
SURF: file contains data for 1 exposure(s) in 10 integrations(s) in 1
measurement(s)
ANALYSIS - Which reduction method /'AVERAGE'/ >
OUT - Name of container file to hold map and time-sequence data > n56_pht_lon
FILE - Name of ASCII file to contain results summary /!/ > n56.txt
```

In this example n56_sky_lon.sdf is processed with scuphot. This observation consisted of 10 integrations and used a 9-point jiggle pattern. The value of each integration was determined by taking the average of the jiggle pattern. In some cases a better signal-to-noise can be achieved by processing the individual two second samples rather than averaging over the nine samples that comprise an integration. For these cases, usually short observations, where the scatter on the averaged data is not representative of the standard deviation of the raw data (small number statistics) ANALYSIS=SAMPLE is recommended.

Information on samples or integrations is written to a text file (n56.txt in this case) and also to n56_pht_lon.sdf. Since photometry observations can use multiple bolometers n56_pht_lon.sdf is in fact a HDS container [21] which contains two NDFs per bolometer: <BOL>_peak contains the photometry data for each integration and <BOL>_map contains the integrated jiggle pattern (assuming the jiggle pattern was on a regular grid – irregular jiggle patterns are written as 1-D images and no map is written for zero offset jiggles). In this example the bolometer used was H7 so that n56_pht_lon.h7_peak would be the NDF containing the integration data (the ascii version of which can be found in n56.txt) and n56_phot_lon.h7_map which would contain the integrated jiggle pattern

Since many photometry observations are usually combined to give the final result the scucat task can be used to concatenate data files that have been produced with scuphot (scucat knows about the _peak NDFs). In this case we have combined the three photometry observations listed in §9.1:

```
% scucat
METHOD - Concatenation method /'SEPARATE'/ >
OUT - Rootname of files to contain concatenated data > 3c279
IN - Name of input file containing photometry data /'n56_pht_lon'/ >
SURF: Found data for the following bolometers: h7
SURF: This is a PHOTOM observation of 3c279. There are 10 integrations
IN - Name of input file containing photometry data /!/ > n57_pht_lon
SURF: Found data for the following bolometers: h7
SURF: This is a PHOTOM observation of 3c279. There are 10 integrations
IN - Name of input file containing photometry data /!/ > n58_pht_lon
SURF: Found data for the following bolometers: h7
SURF: This is a PHOTOM observation of 3c279. There are 10 integrations
IN - Name of input file containing photometry data /!/ >
```

scucat continues to request input data until a null value (!) is given for the IN parameter. Since different bolometers should be processed independently, a new file is created for each bolometer. In this example scucat produces one file called 3c279_h7.sdf; if this data was taken with 2-bolometer chopping there would have been another file called 3c279_h9.sdf (for example). These files can now be analysed with standard statistics packages (e.g. KAPPA stats and kstest).

An alternative to the above for scucat is to use a text file to contain the list of filenames to be processed (useful for scripts):

```
% scucat noloop
METHOD - Concatenation method /'SEPARATE'/ >
OUT - Rootname of files to contain concatenated data > 3c279
IN - Name of input file containing photometry data /'n56_pht_lon'/ > ^in.lis
SURF: Found data for the following bolometers: h7
SURF: This is a PHOTOM observation of 3c279. There are 10 integrations
SURF: Found data for the following bolometers: h7
SURF: This is a PHOTOM observation of 3c279. There are 10 integrations
SURF: Found data for the following bolometers: h7
SURF: This is a PHOTOM observation of 3c279. There are 10 integrations
```

where `in.lis` contains the names of the 3 filenames to be processed (a comma separated list is also allowed).

If you do not want to process different bolometers independently, the METHOD parameter can be set to CATALL, in which case all data will be concatenated together regardless of bolometer and the output filename will match that specified in OUT (rather than being OUT + bolometer name).

9.7.1 SURF photometry and KAPPA

The photometry data reduction system produces one flux measurement per integration per bolometer. Further analysis simply involves finding a self-consistent mean of the merged data set (multiple measurements with a given bolometer can be concatenated together using scucat).

The SURF package supplies two KAPPA scripts to aid with this step of the analysis:

- qdraw displays the data with a $\pm 5\sigma$ range, calculates and draws the 3-sigma lines and reports the mean and error in the mean of the supplied data set. This script uses the KAPPA routines stats, linplot and drawsig. Figure 8 shows the data from the previous section as displayed with qdraw.

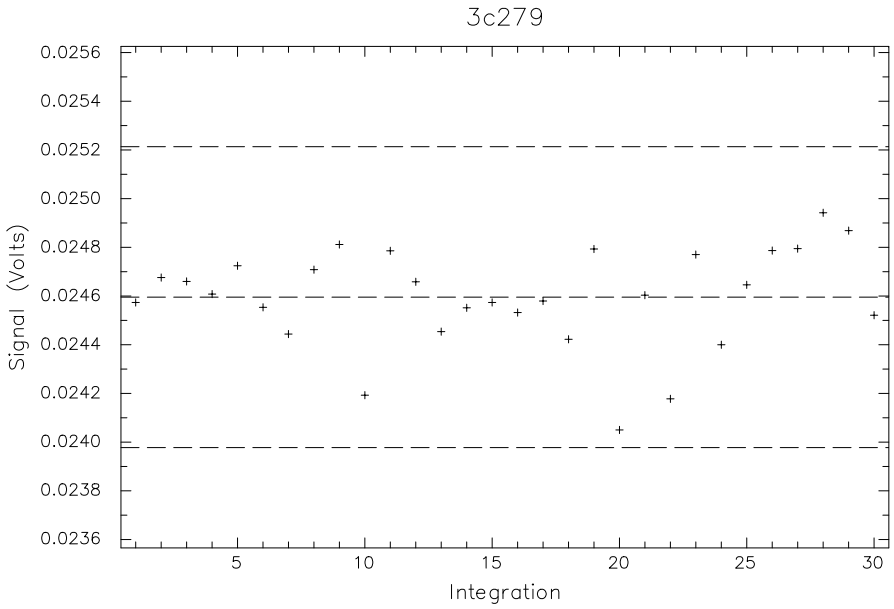

Figure 8: Photometry data of 3C279. This is the concatenated data from three separate observations.

- If the data contains large spikes which are having a significant effect on the standard deviation calculation then sigclip can be used to mark bad all data that are outside a given n-sigma threshold. This script uses the KAPPA routines thresh and stats.

The KAPPA kstest routine can also be used to check the self-consistency of the photometry data by performing a Kolmogorov-Smirnov test on the data (e.g. [26]).

9.8 Scan maps

Scan map data can be taken using two techniques (both based on chopping). The first technique is to chop in the direction of the scan and deconvolve each scan independently (the EKH method [11]). This technique must be used for single pixel mapping although it can also be used for array scan mapping. Problems with this technique are that it is very sensitive to spikes, every scan must be completely off-source at both ends and correlations with adjacent scans/pixels are ignored.

For array scan maps we scan the array across the source whilst chopping in a fixed direction on the sky. Following the work of Emerson[12] we take data using a number of different chop configurations in order to sample as many spatial frequencies as possible (we are not sensitive to structure that is larger than the chop throw). Multiple chop throws in 2 orthogonal directions are used with chop amplitudes chosen so that, except at the origin, the zeroes in the Fourier transform of one do not coincide with the zeroes in the FT of the other up to the spatial frequency limit of the telescope beam. For SCUBA, it is recommended that 6 different chop configurations should be used: Chop throws of 20, 30 and 65 arcsec each with chop position angles of 0 (Dec chopping) and 90 degrees (RA chopping) in a coordinate frame fixed on the sky. This will give

the best coverage of spatial frequencies but reasonable maps can also be obtained by combining four of the chop configurations. This mode also has the advantage that the deconvolution occurs after the images have been regridded; this means that data can be salvaged even if a scan did not go completely off source (by combining with data that does) and small spikes will be averaged out.

During commissioning it has been shown that the new method can result in a substantial improvement in signal-to-noise over the EKH method[13].

9.8.1 Baseline removal

The EKH method guarantees that the mean of every scan should be zero (the transputers remove the mean on-line). In the absence of spikes the data would not need baseline removal but in some cases a large spike can adjust the mean of the scan and the baseline should be recalculated after spike removal (with despike2).

For the "Emerson II" method the situation is more complicated since the mean of each scan is now not guaranteed to be zero (and in fact the transputers do not attempt to remove a baseline in this case). scan_rlb must be run in order to remove the baseline (each bolometer sees a slightly different background). For data where the scans are long enough to be off-source LINEAR baseline removal can be used. For more complicated source structure MEDIAN is worth a try although extremely complicated regions (e.g. OMC-1) may cause problems.

In order to overcome this problem it is also possible to specify specific scans that can be used for calculating the offset level since the DC level appears to be fairly constant during an integration. When the SECTION baseline removal method is selected a SCUBA section (§6) can be used to specify exposure (scan) numbers or actual positions in the data stream. Usually the first and last exposures are used since these are most likely to be 'off-source'. The appendix on scan_rlb contains some examples on the use of SCUBA sections to select baseline regions.

9.8.2 Sky removal

remsky can not be used to calculate the sky contribution for scan map data because it is no longer possible to select bolometers that are guaranteed to be on sky (since most bolometers will see 'source' at some point during the observation).

In order to overcome this problem the source signal must be removed from the data before attempting to calculate the sky. This is achieved with the calcsky task.

For each point in the input datasets calcsky finds the expected flux at that position by comparison with a model of the source and removes that flux from the input data. The source model can be calculated internally by calcsky or an external image can be supplied (usually generated from the same input data using rebin).

The source model is calculated in exactly the same way as for MEDIAN rebinning and despike: the input data are placed in bins related to position on the output image; the median of each bin is then taken to be a good measure of the flux in that region of sky. This approach is an approximation since the bin size (quarter beam width) can accommodate large gradient changes towards point sources but in general these errors are smoothed out by the average taken over the whole array. An alternative approach is to rebin the input data on a fine grid (e.g. 1 arcsec or finer) and use that as the input model (this is especially useful for scan maps since calcsky can add the dual beam response to the data when calculating the model)

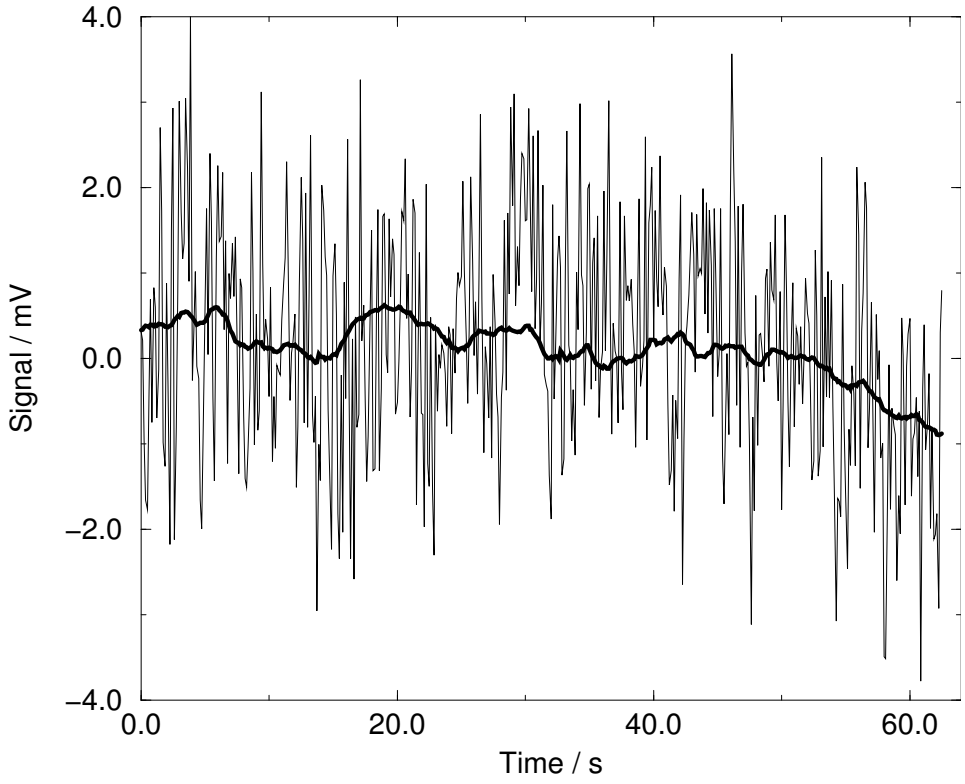

Figure 9: Sky noise calculated by calcsky for a short interval of the M82 data.

Once the source has been removed a sky signal is calculated from the residual signal by finding the average signal across the array for each time. In addition the time series can be smoothed since scan data are sampled much faster (approx. 8 Hz) than the sky emission is expected to vary (a few seconds). These time series are then stored in an extension inside the file (stored in .MORE.REDS.SKY). Once the sky has been calculated it can be removed by using remsky. remsky recognises the presence of a SKY extension and removes this signal from the main data array.

Fig. 9 shows the sky signal for some of the M82 data. In general the sky noise on scan data is below the noise but correlations are visible in the smoothed time series.

This technique is not limited to scan map data. Jiggle maps can benefit from using calcsky in cases where sky bolometers can not be identified or when the sky removal needs to be automated. One caveat is that the quality of the sky removal depends critically on the quality of the sky model. For extreme cases of sky noise in jiggle data where the individual switches are visible as hexagonal patterns across the image, calcsky can not disentangle the source from the hexagonal pattern (no other data are available for that position on the sky) and sky removal will fail.

More information on sky removal for jiggle and scan data can be found in Jenness et al.[13]

9.8.3 Dual beam deconvolution

Chopping whilst scanning results in an image that contains two beams (a plus and minus image of the source). To restore the source profile we must deconvolve the chop from the measured map. The problems associated with this step can best be appreciated by considering the Fourier transform (FT) of the chop function, which is a sine wave with zeroes at the origin and at harmonics of the inverse chop throw. Deconvolving the chop function is equivalent to dividing the FT of the measured map by the FT of the chop and then transforming back to image space. Clearly, problems arise at spatial frequencies where the sine wave of the chop FT has a low value or is zero. Noise at these frequencies is blown up and significantly reduces the signal-to-noise of the restored map [11].

EKH method The restore task must be used to remove the dual beam response whilst chopping in the scan direction. This must be run *before* rebinning. Since the chop direction rotates slowly on the sky (since it is dependent on the scan direction, which is in Nasmyth coordinates, and not the sky orientation) tasks that try to map the chopped data onto a sky plane (despike, calcsky, rebin) can not be used before the dual beam has been removed (despike is useless *after* restoration since spikes propagate through the entire scan and show up as sine waves after restore).

Emerson II method To remove the dual beam signature from "Emerson II" data, rebinned images of each chop configuration must be generated (they can be coadds of lots of observations). These images must have the same map centre, the same pixel scale, the same dimensions and must be regridded in the same coordinate frame as the chop (RJ for RJ, RB and GA data, PL or RD for moving sources). Fig. 10 shows examples of four dual beam images of M82.

Once these images have been generated, they can be processed by remdbm:

```
% remdbm o8?_lon_reb.sdf -out=m82
Starting monoliths...Done
Loop number 1
Chop: PA=90 THROW=20
```

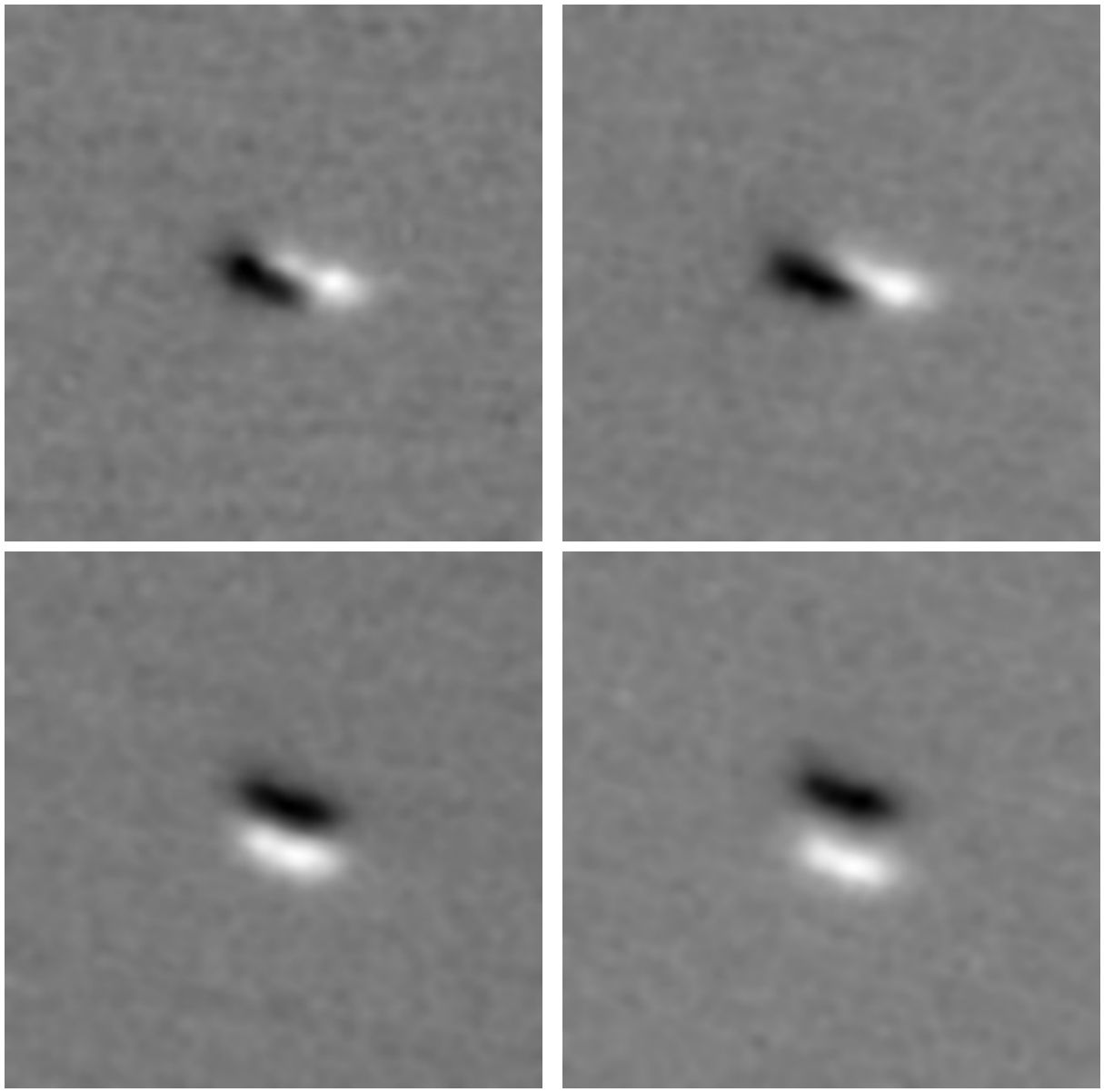

Figure 10: 4 dual beam images of M82. The chop throws are 20 arcsec RA chopping, 30 arcsec RA chopping, 20 arcsec dec chopping and 30 arcsec dec chopping.

```
Doing forward transformation

Loop number 2
Chop: PA=90 THROW=30

Doing forward transformation

Loop number 3
Chop: PA=0 THROW=20

Doing forward transformation

Loop number 4
Chop: PA=0 THROW=30

Doing forward transformation

Maximum difference between estimates of the same Fourier component is
0.02414273.

Doing inverse transformation

Result stored in m82
%
```

Note the use of shell wildcards. The final image can be seen in Fig. 11.

9.9 Polarimetry data reduction

Polarimetry observations are similar to map and photometry observations except that they are broken into measurements of a number of integrations (usually 1) for different positions of a half-wave plate. The wave plate normally steps in 22.5 degree increments. The initial data reduction scheme is identical to standard reduction except that the remip task must be run after extinction to remove the instrumental polarisation. For map observations, the intrebin task must then be used to generate an image for each integration (in practice this means an image per wave-plate position). intrebin ensures that the sky rotation angle and the waveplate angle are stored in the FITS headers (using the ANGROT and WPLATE keywords respectively). At this point the images can either be processed by scripts to calculate the Q and U images[14] or use the POLPACK data reduction system (version 2 or higher) which fits a sine wave to each pixel in the input images. The following example uses POLPACK and is similar to the approach used by the ORAC-DR [27] polarimetry recipes [28].

Assuming the output of intrebin is stored in file `omc1_reb.sdf` (remembering that this file will contain an image per waveplate position named `.i1`, `.i2` etc. There are 16 images in this example), POLPACK must first be told where to find the rotation angle and waveplate position:

```
% polimp table=$SURF_DIR/polimp.scuba omc1_reb
  16 input images to process...
```

[14] Available from your support scientist if required although the ORAC-DR pipeline recipes are now preferred

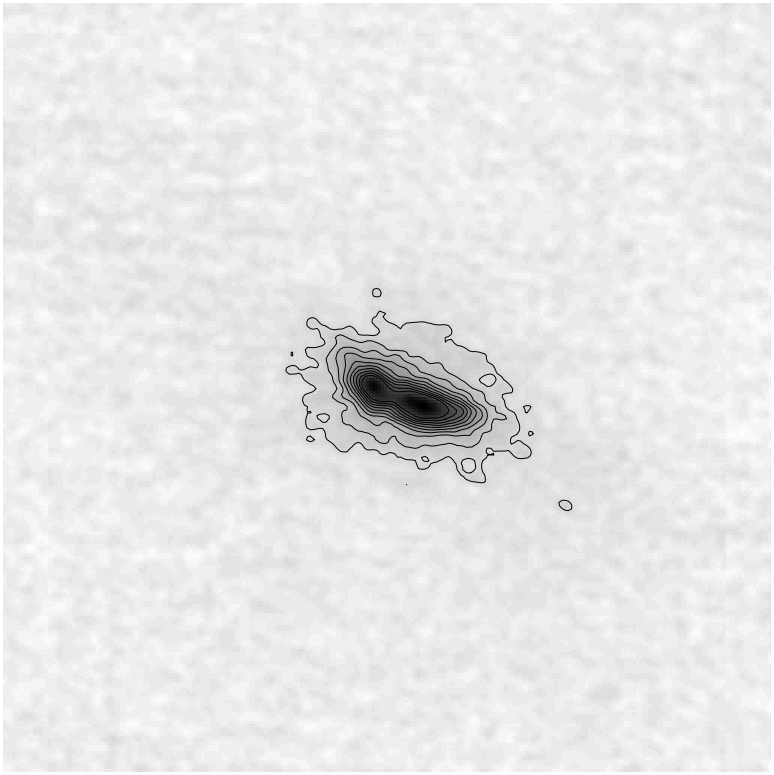

Figure 11: Final image of M82 after single beam restoration.

```
  Processing 'omc1_reb.I1'
     Setting WPLATE to -2.5
     Setting ANGROT to 70.27795
     Setting IMGID to 'omc1_reb.I1'
     Setting FILTER to '850_-2.5'

<cut intervening information>

  Processing 'omc1_reb.I16'
     Setting WPLATE to 335
     Setting ANGROT to 75.46666
     Setting IMGID to 'omc1_reb.I16'
     Setting FILTER to '850_335'
```

SURF provides a suitable import table.

The next stage is to generate the I, Q and U images from these individual waveplate images. This can be done by the polcal task directly:

```
% polcal weights=3 ilevel=2 omc1_reb
   Processing 16 images in single-beam mode...

OUT - Output Stokes cube > omc1_cube

 Iteration: 1...
   Total number of aberrant input pixels rejected: 199

 Iteration: 2...
   Total number of aberrant input pixels rejected: 219

 Iteration: 3...
   Total number of aberrant input pixels rejected: 219

 Iteration: 4...
   Total number of aberrant input pixels rejected: 219

 None of the output pixels failed the test specified by parameter MINFRAC.
```

In this case, we use WEIGHTS=3 to generate the variance information from the fit since the SCUBA variances are unreliable, although in many cases these variances are not under-estimated. polcal can combine images from separate overlapping fields all in one go if desired. If the intention is to mosaic separate fields within polcal intrebin should be run with the TRIM parameter set to some non-zero value to prevent problems with edge effects during the mosaicing. Also, polcal expects all the images to be referenced to the same pixel origin. This can be achieved using the KAPPA wcsalign command but it is easier to do this in intrebin by making sure that all images are regridded relative to the same RA/Dec centre – the resulting images will all be aligned to the same pixel grid.

In many cases, a more reliable approach to calculating the IQU cubes with satisfactory variance information is to use the polstack task on a set of 16 images and use that to generate 4 images with associated variances. These variances are determined directly from the data rather than from the fitting. We have found that running polcal on the resulting 4 images (with WEIGHTS=1

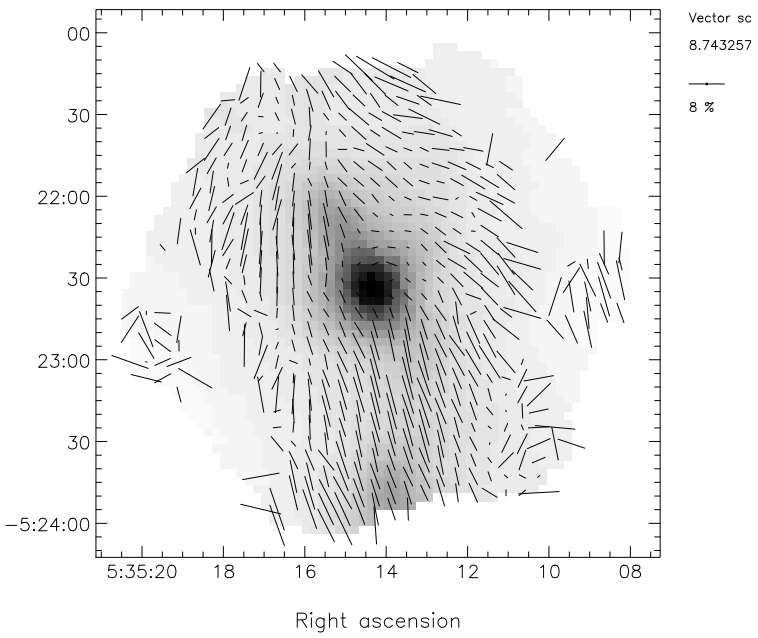

Figure 12: Polarisation E vectors around OMC-1 at 850 microns.

since we now wish to use the supplied variance information) and then mosaicking the resultant IQU cubes (e.g. via CCDPACK makemos) to improve signal-to-noise gives the most robust results and provides variance information that agrees with theory.

Once the IQU cube is made polvec can be used to generate the vectors:

```
% polvec omc1_cube
CAT - Output catalogue > omc1_cat

   2530 vectors written to the output catalogue.
```

This catalogue can then be binned using polbin, sections selected using catselect(part of CURSA) and plotted using polplot. An example image of OMC-1 can be seen in Fig. 12.

For more information on POLPACK see SUN/223 [29].

For photometry observations the output from scuphot can be exported to a single-pixel data reduction system, or alternatively, processed as under-sampled images and reduced through POLPACK as described above.

10 Citing SURF

If you wish to cite SCUBA in a paper the recommended reference is

> Holland W. S., Robson E.I., Gear W.K., Lightfoot J. F., Jenness T., Ivison R. J., Stevens J. A., Cunningham C. R., Ade P. A. R., Griffin M. J., Duncan W. D., Murphy J. A., Naylor D. A., 1999, *MNRAS*, **303**, 659

If you wish to cite this manual the recommended reference is:

> Jenness T., Lightfoot J.F., 2000, Starlink User Note 216, Starlink Project, CLRC

although an alternative *more recognizable* reference to SCUBA data processing can be found at:

> Jenness T., Lightfoot J.F., 1998, "*Reducing SCUBA Data at the James Clerk Maxwell Telescope*", in *Astronomical Data Analysis Software and Systems VII*, ASP Conf. Ser., **145**, 216

The recommended reference for the sky removal algorithm is now:

> Archibald E.N., Jenness T., Holland W.S., Coulson I.M., Jessop N.E., Stevens J.A., Robson E.I., Tilanus R.P.J., Duncan W.D., Lightfoot J.F., 2002, *MNRAS*, **336**, 1

and this supercedes the original paper:

> Jenness T., Lightfoot J. F., Holland W. S., 1998, *"Removing Sky contributions from SCUBA data"* in *Advanced Technology MMW, Radio and Terahertz Telescopes*, Philips T. G. (ed), Proc. SPIE **3357**, 548

The recommended reference for the Emerson 2 deconvolution algorithm as implemented in SURF is:

> Jenness T., Holland W. S., Chapin E., Lightfoot J.F., Duncan W. D., 2000, *"Dual-beam rastering and deconvolution techniques for SCUBA"*, in *Astronomical Data Analysis Software and Systems X*, ASP Conf. Ser., **216**, 559

The recommended reference for the ORAC-DR SCUBA data reduction pipeline is:

> Jenness T., Economou F., 1999, "*The SCUBA Data Reduction Pipeline: ORAC-DR at the JCMT*", in *Astronomical Data Analysis Software and Systems VIII*, ASP Conf. Ser., **172**, 171

The SURF software package is registered with the Astrophysics Source Code Library as `ascl:1403.008`.

11 Future Work

The SURF software is now in maintenance mode at the Joint Astronomy Centre. Bugs are fixed but new features are only added if there is a strong demand. New releases will be announced on the JCMT software web pages and through Starlink. Upgrades currently on the work list but which may not be completed due to other developments at the JAC are:

- Upgrades to the sky removal software to allow removal of planes.
- Support for heterodyne receiver beam maps.

Additional information on writing SURF extensions can be found in SSN/72 [30].

12 Release Notes

12.1 Changes in Version 1.6-11

- Now includes a new version of the scunoise application.
- A small error was found and fixed in the equation used by remip. Essentially the flux at all waveplate angles should have been reduced by a further small (constant) fraction determined by the level of instrumental polarization at the observing wavelength. The net result is that source polarizations will have been very slightly underestimated. For example, a source polarization of 1.00% at 850 microns should in fact have been 1.01% and a source polarization of 1.00% at 450 microns should have been 1.03%. This effect is smaller than measurement errors unless the source polarization exceeds $\approx$ 10%.
- A bug was fixed to allow 256 maps to be coadded in rebin. (previously the limit was 256 but another limit was reached after 173 maps).

12.2 Changes in Version 1.6-10

- Fix problem in bolrebin on linux (unintialized pointer).
- Fix remip problem with aborted polarimeter observations.

12.3 Changes in Version 1.6-9

- Fix more problems with scuba2mem when using SC (EKH) scanning.
- Correctly rebin photometry observations taken with AZ jiggling. [previously AZ offsets were simply ignored unless pointing corrections were being applied].

12.4 Changes in Version 1.6-8

- New version of the mapping cookbook (SC/11) now includes scan mapping.
- Update remdbm to support KAPPA V0.18.
- Use KAPLIBS rather than private copies of KAPPA routines.

12.5 Changes in Version 1.6-7

This is a bug fix release ov V1.6:

- Add support for raster skydips.
- Minor fixes for scuba2mem with EKH scanning.
- Don't calculate clock correction when using AZ.

12.6 Changes in Version 1.6

This includes important changes to the skydip task (relating to default values of fitting parameters) and a fix for the SCUVAX clock error problem.

New Tasks

- scuclkerr can be used to determine possible clock errors in the acquisition system.

Changes to existing tasks

- Add correction for the SCUVAX clock error problem.
- Skydips now 'know' the correct values to use as defaults for ETA_TEL, T_COLD and T_HOT.
- In remsky the outer ring of bolometers can be specified using R-1 (i.e. it counts from the outside in if you use a negative ring number)
- scuover is now a little cleverer (and the text can be a different color to the circles) and uses PGPLOT rather than the old SGS plotting system.
- scunoise works on Windows NT.
- If the second LST provided to remsky is less than the first LST it is now assumed that the time refers to the following day.

Bug Fixes

- Fixed error when scuphot runs in the pipeline where occasionally the parabola fit of the complete coadd could give incorrect answers.
- Can now combine data taken at almost the same wavelengths (a 20 micron difference is allowed) when using rebin.
- Output file from remdbm now no longer contains CHOP_* keywords

12.7 Changes in Version 1.5

This is a minor update.

New Tasks

- scuba2mem officially released (previously it was available but not advertised).
- The SURF programming guide (SSN/72) now available.

Changes to existing tasks

- sculog and related tools rewritten to handle data from multiple UT dates in a single directory. Extended support for POLMAP and POLPHOT observing modes.
- Improve support of external data model in calcsky. Can now import image of arbritrary coordinates and automatically add chop functions.
- add_dbm can now be used to add a triple beam.

- Scripts are now compatible with KAPPA version 0.14.

Bug fixes

- Fix bug in remdbm when using filtering when data have a pixel origin that is not in the middle of the array.

12.8 Changes in Version 1.4

The main purpose of this upgrade is to add polarimetry support to SURF.

New Tasks

- remip can be used to remove instrumental polarisation.
- add_dbm can be used to generate simulated dual beam images
- scusetenv for setting environment variables at the JAC.

Changes to existing tasks

- Units should now be propagated correctly through all tasks (ie calibration units are not lost after rebin or scuphot)
- SURF version number is now written to history information
- scan_rlb: Area to use for baseline removal can now be specified as a SCUBA section.
- remdbm : The `-filter` option will filter out high frequencies before inverting the Fourier transform.
- rebin:
  - Add TRIM parameter to trim edge regions from rebinned images (useful when trying to mosaic)
  - Astrometry information is now entirely contained in the AST/WCS component. No longer written to FITS or IRAS90 extensions. Also, the pixel origin is now centred on the specified RA/Dec centre of the image and not the bottom left hand corner.
  - REFPIX parameter has been added to make it easier to specify the reference pixel location when changing the map size (in the past the reference pixel was always the middle of the map when specifying the map size)
  - The output file is now propagated from the input when processing a single file (keeps history intact)
- intrebin: Waveplate position and sky rotation angle are now written to the fits headers for polarimetry observations.
- extinction: Can process FAST_AXIS polarimetry information correctly.
- skydip: Add preliminary support for RASTER mode (not yet stable)
- obssum: POLMAP and POLPHOT are now supported modes.
- scuphot: now recognizes measurements as well as integrations (required for polarimetry observing)
- scumakewt: Now can make a weights image like a reference image (ie same size, chop throw and position angle). See the LIKE parameter.

12.9 Changes in Version 1.3

This is only a minor upgrade. All scripts have been updated so that they are compatible with KAPPA V0.13.

New Tasks

- Noise data can now be processed with the reduce_noise task.

Changes to existing tasks

- scunoise has been modified so that it can read files generated by reduce_noise.
- Images produced by rebin now include world-coordinate information via the AST library (WCS extension).
- The guard ring has been turned on for LINEAR and GAUSSIAN regridding. (It had been turned off in v1.2). A new parameter (GUARD) can be used to turn the bolometer guard ring on or off.
- Axis information is now written to the output files from REMDBM.

Minor fixes

- rebin can now combine 256 files.
- sculog now formats the RA field correctly.
- The documentation has been updated to reflect the addition of reduce_noise and the use of AST.

12.10 Changes in Version 1.2

New Tasks

- Sky removal for SCAN map is now available using the calcsky task.
- Dual beam images taken using the new SCAN map observing mode can now be reduced using the remdbm task (also uses scumakewt).
- The offset between the arrays can be compensated for by using change_nacentre.
- Noise data can now be displayed with scunoise.
- Bolometer weights can be set with setbolwt.

Changes to existing tasks

- scucat can now accept a comma separated list of input files or a text file containing a list of files rather than having to supply one at a time. Also, there is now a METHOD option in scucat to control whether bolometers are treated independently or combined regardless of bolometer name.
- scuphot can now propagate all samples to the output file. This is necessary for observations where the number of integrations is small and the variance can not be calculated reliably.

- scan_rlb now has two extra modes for baseline removal (MEAN and MEDIAN).
- A Gaussian regridding option has been added to rebin (bolrebin, intrebin). Also, the radius and footprint size of the convolution functions can now be configured.
- A median regridding option is available. This option simply calculates the median value of all points in an output cell.
- A histogram of the distribution of data samples on the output image can be obtained with the TIMES parameter in rebin.
- Bolometer weighting has been added to rebin. This is still in alpha test since it has been shown not to conserve flux for small data sets (for larger datasets – hours – there is a signal-to-noise gain without turning off bad pixels).
- skydip now provides an estimate of the errors.

Minor fixes

- despike can now be told to write output files automatically via the DEFOUT parameter.
- scuclip now performs an iterative clip by default.
- Units are propagated through scuphot.
- sdip now resets the linplot colour settings to their original values after use.
- The size of the 'IN' parameter has been increased in change_quality and change_data.
- A memory leak has been fixed in despike.

12.11 Changes in Version 1.1

General changes

- Output files are now as small as possible. In version 1.0-0 output files were the same size as the input file.
- Observation numbers, rather than the full filename, can now be given to tasks that process the raw demodulated data (reduce_switch, skydip, sdip, scuquick). This feature requires the SCUBA_PREFIX environment variable.
- All tasks now supply a default output filename. The form of this filename is governed by the SCUBA_SUFFIX environment variable.
- The MAP_X, MAP_Y and LOCAL_COORDS observing parameters are now supported.

New tasks

- A despiking task has been added for JIGGLE/MAP data. (despike)
- An experimental despiking task is available for SCAN/MAP data (despike2).
- The data clipping functionality has been moved from remsky to a stand-alone task (scuclip).
- There is now a task for extracting flatfield information from data files. (extract_flat).
- Data suffering from the 'data shift' problem (mainly Semester 97a) can be fixed with the scushift task.

- The experimental task, scan_rlb, can be used to remove linear baselines from SCAN/MAP data.
- The addition of some interactive despiking and data inspection tools (dspbol, pltbol, and rlinplot).

Changes to existing tasks

- skysum is now officially released with documentation.
- SKYDIP data can now be processed with reduce_switch and change_quality. This allows bad skydip points to be removed prior to fitting with skydip. This required changes to reduce_switch (cold load temperatures are requested) and skydip.
- reduce_switch now creates axis information (instead of extinction).
- For SCAN/MAP data scuover now displays the position of the array at the start of a scan
- skydip now reads default values for ETA_TEL from the observation header and allows the T_HOT value to be modified. Additionally, the fit results are stored as output parameters.
- extinction now reads default values for FIRST_TAU from the observation header and supplies a default for SECOND_TAU (the value accepted for FIRST_TAU.)
- remsky now adds the mean sky level back onto the data in order to minimise the removal of flux from the image.
- remsky no longer despikes the data. This facility is now provided by the scuclip/despike tasks.
- Bolometer groups (e.g. ring 1, ring 2, all) can now be used to specify bolometer lists for remsky.
- The size of the output map can now be specified in rebin.
- The filenaming system used by scuquick has been modified slightly so that it conforms with the SCUBA_SUFFIX=long mode. scuquick now also recognizes SKYDIPs.

12.12 Version 1.0–0

First public release of SURF.

Glossary

chopping The secondary mirror is continuously moved on and off source at approximately 7 Hz in order to remove the sky to zeroth order. This is done in addition to standard jiggling.

demodulation Removal of the chop signal by the transputers. At this time, the raw data can not be accessed, only the demodulated data are stored.

exposure An exposure is the result from a complete set of switches. For example, in a JIGGLE/MAP or PHOTOM observation where the telescope is nodding the source between left and right beams, the data from each nod position is a switch and the reduced result 'left switch' - 'right switch' say, is an exposure. In a SCAN/MAP observation there is no beam switching so, in this case, an exposure is the same as a switch.

integration An integration means different things for different observations.

For one of the mapping modes it means the data from one fully-sampled coverage of the map area. In a JIGGLE/MAP, where full sampling is achieved by jiggling the secondary mirror, an integration is generally the results from one pass through the complete jiggle pattern. An integration is made up of one or more exposures.

Similarly, an integration for a SCAN/MAP observation is made up of data from the raster scans that cover the map area once.

For PHOTOM observations an integration is usually the average of a 9 point mini-jiggle.

For a SKYDIP observation, an integration is the data from a single revolution of the sector chopper in front of the cryostat window.

jiggle In order to sample an image fully the secondary mirror is moved once a second (whilst chopping) to move the position of the array on the sky; this is called 'jiggling.' There are a complete set of jiggle positions for each integration. A PHOTOM observation can also jiggle in order to correct for seeing effects.

measurement A measurement is a group of integrations. Most MAP or PHOTOM observations will consist of only one measurement.

A FOCUS or ALIGN observation consists of five measurements (one for each secondary mirror position). A SKYDIP observation consists of one measurement at each elevation.

nod In order to correct for atmospheric variation the telescope is moved off-source in each exposure so that sky can be measured.

ODF The observation definition file (ODF) is a file containing a list of instructions for an observation with SCUBA.

sub-instrument SCUBA contains bolometer arrays and photometric pixels that can operate at several wavelengths simultaneously. Each of these is called a sub-instrument. They are:

- SHORT - the short wave array containing 91 bolometers
- LONG - the long wave array containing 37 bolometers
- P1100 - the single bolometer optimised for 1100μm.

- P1350 - the single bolometer optimised for 1350μm.
- P2000 - the single bolometer optimised for 2000μm.

switch The switch is the fundamental unit of data-taking in an observation. For example in a JIGGLE/MAP or PHOTOM observation each chunk of jiggle positions measured with the object in the beam of a telescope is a switch. Each scan across the source in a SCAN/MAP observation is also a switch.

tau (τ) Submillimetre extinction is measured using the zenith optical depth, tau or τ, this is a measure of the amount of water vapour present in the atmosphere. For a tau, τ at a given airmass, A, the attenuation due to the atmosphere is given as $e^{-A\tau}$. Note that tau is wavelength dependent and that the value quoted by the Caltech Submillimetre Observatory (CSO) is the τ at 225 GHz and will therefore be different at the other wavelengths used by SCUBA (see [31] for details of the variation with SCUBA filters; or [32] for details on the variation seen with UKT14).

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A An alphabetical summary of SURF commands

B Classified SURF commands

SURF applications may be classified in terms of their function as follows:

Observation summaries:

SCULOG: Provide detailed descriptions of all observation data.

OBSSUM: Summarize all observations.

MAPSUM: Summarize mapping observations.

PHOTSUM: Summarize photometry observations.

POINTSUM: Summarize pointing observations.

SKYSUM: Summarize skydip observations.

Miscellaneous:

EXTRACT_FLAT: Write the flatfield information to a text file.

REDUCE_NOISE: Process demodulated noise data.

SCUBA2MEM: Calculate bolometer positions

SCUCLKERR: Determine potential inconsistency in the SCUBA time headers

SCUHELP: Interactive help system.

SCUPA: Show position angle of array (requires KAPPA).

SCUSETENV: Set SCUBA environment variables (JAC only)

SCUQUICK: Semi-automated data reduction pipeline.

SCUSHIFT: Shift data along an A-to-D card.

SDIP: Script to reduce and display skydip data (requires KAPPA).

SKYDIP: Calculate sky opacity from skydip data.

Initial Processing:

REDUCE_SWITCH: Convert raw demodulated data to standard format and process individual switches.

FLATFIELD: Multiply the data array by the flatfield volumes.

EXTINCTION: Correct the data for atmospheric extinction.

CALCSKY: Calculate sky signal.

Processing JIGGLE data:

DESPIKE: Despike JIGGLE data.

REMSKY: Remove sky contribution from each jiggle.

SCUCLIP: Sigma clip photometry data and maps of weak sources.

Processing SCAN/MAP data:

ADD_DBM: Add dual-beam to single-beam data.
DESPIKE2: Despike SCAN/MAP data.
REMDBM: Remove dual-beam response from SCAN/MAP images (requires KAPPA).
RESTORE: Remove dual-beam response from SCAN/MAP data (EKH method).
SCAN_RLB: Remove baselines from scans.
SCUMAKEWT: Generate Fourier weights (used by remdbm).

Polarimetry:

REMIP: Remove instrumental polarisation from polarimetry data.

Data inspection:

PLTBOL: Interactive bolometer display (requires KAPPA)
RLINPLOT: Interactive display via mlinplot(requires KAPPA).
SCUNOISE: Plot SCUBA noise data.
SCUPLOT: Interactive display and despiking (requires KAPPA).

Data modification:

CHANGE_DATA: Change data (or variance) values in a dataset.
CHANGE_FLAT: Change the stored flatfield information.
CHANGE_NACENTRE: Change Nasmyth coordinates of array centre.
CHANGE_POINTING: Change Az and El pointing offsets for map data.
CHANGE_QUALITY: Change data quality.
DSPBOL: Interactive despiking (requires KAPPA).

Mapping:

REBIN: Rebin all data onto a rectangular grid.
BOLREBIN: Generate a separate regridded image for each bolometer.
INTREBIN: Generate a separate regridded image for each integration.
EXTRACT_DATA: Write bolometer positions and data to text file.
SCUOVER: Overlay bolometer array on image.
SETBOLWT: Calculate and set bolometer weights (Requires KAPPA).

Photometry:

SCUPHOT: Reduces photometry data to a single point per integration.
SCUCAT: Concatenate photometry results into a single NDF.
QDRAW: Plot photometry data (requires KAPPA).
SIGCLIP: Remove spikes from photometry data (requires KAPPA).

C Complete routine descriptions

The SURF routines are described in the following pages:

ADD_DBM
Generate a chopped image from a single beam map

Description:

Create a chopped image from a single beam input map. Can be used to create a dual-beam (e.g. a simlated scan map image) or a triple-beam map (e.g. a simulated jiggle map image).

For dual-beam it simply finds the signal detected at each pixel by looking at the difference between the pixels nearest to each chop beam. This calculates a middle beam response. (ie the response at each pixel is the difference between the L and the R beams).

For the triple-beam response the signal is the difference between the middle pixel and half the values measured in the negative beams. Set NBEAMS to 3 to use triple-beam response.

This task can be used to generate test data for remdbm.

Usage:

```
add_dbm in chop pa out
```

Parameters:

CHOP = REAL (Read)
Chop throw in pixels of the input image. There is no default. The range of this parameter should lie between 1 and the size of the input image.

IN = NDF (Read)
Input single beam image.

MSG_FILTER = CHAR (Read)
Message filter level. Options are QUIET, NORMAL and VERBOSE. Default is NORM.

NBEAMS = INTEGER (Read)
When NBEAMS=2 a dual-beam response is calculated. When NBEAMS=3 a triple-beam response is calculated. Default is 3.

OUT = NDF (Write)
Output Dual beam image. Default output name is input name plus _dbm_int(pa)_int(chop).

PA = REAL (Read)
Position angle of chop throw. Positive is anti-clockwise starting from North. The angle should be specified in degrees.

PIXSIZE = REAL (Read)
Pixel size in arcseconds. This is required for compatibility with remdbm (since the CHOP_THR FITS keyword has to be in arcseconds rather than pixels and REMDBM requires SCUPIXSZ FITS keyword). A null value will be treated as 1 arcsec. Default is to use the value of SCUPIXSZ from the FITS header (if present).

Examples:

```
add_dbm gaussian 0 30 dbm_out
```

Generate a dual beam image from the single beam 'gaussian' input NDF using a 30 pixel chop at 0 degrees. Write the resulting image to dbm_out.sdf.

```
add_dbm image 90 45 3bm_out nbeams=3
```

Generate a triple-beam image with throw 45 and position angle 90 degrees.

Notes:

- The output images are compatible with REMDBM.
- All extensions and AST/WCS information are propogated to the output image.
- A variance array is created if present in the input image.
- If a quality array is present in the input image it is used to generate a bad pixel mask in the output image and is removed.
- Bad pixels in the input image are treated as zeroes for the dual beam calculation.

Related Applications :

SURF: remdbm

BOLREBIN
Generate a separate regridded image for each bolometer

Description:

This routine rebins the demodulated data from SCUBA MAP observations onto a rectangular mesh by a variety of methods. Currently convolution by weighting functions, spline interpolation and median are supported.

- Weighting functions:
  Currently linear, Bessel and Gaussian weighting functions are supported. The width of the Bessel function is such that it should preserve all spatial information obtained by the telescope at the wavelength of observation, but suppress higher spatial frequencies. To minimise edge effects the Bessel function is truncated at a radius of 10 half-widths from the centre (although this is configurable), and apodized over its outer third by a cosine function. Viewed in frequency space the method consists of Fourier transforming the input dataset(s), multiplying the transform by a cylindrical top-hat (the F.T. of the Bessel function), then transforming back into image space. A linear weighting function is also available which works out to one half-width - this has the advantage that it is much faster to process and is much less susceptible to edge effects. The Gaussian weighting function is probably the best compromise between the Bessel (slow and prone to edge effects) and Linear (fast but the point spread function is non-trivial for modeling).
  The radius and size of 'footprint' for the weighting functions are configurable using the WTFNRAD and SCALE parameters.
- Splines:
  Additionally, spline interpolation and smoothing routines are also available. Note that the spline routines work on each integration in turn, whereas the weighting function routines work on all the input data in one go. At present the spline routines are experimental and comments are welcomed.
- Median:
  A regridding option derived from despike is available. This method simply puts all data points in an output grid and calculates the median of each output cell. Small pixel scales require large datasets (since not all cells in a 1 arcsecond grid will contain data points) although the KAPPA commands fillbad and glitch can be used to smooth over bad pixels.

Usage:

```
bolrebin ref
```

Parameters:

GUARD = LOGICAL (Read)

Controls whether the bolometer guard ring should be used during the regridding process. The guard ring enforces zero flux at the edge of the regridded image. Should be turned off if flux is present at the edge. Default is to use the guard ring for LINEAR, BESSEL and GAUSSIAN rebin modes.

IN = CHAR (Read)
The name of the input file to be rebinned. This parameter is requested repeatedly until a NULL value (!) is supplied. LOOP must be TRUE. IN can include a SCUBA section. Like the REF parameter this parameter accepts a text file.

LAT_OUT = CHAR (Read)
The latitude of the output map centre. The supplied default value is that of the map centre of the first map.

LONG_OUT = CHAR (Read)
The longitude of the output map centre. The supplied default value is that of the map centre of the first map.

LOOP = LOGICAL (Read)
Task will ask for multiple input files if true. Only REF is read if noloop.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)
This is the name of the HDS container file that will contain the rebinned images. The map for each bolometer is stored in an NDF inside this NDF container. The maps can be accessed as '`out.name`' where `name` is the bolometer name (e.g. H7 or G1 etc.).

OUT_COORDS = CHAR (Read)
The coordinate system of the output map. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (e.g. Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)
- GA: Galactic coordinates (J2000)

For RD current epoch is taken from the first input file.

OUT_OBJECT = CHAR (Read)
The name of the object (ie the NDF title).

PIXSIZE_OUT = REAL (Read)
Size of pixels in the output map. Units are arcsec.

REBIN_METHOD = CHAR (Read)
The rebin method to be used. A number of regridding methods are available:

- LINEAR: Linear weighting function
- GAUSSIAN: Gaussian weighting function
- BESSEL: Bessel weighting function
- SPLINE1: Interpolating spline (PDA_IDBVIP)
- SPLINE2: Smoothing spline (PDA_SURFIT)
- SPLINE3: Interpolating spline (PDA_IDSFFT)
- MEDIAN: Median regridding

Please refer to the PDA documentation (SUN/194) for more information on the spline fitting algorithms.

REF = CHAR (Read)
The name of the first NDF to be rebinned. The name may also be the name of an ASCII text file containing NDF and parameter values. See the notes. REF can include a SCUBA section.

REFPIX (2) = INTEGER (Read)
The coordinate of the reference pixel in the output data array. This corresponds to the pixel associated with the specified RA/Dec centre. Default is to use the middle pixel if a size is specified or the optimal pixel if the default size is used (see the SIZE parameter).

TRIM = INTEGER (Read)
This parameter determines the amount of good data that should be trimmed from the final image to correct for edge effects. The supplied value should be in arcseconds. All pixels closer to a bad pixel than this distance will be set to bad in the output image (by setting bit 1 in the quality array). Default is 0.0.

SCALE = REAL (Read)
Radius of one scale size in arcsec. This effectively governs the size of the weighting function. For LINEAR one scale size corresponds to the zero of the cone, for BESSEL it is the first zero of the Bessel function (π) and for Gaussian it is the half-width half maximum (HWHM).

SIZE (2) = INTEGER (Read)
This array parameter sets the size of the output grid in pixels (nx, ny). The default values are the minimum dimensions required to display the entirety of the mapped area.

SHIFT_DX = REAL (Read)
The pointing shift (in X) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

SHIFT_DY = REAL (Read)
The pointing shift (in Y) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

TIMES = LOGICAL (Read)
Store an extra NDF in the output map containing the 2-D histogram of the data. This can be used to make an estimate of the actual number of samples responsible for each point in the output grid. Note that, in general, the number of pixels in the output grid exceeds the number of independent beams in the image. The data can be accessed as OUT.more.reds.times. Default is FALSE.

WEIGHT = REAL (Read)
The relative weight that should be assigned to each dataset.

WEIGHTS = LOGICAL (Read)
This parameter governs whether the convolution weights array will be stored in the output NDF. The default is FALSE (i.e. do not store the weights array).

WTFNRAD = INTEGER (Read)
Size of the weighting function in scale sizes. This parameter is irrelevant for LINEAR regridding. For Gaussian the default is 3 (i.e. a diameter of 3 FWHM for the footprint),

and for Bessel it is 10. The smaller the weighting function is (a combination of WTFNRAD and SCALE) the faster the regridding goes.

Examples:

```
bolrebin rebin_method=LINEAR out_coords=RJ
```

Rebin the maps with LINEAR weighting function in J2000 RA/Dec coordinates. You will be asked for input datasets until a null value is given.

```
bolrebin rebin_method=BESSEL out=map
```

Rebin the maps with Bessel weighting function. Each bolometer is rebinned separately and placed in an NDF in the output container file map.sdf. Bolometer H7 can be accessed by displaying map.h7.

```
bolrebin noloop ref=test.bat
```

Rebin each bolometer using the data specified in the file test.bat.

Notes:

For each file name that is entered, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY are requested.

- The application can read in up to 256 separate input datasets.
- The output map will be large enough to include all data points.
- Spline regridding may have problems with SCAN/MAP (since integrations contain lots of overlapping data points).
- SCUBA sections can be given along with any input NDF
- The relative weights associated with each point in the output map are stored in a WEIGHTS NDF in the REDS extension of the output data (For WEIGHTS=TRUE). For spline rebinning each point is equivalent to the number of integrations added into the final data point. For weight function regridding the situation is more complicated. The actual number of points contributing to each cell can be stored using the TIMES parameter.
- Bolometer weights will be used if a BOLWT extension is found in the input data file (usually set with setbolwt).
- Astrometry information is stored in the WCS component and not the FITS extension.

ASCII input files :

The REF and IN parameters accept ASCII text files as input. These text files may contain comments (signified by a #), NDF names, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY, and names of other ASCII files. There is one data file per line. An example file is:

```
file1{b5}   1.0  0.5  0.0  # Read bolometer 5 from file1.sdf
file2                     # Read file 2 but you will still be
                          # prompted for WEIGHT, and shifts.
file3{i3}-  1.0  0.0  0.0  # Use everything except int 3
test.bat                  # Read in another text file
```

Note that the parameters are position dependent and are not necessary. Missing parameters are requested. This means it is not possible to specify SHIFT_DX (position 3) without specifying the WEIGHT. If the file has the .txt extension the NDF system will attempt to convert it to NDF format before processing – this is probably not what you want.

Related Applications :

SURF: rebin, intrebin, extract_data

CALCSKY
Calculate sky contribution from median image

Description:

This routine calculates the sky contribution by attempting to remove the source from the input data stream. The source signal can either be calculated by this routine or by reading in a model of the source from a file.

When calculating the source structure internally a similar method to that used by DESPIKE is employed. The input data are placed into bins of size one quarter beamwidth. The median of each bin is calculated and this is treated as the source model (cf. REBIN_METHOD=MEDIAN in rebin).

Once the source model is available, it is removed from all of the input data. The source-removed data are then analysed with the sky emission derived from the mean of the signal across the array for all the sample times.

Since the sky signal is expected to vary on timescales of the order of one second, an option is included for smoothing the sky signal. This is especially useful for scan map data where samples are taken at 7.8∼Hz.

Usage:

```
calcsky ref
```

Parameters:

BOXSZ = INTEGER (Given)
Size of smoothing box in seconds. This is used to smooth the time series. Default is 2.0 seconds.

IN = CHAR (Read)
The name of the input file to be processed. This parameter is requested repeatedly until a NULL value (!) is supplied. LOOP must be TRUE. IN can include a SCUBA section. Like the REF parameter this parameter accepts a text file.

LOOP = LOGICAL (Read)
Task will ask for multiple input files if true. Only REF is read if noloop.

MODEL = NDF (Read)
NDF containing the model of the source. The astrometry is read from this file. The model must have been generated by SURF since it relies on the presence of certain FITS keywords.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM.

NOSRC = NDF (Write)
File to store source removed data. This can be used to check the source removal. Note that this output file can not be used directly by SURF for further processing since the header is incomplete. No file is written by default.

OUT_COORDS = CHAR (Read)
The coordinate system to be used for the model determination. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (e.g. Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)
- GA: Galactic coordinates (J2000)

For RD current epoch is taken from the first input file.

REF = CHAR (Given)
The name of the first NDF to be processed. The name may also be the name of an ASCII text file containing NDF and parameter values. REF can include a SCUBA section. See rebin for more information on the format of the ASCII input file.

SHIFT_DX = REAL (Read)
The pointing shift (in X) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

SHIFT_DY = REAL (Read)
The pointing shift (in Y) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

WEIGHT = REAL (Read)
This parameter does nothing in calcsky. It must be present when using text file input. Any value is allowed.

Examples:

```
calcsky test_rlb model=!  \\
```

Calculate sky for test_rlb.sdf. Only read in one file and don't use an external source model.

```
calcsky list.inp model=m82 noloop\\
```

Read in the files specified in list.inp and use m82.sdf as a model of the source.

```
calcsky file nosrc=nosrc boxsz=10.0 \\
```

Calculate sky for file.sdf. Store the source subtracted image in nosrc.sdf. Use a smoothing size of 10 seconds.

Notes:

- The model itself is only an approximation to the data (since the data points can fall anywhere within a given cell) so some source signal will remain after source subtraction.

- If a model is supplied externally (via MODEL parameter) the cell size of the model is used for the source subtraction.
- The sky signal is stored in an NDF extension (.MORE.REDS.SKY). The file must be processed by remsky to actually remove the sky contribution.

Related Applications :

SURF: remsky

CHANGE_DATA
Set SCUBA data to any value

Description:

This application is used to set SCUBA data to any value by using SCUBA sections to specify a subset of the full data. Data, Variance and Quality arrays can be modified.

Once the data specification has been decoded the application will read from parameter VALUE the value of the data that should be used. All data specified by the section (or by the inverse of this section if specified) will be set to this value.

Usage:

```
change_data ndf{spec1}{spec2}{specn} value out
```

Parameters:

COMP = LITERAL (Read)

The name of the NDF array component which should be changed: "Data","Error", "Quality" or "Variance" (where "Error" is the alternative to "Variance" and causes the square root of the variance values to be taken). The default component is always DATA. If "Quality" is specified, then the quality values are treated as numerical values (in the range 0 to 255).

IN = CHAR (Read)

Name of data set and the specification of the data to be changed. Usually of the form 'ndf{spec1}{spec2}' where ndf is the filename and spec1...n are the section specifications. The section can be read from the SECTION parameter if the SCUBA section is omitted.

MSG_FILTER = CHAR (Read)

Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages

OUT = NDF (Write)

Name of the NDF that stores the modified data.

SECTION() = CHAR (Read)

This parameter can be used to specify SCUBA sections. Curly brackets must still be given. Since this is an array parameter square brackets must be used to specify more than one component:

```
SECTION > [ {b3} , {i2} ]
```

would supply two SECTIONS of {b3} and {i2}. Only {b3} will be used if the square brackets are not used. Care must also be taken when using commas in SCUBA sections - the parameter system will split multiple entries on commas unless the entire section is quoted:

```
SECTION > [ "{b3,5}" , {i2} ]
```

If necessary the negation character should come after a section (ie after the closing curly bracket) and that negation applies to the combined section and not just the string containing the negation character:

```
SECTION > [ {b3}-, {i2} ]
```

implies that the section consists of everything except bolometer 3 and integration 2. This parameter is only used when no SCUBA section was specified via the IN parameter.

VALUE = LITERAL (Read)

Value to which all selected data points should be set. A value of 'bad' will set the data point to VAL__BAD (Starlink bad data value). For COMP=Quality only numbers 0 to 255 are allowed - numbers outside this range are assumed to be bad values.

Examples:

```
change_data 'ndf{b2}' bad changed
```

Copy all data in ndf.sdf to changed.sdf and change all data in bolometer 2 to bad.

```
change_data 'ndf{}' comp=variance value=0.0001
```

Copy ndf.sdf to the output file (asked for explicitly) and set all variance values to 0.0001.

```
change_data test section='[{b47},{i3}]' value=1.02
```

Select data from bolometer 47 and integration 3 in test.sdf and set this to a value of 1.02. This method of selecting a section is not recommended given the complication using commas and square brackets.

```
change_data test2 section='["{b2,5}", {i2}-]' value=0.2 comp=err
```

Select everything except integration 2 and bolometers 2 and 5. Set the error for this section to 0.2

```
change_data 'phot{i2:6}{b3}' comp=quality value=8
```

Explicitly set the quality array to 8 for integrations 2 through 6 and bolometer 3. The task change_quality is recommended in this case since then only bit 3 is affected.

```
change_data 'map{i2,5}-' value=0.0
```

Set everything except integrations 2 and 5 to zero.

Notes:

- This software sets the actual value in the specified component and so, unlike change_quality, is not reversible. For this reason a new output file is created.
- This task does not attempt to create a component if the specified component is missing. A Variance array can be created using the KAPPA task setvar if necessary.

- The SECTION parameter is not used if a SCUBA section was given via the IN parameter.

Related Application :

SURF: change_quality, rebin, scuphot

CHANGE_FLAT
Change the flatfield in a SCUBA datafile

Description:

The flatfield information is stored inside each demodulated data file and this task can be used to change the flatfield that is stored internally. The new flatfield is read from a text file.

Usage:

```
change_flat in new_flat
```

Parameters:

IN = NDF (Read)
Name of NDF to change.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM.

NEW_FLAT = CHAR (Read)
Name of the new flatfield file.

Examples:

```
change_flat test newflat.dat
```

This will change the flatfield stored in test.sdf to that stored in newflat.dat.

Related Application :

SURF: flatfield, scuquick

CHANGE_NACENTRE
Shift the Nasmyth centre of the array

Description:

This routine shifts the position of the Nasmyth centre of a SCUBA array. It can be used to take out the small difference between the centres of the LONG and SHORT wave arrays. Should be run after extinction.

Usage:

```
change_nacentre [-h | -v] infile dx dy
```

Parameters:

−h
Return a help message only.

−v
Return the version number of scunoise

infile
Input file name. The file is modified in place.

dx Shift in Nasmyth X (du3) direction

dy Shift in Nasmyth Y (du4) direction

Examples:

```
change_nacentre
```

Will prompt for input file name and shift

```
change_nacentre file 5 −3
```

Will move the array centre of file.sdf by (5,−3) arcsec.

Notes:

This command can only be reversed by running change_nacentre with minus the previous X,Y shift. extinction must have been run on the input file (otherwise the file will contain more than 1 array) – this is not checked for explicitly.

Related Applications :

SURF: rebin

CHANGE_POINTING
Change the pointing corrections to map data

Description:

This application is used to change the pointing corrections to map data.

If the observing mode of the input datafile is 'MAP' the application will search for pointing corrections in the file and, if it finds any, report them. You will be asked if you wish to change the pointing correction data in the file. 'No' will result in the data remaining unaltered, 'yes' will then ask you for the time of the pointing offset (LST in hh mm ss.ss format) and the azimuth and elevation correction (in arcseconds) that would have to be added to the observation position to correct the pointing at that time. If you supply no data the existing pointing corrections will be removed. Corrections will be requested until a negative number is given for the local sidereal time.

Usage:

```
change_pointing in change_point
```

Parameters:

CHANGE_POINT = CHAR (Read)
If true you will be prompted for pointing corrections otherwise the program will exit after listing the current pointing corrections.

IN = NDF (Read)
Name of NDF to change.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM.

POINT_DAZ = REAL (Read)
The Azimuth pointing correction (arcsec).

POINT_DEL = REAL (Read)
The elevation pointing correction (arcsec).

POINT_LST = CHAR (Read)
The sidereal time of the pointing correction. Pointing corrections are asked for repeatedly until a NULL (!) or negative value are given for POINT_LST.

Notes:

- Pointing corrections are erased when new items are written.
- Pointing corrections can be removed completely by issuing null (!) in response to POINT_LST when first prompted. (ie pointing corrections are removed if no corrections are given)
- Use ABORT (!!) if you don't want to change the pointing corrections once you have started entering values.
- Pointing corrections must be given in LST order.

Related Application :

SURF: rebin

CHANGE_QUALITY
Set SCUBA data quality bad or good

Description:

This application is used to set SCUBA data quality bad or good by using SCUBA sections to specify a subset of the full data.

Once the data specification has been decoded the application will read from parameter BAD_QUALITY whether quality should be set good or bad. A 'yes' answer will mark the area bad, a 'no' answer will mark the area good (an area will only be good if no other QUALITY bits are set - change_quality only uses QUALITY bit 3). The section can be inverted by using the negation character at the end of the section.

Usage:

```
change_quality ndf{spec1}{specn} bad_quality
```

Parameters:

BAD_QUALITY = LOGICAL (Read)

Set quality to BAD. Answering this question with a 'yes' will mean that the selected data will be set to BAD. 'no' will set them to good.

IN = CHAR (Read)

Name of data set and the specification of the data to be changed. Usually of the form 'ndf{spec1}{spec2}' where ndf is the filename and spec1...n are the section specifications. The section can be read from the SECTION parameter if the SCUBA section is omitted.

MSG_FILTER = CHAR (Read)

Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM.

SECTION() = CHAR (Read)

This array parameter can be used to specify SCUBA sections. Curly brackets must still be given. Since this is an array parameter square brackets must be used to specify more than one component:

```
SECTION > [ {b3} , {i2} ]
```

would supply two SECTIONS of {b3} and {i2}. Only {b3} will be used if the square brackets are not used. Care must also be taken when using commas in SCUBA sections - the parameter system will split multiple entries on commas unless the entire section is quoted:

```
SECTION > [ "{b3,5}" , {i2} ]
```

If necessary the negation character should come after a section (ie after the closing curly bracket) and that negation applies to the combined section and not just the string containing the negation character:

```
SECTION > [ {b3}-, {i2} ]
```

implies that the section consists of everything except bolometer 3 and integration 2.

This parameter is only used when no SCUBA section was specified via the IN parameter.

Examples:

```
change_quality 'ndf{}' BAD_QUALITY=false
```

Select the entire array and unset bit 3.

```
change_quality 'ndf{b2}' BAD_QUALITY
```

Select the second bolometer and mark it bad.

```
change_quality 'ndf{b2;i3}-' BAD_QUALITY
```

Select the third integration of bolometer two but set all other data points bad by inverting the section.

```
change_quality 'ndf{b16}{i2}' BAD_QUALITY
```

Select all of bolometer 16 and the whole of integration 2.

```
change_quality 'ndf{e5,16:18}' MSG_FILTER=quiet
```

Select exposure 5 and 16 through 18. Messaging is turned off.

```
change_quality ndf
```

Since no section has been specified, the user will be prompted for a section later.

```
change_quality test SECTION='["{b41,52}",{i3}]' BAD_QUALITY
```

Set bolometers 41 and 52 as well as integration 3 to bad quality. Use of SECTION here is not recommended given the complication when using commas and square brackets.

```
change_quality test SECTION='[{b2;i2}-]' BAD_QUALITY
```

Set everything bad except bolometer 2 and integration 2.

Notes:

Samples are marked bad by setting bit 3 of the quality array. The effects of change_quality can be removed by changing the value of the bad bit mask (with the KAPPA task setbb or by running change_quality on the entire array [section is {} for entire array] but with BAD_QUALITY=false) so that bit 3 (decimal value of 8) is no longer used as a masking bit.

Related Application :

SURF: change_data, rebin, scuphot;
KAPPA: setbb

DESPIKE
Despike data by position

Description:

This routine despikes demodulated data by comparing points that lie in the same region of sky. Each point is placed in the output grid (similar to rebin but without the smoothing) depending on its position. The points in each cell are then compared with each other and spikes are detected if any points lie more than NSIGMA from the mean.

Optionally, a plot is provided showing the points in each bin along with the clipping level to be used for despiking. In order to provide a 2-dimensional plot of 3-dimensional data the grid is unwrapped such that all the cells are plotted in one axis. The unwrapping order is governed by the DMODE parameter.

More details on despike can be found in appendix G.

Usage:

```
despike
```

Parameters:

DEFOUT = LOGICAL (Read)
Determines whether output files should be written automatically (using the default output names) or whether the user should be prompted. Default is FALSE.

DEVICE = DEVICE (Read)
The device on which to display the binned data. Can be null (!)

DMODE = CHAR (Given)
For display purposes the points in each cell are plotted sequentially on a 1-dimensional plot. This parameter governs the way in which the cells are extracted from the grid. Allowed values are:

- SPIRAL: A Spiral outwards from the reference pixel
- XLINEAR: unfold each X strip in turn for each Y
- YLINEAR: unfold each Y strip in turn for each X
- DIAG1: diagonal strips starting at position (1,1)
- DIAG2: diagonal strips starting at positions (nx,1)

This parameter is also required if SMODE is not equal to 'NONE' since the smoothing depends on the order that the points are extracted from the grid.

IN = CHAR (Read)
The name of the input file to be despiked. This parameter is requested repeatedly until a NULL value (!) is supplied. LOOP must be TRUE. IN can include a SCUBA section. Like the REF parameter this parameter accepts a text file.

LOOP = LOGICAL (Read)
Task will ask for multiple input files if true. Only REF is read if noloop.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. In VERBOSE mode the positions of detected spikes are listed.

NSIGMA = REAL (Read)
The sigma clipping level used for despiking each cell.

SMODE = CHAR (Given)
This parameter controls the mode used for smoothing of the clipping envelope. If smoothing is selected, the extraction mode (DMODE) is used to determine the pixels that are adjacent to each other.

Allowed modes are:

- NONE: No smoothing
- HANN: Hanning smoothing

OUT = NDF (Write)
This is the name of the NDF that will contain the despiked data. There will be one prompt per input filename (assuming spikes were detected).

OUT_COORDS = CHAR (Read)
The coordinate system of the output grid. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (eg Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)
- GA: Galactic coordinates (J2000)

For RD current epoch is taken from the first input file.

REF = CHAR (Read)
The name of the first NDF to be rebinned. The name may also be the name of an ASCII text file containing NDF and parameter values. See the notes. REF can include a SCUBA section.

SHIFT_DX = REAL (Read)
The pointing shift (in X) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

SHIFT_DY = REAL (Read)
The pointing shift (in Y) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

WEIGHT = REAL (Read)
The relative weight that should be assigned to each dataset.

XRANGE = INTEGER (Read)
The X-range of the plot. This parameter loops indefinitely until a null response is provided (!).

Examples:

```
despike out_coords=RJ smode=none device=!
```

Despike the maps by placing points onto an RJ grid. Do not plot the data points before despiking and do not smooth the clipping envelope. You will be asked for input datasets until a null value is given.

```
despike device=!  out_coords=RB smode=hann dmode=sp nsigma=4.0
```

Despike on a RB grid with hanning smoothing. Use a 4.0 sigma clip and do not display. Note that the smoothing uses the spiral mode for grid unwinding.

```
despike device=xwindows dmode=x nsigma=3.0
```

Unwind with XLINEAR mode and display the data before despiking.

```
despike noloop accept ref=test.bat
```

Despike the files specified in test.bat using an RJ grid.

Notes:

For each file name that is entered, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY are requested.

- The application can read in up to 100 separate input datasets.
- The output grid will be large enough to include all data points.
- SCUBA sections can be given along with any input NDF

ASCII input files :

The REF and IN parameters accept ASCII text files as input. These text files may contain comments (signified by a #), NDF names, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY, and names of other ASCII files. There is one data file per line. An example file is:

```
file1{b5}   1.0  0.5  0.0  # Read bolometer 5 from file1.sdf
file2                     # Read file 2 but you will still be
                          # prompted for WEIGHT, and shifts.
file3{i3}-  1.0  0.0  0.0  # Use everything except int 3
test.bat                  # Read in another text file
```

Note that the parameters are position dependent and are not necessary. Missing parameters are requested. This means it is not possible to specify SHIFT_DX (position 3) without specifying the WEIGHT. If the file has the .txt extension the NDF system will attempt to convert it to NDF format before processing – this is probably not what you want.

Related Applications :

SURF: rebin, despike2, scuclip, sigclip

DESPIKE2
Remove spikes from SCAN/MAP observations

Description:

This routine removes spikes from SCAN/MAP observations. The scan map differential despiking algorithm uses 2 criteria to decide which points are spikes.

First, for each bolometer used a pass is made through each scan calculating for each point:-

$$\mathrm{diff}(i) = \mathrm{point}(i) - \frac{\mathrm{point}(i-1) + \mathrm{point}(i+1)}{2.0}$$

Values of 'diff()' for the first and last points in the scan are calculated in a similar way but subtracting the mean of points 2 and 3 and points n-1 and n-2 respectively.

The mean and standard deviation of 'diff()' are calculated by coadding the 10 points at each end of the scan where, hopefully, there is no source emission. Spikes in these regions are handled by removing points from the coadd that lie further than 3 sigma from the mean, then redoing the calculation recursively until no further points need be removed.

The first criterion for a spike is that it's 'diff()' value should be further from the mean of 'diff()' by NSIGMA times the sigma derived from the endpoints.

The problem with this simple approach is that bright sources in the scan themselves lead to excursions in 'diff()' that can be wrongly identified as spikes. To prevent this happening a second criterion is used. In this the scan values are convolved with a 3 sample wide box so that each 'box()' point is the average of the point itself and the points on either side of it. 'Box()' is expected to increase faster for real sources than for spikes because in them the increase will be spread over all 3 averaged points rather than just 1.

The second criterion for a spike is met, therefore, if a point's 'diff()' is further from the 'diff()' mean than the value of 'box()' at that point.

Fixed-up values for points that have been identified as spikes are calculated by interpolating between the closest healthy points on either side.

The second spike criterion also means unfortunately that the technique is less sensitive to spikes on bright sources than elsewhere. In addition, it is still possible to clip bright sources if too low a value for NSIGMA is used. It is recommended to run despike several times with different values of NSIGMA. Begin with NSIGMA=5, look at the result to see how effective despiking has been, then repeat the process with NSIGMA=4.5, 4.0 etc. until you start to clip source information.

Usage:

```
restore in out nsigma
```

Parameters:

IN = NDF (Read)

The name of the input file containing demodulated SCUBA data.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. No verbose messages are used.

NSIGMA = REAL (Read)
Nsigma from mean at which 'spikes' begin.

OUT = NDF (Write)
The name of the output file to contain the processed data. A default output name is suggested that is derived from the input.

Examples:

```
restore o37 o37_des 5.0
```

Despike o37.sdf at 5.0 sigma.

```
restore o37 \
```

Despike using the default sigma level and writing to the default output file.

Notes:

Care must be taken when despiking bright sources.

Related Applications :

SURF: despike, scuclip, sigclip, restore

DSPBOL
Interactive display and despiking

Description:

dspbol (or any d∗ link to scuplot) can be used to interactively despike bolometers. While it is not as fast as a completely integrated routine would be, it makes interactive despiking much easier by hiding the cycle between linplot and change_quality for the user. The most common use is to zoom in on the region with the spike via the 'X' menu option (either typing the input or using the cursor) and subsequently to flag the offending point (just type the coordinate of the point, a range, or use the cursor; *in general the coordinate is to the right of the plotted point*). The routine will overlay the despiked data, prompt the user to accept the new set and de-zoom to the original scale. To reset a previously flagged point, flag the point again but do *not* accept it: the point will be set to GOOD again. Please read the note below the description of the menu on the use of the mouse.

The menu consists of:

[M. H]	Redisplay menu
[Q]	Quit
[N]	Next bolometer
[B#]	Switch to bol #
[X min max], [X cen]	X-axis from min:max or cen+/-10
	Just 'x' activates the cursor.
[R]	Reset X-axis
[Y min max], [Y lim]	Y-axis from min:max or -lim:+lim
[U]	Reset Y-axis
[#], [#:#], [#-#]	Despike point or range of points;
	Just 'p' activates the cursor.

Option >

Note that a X center defined with the cursor or [X cen] defaults to a 20 points window around cen, the position of the spike. Using the CURSOR, the Left Mouse button always defines the point, the Right Mouse button exits the cursor task while accepting the last point clicked.

Usage:

```
dspbol [-f sdf_file] [-d sdf_file2] [-s min max] [bol [bol [bol] ...]]
```

Parameters:

-h[elp]
Print the help information.

-f file
name of NDF file (.sdf may be included in the name).

-d file2
name of a second file: e.g. the despiked version of the NDF file. The same bolometers will be plotted in a second window or overlaid for comparison.

-s min max
Y-axis scales for plot (can be changed via menu).

bol
list of bolometers to plot. Type 'all' for 1..37 and 'alls' for 1..91. Can be added via menu if mode = 'r'.

Examples:

```
scuplot
```

The user will be asked for an input file and bolometer list before proceeding.

```
dspbol-f o39_lon_ext
```

Interactive despiking on o39_lon_ext.sdf. A bolometer list will be requested.

```
dspbol -f s14_lon_ext 12 13 18 20 25 26 19
```

Use file s14_lon_ext.sdf. Plot bolometers 12,13, 18, 20, 25, 26 and 19.

Notes:

- If the overlay comes up scrambled, delete the agi_xxx files in your home directory and if that does not work also files like linplot.sdf in the /home/you/adam subdirectory.
- Figaro's sclean is a more efficient alternative.

Related Applications :

SURF: pltbol, rlinplot, change_quality, despike;
KAPPA: linplot, cursor;
FIGARO: sclean

Bugs:

Freezes when asked to plot a bad bolometer.

EXTINCTION
Remove the effect of atmospheric extinction from a SCUBA observation

Description:

This application extracts from a demodulated-data file data for a specified SCUBA sub-instrument and corrects it for the effect of atmospheric extinction. The airmass at which each bolometer measurement was made is calculated, then multiplied by the zenith sky extinction at the time of the measurement to give the extinction optical depth along the line of sight. The data point in question is then multiplied by the exponential of the optical depth to give the value that would have been measured in the absence of the atmosphere.

The zenith optical depth is assumed to vary linearly with time between the values input in parameters FIRST_TAU and LAST_TAU. If the measurement was taken at a time outside the range covered by FIRST_TAU and LAST_TAU then the value closest in time will be used.

Usage:

```
extinction in sub_instrument first_tau first_lst second_tau second_lst out
```

Parameters:

FIRST_LST = CHAR (Read)
The local sidereal time at which FIRST_TAU was the zenith sky opacity, in hh mm ss.ss format.

FIRST_TAU = REAL (Read)
The zenith sky opacity before the observation. The default value is the zenith tau value accepted by the on-line system before the observation.

IN = NDF (Read)
The name of the input file containing demodulated SCUBA data.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)
The name of the output file to contain the extinction corrected data for the specified sub-instrument.

SECOND_LST = CHAR (Read)
The local sidereal time at which SECOND_TAU was the zenith sky opacity, in hh mm ss.ss format. The default value is that of FIRST_LST (usually the case for a constant tau). If this value is less than FIRST_LST it is assumed you are referring to the following day.

SECOND_TAU = REAL (Read)
The zenith sky opacity after the observation. The default value is that of FIRST_TAU.

SUB_INSTRUMENT = CHAR (Read)
The name of the sub-instrument whose data are to be selected from the input file and

extinction corrected. Permitted values are SHORT, LONG, P1100, P1350 and P2000. This parameter is only used if more than one sub-instrument is present in the file.

Examples:

```
extinction flat long 0.24 '01 00 00' 0.3 '02 00 00' corr
```

Process the LONG sub-instrument from flat.sdf using the knowledge that the 850 tau (assuming LONG refers to the 850 micron filter) was 0.24 at 1h LST and 0.3 at 2h LST. The output is written to corr.sdf

```
extinction test short 0.6 0 0.6 0 test2
```

Process the SHORT sub-instrument from test.sdf assuming a constant tau of 0.6 (since FIRST_LST = SECOND_LST) and write the result to test2.sdf

Related Applications :

SURF: rebin, scuphot, skydip, scuquick

EXTRACT_DATA
Write bolometer positions and values to text file

Description:

This routine writes the value, variance and position of each data point to a ASCII file. The interface is the same as that used in the rebin task. The data and variance are in volts. The positions are in radians. The data are written out as columns: RA DEC DATA VAR

Parameters:

FILE = FILENAME (Write)
The name of the ASCII file used for storing the data.

IN = CHAR (Read)
The name of the input file to be rebinned. This parameter is requested repeatedly until a NULL value (!) is supplied. LOOP must be TRUE. IN can include a SCUBA section. Like the REF parameter this parameter accepts a text file.

LAT_OUT = CHAR (Read)
The latitude of the output map centre. The supplied default value is that of the map centre of the first map.

LONG_OUT = CHAR (Read)
The longitude of the output map centre. The supplied default value is that of the map centre of the first map.

LOOP = LOGICAL (Read)
Task will ask for multiple input files if true. Only REF is read if noloop.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT_COORDS = CHAR (Read)
The coordinate system of the output map. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (e.g. Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)
- GA: Galactic coordinates (J2000)

REF = CHAR (Read)
The name of the first NDF to be rebinned. The name may also be the name of an ASCII text file containing NDF and parameter values. See the notes. REF can include a SCUBA section.

SHIFT_DX = REAL (Read)
The pointing shift (in X) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

SHIFT_DY = REAL (Read)
The pointing shift (in Y) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

WEIGHT = REAL (Read)
The relative weight that should be assigned to each dataset.

Notes:

For each file name that is entered, values for the parameters SELECT_INTS, WEIGHT, SHIFT_DX and SHIFT_DY are requested.

- The application can read in up to 256 separate input datasets.
- No data is returned if the DATA or positions are bad. Data is still returned if Variance is bad.

ASCII input files :

The REF and IN parameters accept ASCII text files as input. These text files may contain comments (signified by a #), NDF names, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY, and names of other ASCII files. There is one data file per line. An example file is:

```
file1{b5}   1.0  0.5  0.0  # Read bolometer 5 from file1.sdf

file2                     # Read file 2 but you will still be

                          # prompted for WEIGHT, and shifts.

file3{i3}-  1.0  0.0  0.0  # Use everything except int 3

test.bat                  # Read in another text file
```

Note that the parameters are position dependent and are not necessary. Missing parameters are requested. This means it is not possible to specify SHIFT_DX (position 3) without specifying the WEIGHT. Also note that SCUBA sections can be specified with any input NDF.

Related Applications :

SURF: rebin, bolrebin, intrebin, change_quality

EXTRACT_FLAT
Extract a flatfield from a SCUBA demodulated data file

Description:

This routine extracts the flatfield information from a SCUBA demodulated data file and writes it out in a format suitable for use by CHANGE_FLAT. The full flatfield is extracted: Bolometer positions and relative responsivities.

Usage:

```
extract_flat in file
```

Parameters:

IN = NDF (Read)
The name of the NDF containing the demodulated data with the required flatfield.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

FILE = FILE (Write)
The name of the ascii file to which the flatfield information will be written

Examples:

```
extract_flat 19971017_dem_0002 oldflat.dat
```

This will read the flatfield from 19971017_dem_0002.sdf and write it to a text file

Related Applications :

SURF: change_flat, flatfield

FLATFIELD
Flatfield demodulated SCUBA data

Description:

This routine flatfields SCUBA demodulated data. The data must previously have been processed by reduce_switch.

Usage:

```
flatfield in out
```

Parameters:

IN = NDF (Read)
The name of the NDF containing the demodulated data to be flatfielded. This file should already have been run through the reduce_switch application.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)
The name of the NDF to which the flatfielded data are to be written.

Examples:

```
flatfield redsw flat
```

This will flatfield the data from redsw.sdf and write it to flat.sdf

Related Applications :

SURF: change_flat, scuquick

INTREBIN
Generate a separate regridded image for each integration

Description:

This routine rebins the demodulated data from SCUBA MAP observations onto a rectangular mesh by a variety of methods. Currently convolution by weighting functions, spline interpolation and median are supported.

- Weighting functions:
  Currently linear, Bessel and Gaussian weighting functions are supported. The width of the Bessel function is such that it should preserve all spatial information obtained by the telescope at the wavelength of observation, but suppress higher spatial frequencies. To minimise edge effects the Bessel function is truncated at a radius of 10 half-widths from the centre (although this is configurable), and apodized over its outer third by a cosine function. Viewed in frequency space the method consists of Fourier transforming the input dataset(s), multiplying the transform by a cylindrical top-hat (the F.T. of the Bessel function), then transforming back into image space. A linear weighting function is also available which works out to one half-width - this has the advantage that it is much faster to process and is much less susceptible to edge effects. The Gaussian weighting function is probably the best compromise between the Bessel (slow and prone to edge effects) and Linear (fast but the point spread function is non-trivial for modeling).
  The radius and size of 'footprint' for the weighting functions are configurable using the WTFNRAD and SCALE parameters.
- Splines:
  Additionally, spline interpolation and smoothing routines are also available. Note that the spline routines work on each integration in turn, whereas the weighting function routines work on all the input data in one go. At present the spline routines are experimental and comments are welcomed.
- Median:
  A regridding option derived from despike is available. This method simply puts all data points in an output grid and calculates the median of each output cell. Small pixel scales require large datasets (since not all cells in a 1 arcsecond grid will contain data points) although the KAPPA commands fillbad and glitch can be used to smooth over bad pixels.

Usage:

```
intrebin ref
```

Parameters:

GUARD = LOGICAL (Read)

Controls whether the bolometer guard ring should be used during the regridding process. The guard ring enforces zero flux at the edge of the regridded image. Should be turned off if flux is present at the edge. Default is to use the guard ring for LINEAR, BESSEL and GAUSSIAN rebin modes.

IN = CHAR (Read)
The name of the input file to be rebinned. This parameter is requested repeatedly until a NULL value (!) is supplied. LOOP must be TRUE. IN can include a SCUBA section. Like the REF parameter this parameter accepts a text file.

LAT_OUT = CHAR (Read)
The latitude of the output map centre. The supplied default value is that of the map centre of the first map.

LONG_OUT = CHAR (Read)
The longitude of the output map centre. The supplied default value is that of the map centre of the first map.

LOOP = LOGICAL (Read)
Task will ask for multiple input files if true. Only REF is read if noloop.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)
This is the name of the HDS container file that will contain the rebinned images. The map for each integration is stored in an NDF inside this NDF container. The maps can be accessed as '`out.name`' where `name` is the integration name (i.e. i1, i2, i3, etc.).

OUT_COORDS = CHAR (Read)
The coordinate system of the output map. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (e.g. Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)
- GA: Galactic coordinates (J2000)

For RD current epoch is taken from the first input file.

OUT_OBJECT = CHAR (Read)
The name of the object (ie the NDF title).

PIXSIZE_OUT = REAL (Read)
Size of pixels in the output map. Units are arcsec.

REBIN_METHOD = CHAR (Read)
The rebin method to be used. A number of regridding methods are available:

- LINEAR: Linear weighting function
- GAUSSIAN: Gaussian weighting function
- BESSEL: Bessel weighting function
- SPLINE1: Interpolating spline (PDA_IDBVIP)
- SPLINE2: Smoothing spline (PDA_SURFIT)
- SPLINE3: Interpolating spline (PDA_IDSFFT)
- MEDIAN: Median regridding

Please refer to the PDA documentation (SUN/194) for more information on the spline fitting algorithms.

REF = CHAR (Read)
The name of the first NDF to be rebinned. The name may also be the name of an ASCII text file containing NDF and parameter values. See the notes. REF can include a SCUBA section.

REFPIX (2) = INTEGER (Read)
The coordinate of the reference pixel in the output data array. This corresponds to the pixel associated with the specified RA/Dec centre. Default is to use the middle pixel if a size is specified or the optimal pixel if the default size is used (see the SIZE parameter).

TRIM = INTEGER (Read)
This parameter determines the amount of good data that should be trimmed from the final image to correct for edge effects. The supplied value should be in arcseconds. All pixels closer to a bad pixel than this distance will be set to bad in the output image (by setting bit 1 in the quality array). Default is 0.0.

SCALE = REAL (Read)
Radius of one scale size in arcsec. This effectively governs the size of the weighting function. For LINEAR one scale size corresponds to the zero of the cone, for BESSEL it is the first zero of the Bessel function (π) and for Gaussian it is the half-width half maximum (HWHM).

SIZE (2) = INTEGER (Read)
This array parameter sets the size of the output grid in pixels (*nx*, *ny*). The default values are the minimum dimensions required to display the entirety of the mapped area.

SHIFT_DX = REAL (Read)
The pointing shift (in X) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

SHIFT_DY = REAL (Read)
The pointing shift (in Y) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

TIMES = LOGICAL (Read)
Store an extra NDF in the output map containing the 2-D histogram of the data. This can be used to make an estimate of the actual number of samples responsible for each point in the output grid. Note that, in general, the number of pixels in the output grid exceeds the number of independent beams in the image. The data can be accessed as OUT.more.reds.times. Default is FALSE.

WEIGHT = REAL (Read)
The relative weight that should be assigned to each dataset.

WEIGHTS = LOGICAL (Read)
This parameter governs whether the convolution weights array will be stored in the output NDF. The default is FALSE (i.e. do not store the weights array).

WTFNRAD = INTEGER (Read)
Size of the weighting function in scale sizes. This parameter is irrelevant for LINEAR regridding. For Gaussian the default is 3 (i.e. a diameter of 3 FWHM for the footprint),

and for Bessel it is 10. The smaller the weighting function is (a combination of WTFNRAD and SCALE) the faster the regridding goes.

Examples:

```
intrebin rebin_method=LINEAR out_coords=RJ
```

Rebin the maps with LINEAR weighting function in J2000 RA/Dec coordinates. You will be asked for input datasets until a null value is given.

```
intrebin rebin_method=BESSEL out=map
```

Rebin the maps with Bessel weighting function. Each integration is rebinned separately and placed in an NDF in the output container file map.sdf. Integration 2 can be accessed by displaying `map.i1`.

```
intrebin noloop ref=test.bat
```

Rebin each integration using the data specified in the file test.bat.

Notes:

For each file name that is entered, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY are requested.

- The application can read in up to 256 separate input datasets.
- The output map will be large enough to include all data points.
- Spline regridding may have problems with SCAN/MAP (since integrations contain lots of overlapping data points).
- SCUBA sections can be given along with any input NDF
- The relative weights associated with each point in the output map are stored in a WEIGHTS NDF in the REDS extension of the output data (For WEIGHTS=TRUE). For spline rebinning each point is equivalent to the number of integrations added into the final data point. For weight function regridding the situation is more complicated. The actual number of points contributing to each cell can be stored using the TIMES parameter.
- Bolometer weights will be used if a BOLWT extension is found in the input data file (usually set with setbolwt).
- Astrometry information is stored in the WCS component and not the FITS extension.

ASCII input files :

The REF and IN parameters accept ASCII text files as input. These text files may contain comments (signified by a #), NDF names, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY, and names of other ASCII files. There is one data file per line. An example file is:

```
file1{b5}   1.0  0.5  0.0  # Read bolometer 5 from file1.sdf
file2                     # Read file 2 but you will still be
                          # prompted for WEIGHT, and shifts.
file3{i3}-  1.0  0.0  0.0  # Use everything except int 3
test.bat                  # Read in another text file
```

Note that the parameters are position dependent and are not necessary. Missing parameters are requested. This means it is not possible to specify SHIFT_DX (position 3) without specifying the WEIGHT. If the file has the .txt extension the NDF system will attempt to convert it to NDF format before processing – this is probably not what you want.

Related Applications :

SURF: rebin, bolrebin, extract_data

MAPSUM
Produce one-line summary of SCUBA map observations

Description:

Mapsum goes through all the sdf files in the current directory and, optionally, DATADIR (defined in an environment variable) and summarizes files containing map observations.

In the absence of the −all flag, a numeric range is requested. This range only has an effect on raw data or reduced files which have the run number embedded into the file name. Filenames with no numbers are treated as scan 0.

Usage:

```
mapsum [-h] [-demod] [-reduced] [-all|[-begin nn -end nn]]
```

Parameters:

−**h[elp]**
: Return a help message only. More help can be obtained by using 'showme sun216' or 'scuhelp mapsum'.

−**all**
: List all map files in the current directory and $DATADIR

−**demod**
: Only list demodulated data files (signified by _dem_ file name)

−**reduced**
: Only list reduced data files (signified by _red_ file name)

−**begin nn**
: First scan number to be considered (same as −−begin==nn)

−**end nn**
: Final scan number to be considered (same as −−end=nn)

Examples:

```
mapsum
```

Ask for a range of scan numbers and then give a summary of every MAP file matching this criterion in DATADIR and the current directory.

```
mapsum −all
```

Generate a summary of all map files in the current and DATADIR directory.

```
mapsum −−begin=5 −−end=100
```

Generate a summary of all map data from scans 5 to 100 inclusive.

```
mapsum −all −reduced
```

Produce a one line summary of all reduced (_red_) map files.

```
mapsum −all −reduced > log.txt
```

Produce a one line summary of all the reduced map files and store the output in the text file log.txt (note this example is shell specific).

```
mapsum −all −reduced −demod
```

Produce a summary of all reduced (_red_) and demodulated (_dem_) map data files (ie not files produced during off-line data reduction).

Notes:

- mapsum only displays map data.
- Files are drawn from the current working directory and the directory indicated by the $DATADIR environment variable.
- Data reduced by the off-line system will all be treated as run 0 for the purposes of listing unless numbers are present in the filename.
- The output can be stored in a file by using unix redirection as long as the search range is fully specified (either as '−all' or with '−begin' and '−end').
- Command line options can be abbreviated.
- Options that take values can be used either as '−flag option' or as '−−flag=option'

Related Applications :

SURF: sculog, photsum, pointsum, obssum, skysum

OBSSUM
Produce one-line summary of SCUBA observations

Description:

obssum goes through all the sdf files in the current directory and, optionally, DATADIR (defined in an environment variable) and extracts information from any FITS entries that may be present.

In the absence of the −all flag, a numeric range is requested. This range only has an effect on raw data or reduced files which have the run number embedded into the file name. Filenames with no numbers are treated as scan 0.

Usage:

```
obssum [-h] [-demod] [-reduced] [-mode ??]  [-all|[-begin nn -end nn]]
```

Parameters:

−**h[elp]**
: Return a help message only. More help can be obtained by using 'showme sun216' or 'scuhelp obssum'.

−**all**
: List all files in the current directory and $DATADIR

−**demod**
: Only list demodulated data files (signified by _dem_ file name)

−**reduced**
: Only list reduced data files (signified by _red_ file name)

−**begin nn**
: First scan number to be considered (same as −−begin==nn)

−**end nn**
: Final scan number to be considered (same as −−end=nn)

−**mode obs**
: Select only specified observation modes for listing. The list should be comma separated. (same as −−mode=obs)

Examples:

```
obssum
```

Ask for a range of scan numbers and then give a summary of every sdf file matching this criterion in DATADIR and the current directory.

```
obssum −all
```

Generate a summary of all sdf files in the current and DATADIR directory.

```
obssum −−begin=5 −−end=100
```

Generate a summary of all data from scans 5 to 100 inclusive.

```
obssum −all −reduced
```

Produce a one line summary of all reduced (_red_) files.

```
obssum −all −reduced > log.txt
```

Produce a one line summary of all the reduced files and store the output in the text file log.txt (note this example is shell specific).

```
obssum −all −reduced −demod
```

Produce a summary of all reduced (_red_) and demodulated (_dem_) data files (ie not files produced during off-line data reduction).

```
obssum −all −mode pointing
```

Produce a one line summary of all pointing observations

```
obssum −reduced −begin 100 −end 200 −−mode=photom,skydip
```

Produce a one line summary of the photom and skydip observations of reduced files with scan numbers 100 to 200. This is similar to photsum except that the signal and signal-to-noise will not be displayed even if reduced files are being listed.

Notes:

- obssum only uses information stored in the FITS header of reduced and raw data files and does not provide summaries of reduced (RO) data such as photometry results (essentially for reasons of clarity). 'photsum' must be used to generate a summary of photometry observations that includes reduced data.
- Files are drawn from the current working directory and the directory indicated by the $DATADIR environment variable.
- Data reduced by the off-line system will all be treated as run 0 for the purposes of listing unless numbers are present in the filename.
- The output can be stored in a file by using unix redirection as long as the search range is fully specified (either as '−all' or with '−begin' and '−end').
- Command line options can be abbreviated.
- Options that take values can be used either as '−flag option' or as '−−flag=option'

Related Applications :

SURF: sculog, photsum, pointsum, mapsum, skysum

PHOTSUM
Produce one-line summary of SCUBA photometry observations

Description:

Photsum goes through all the sdf files in the current directory and, optionally, DATADIR (defined in an environment variable) and summarizes files containing photometry observations.

In the absence of the −all flag, a numeric range is requested. This range only has an effect on raw data or reduced files which have the run number embedded into the file name. Filenames with no numbers are treated as scan 0.

Usage:

```
photsum [-h] [-demod] [-reduced] [-all|[-begin nn -end nn]]
```

Parameters:

−**h[elp]**
: Return a help message only. More help can be obtained by using 'showme sun216' or 'scuhelp photsum'.

−**all**
: List all photometry files in the current directory and $DATADIR

−**demod**
: Only list demodulated data files (signified by _dem_ file name)

−**reduced**
: Only list reduced data files (signified by _red_ file name)

−**begin nn**
: First scan number to be considered (same as −−begin==nn)

−**end nn**
: Final scan number to be considered (same as −−end=nn)

Examples:

```
photsum
```

Ask for a range of scan numbers and then give a summary of every PHOTOM file matching this criterion in DATADIR and the current directory.

```
photsum −all
```

Generate a summary of all photometry files in the current and DATADIR directory.

```
photsum −−begin=5 −−end=100
```

Generate a summary of all photometry data from scans 5 to 100 inclusive.

```
photsum −all −reduced
```

Produce a one line summary of all reduced (_red_) photometry files. This will include the photometry results calculated by the on-line system.

```
photsum −all −reduced > log.txt
```

Produce a one line summary of all the reduced photometry files and store the output in the text file log.txt (note this example is shell specific).

```
photsum −all −reduced −demod
```

Produce a summary of all reduced (_red_) and demodulated (_dem_) photometry data files (ie not files produced during off-line data reduction).

Notes:

- If task is run on reduced data ('_red_' files) then the photometry results will be listed.
- Skydip data is printed for convenience.
- Files are drawn from the current working directory and the directory indicated by the $DATADIR environment variable.
- Data reduced by the off-line system will all be treated as run 0 for the purposes of listing unless numbers are present in the filename.
- The output can be stored in a file by using unix redirection as long as the search range is fully specified (either as '−all' or with '−begin' and '−end').
- Command line options can be abbreviated.
- Options that take values can be used either as '−flag option' or as '−−flag=option'
- It may be necessary to set the HDS_SCRATCH environment variable if files are being logged from directories for which write access is denied (e.g. `setenv HDS_SCRATCH /tmp`)

Related Applications :

SURF: sculog, mapsum, pointsum, obssum, skysum

PLTBOL
Interactive bolometer display

Description:

pltbol (or any p∗ link to scuplot) is a wrapper around the KAPPA utility linplotand facilitates data inspection. It allows plots of a whole series of bolometers one by one, optionally overlaying them with the same bolometer from a second file. Obvious overlays are despiked on non-despiked data or data from different exposures to check the noise.

The menu items are:

[M. H]	Redisplay menu
[Q]	Quit
[N]	Next bolometer
[B#]	Switch to bol #
[X min max], [X cen]	X-axis from min:max or cen+/-10
	Just 'x' activates the cursor.
[R]	Reset X-axis
[Y min max], [Y lim]	Y-axis from min:max or -lim:+lim
[U]	Reset Y-axis

Option >

Note that a X center defined with the cursor or [X cen] defaults to a 20 points window around cen, the position of the spike. Using the CURSOR, the Left Mouse button always defines the point, the Right Mouse button exits the cursor task while accepting the last point clicked.

Usage:

```
pltbol [-f sdf_file] [-d sdf_file2] [-s min max] [bol [bol [bol] ...]]
```

Parameters:

-h[elp]
Print the help information.

-f file
name of NDF file (.sdf may be included in the name).

-d file2
name of a second file: e.g. the despiked version of the NDF file. The same bolometers will be plotted in a second window or overlaid for comparison.

-s min max
Y-axis scales for plot (can be changed via menu).

bol
list of bolometers to plot. Type 'all' for 1..37 and 'alls' for 1..91. Can be added via menu if mode = 'r'.

Examples:

```
pltbol
```

The user will be asked for an input file before proceeding to the menu.

```
pltbol -f o39_lon_ext
```

Plot bolometers from o39_lon_ext.sdf and ask for the bolometer list.

```
pltbol -f s14_lon_ext 12 13 18 20 25 26 19
```

Use file s14_lon_ext.sdf. Plot bolometers 12,13, 18, 20, 25, 26 and 19.

Notes:

- If the overlay comes up scrambled, delete the agi_xxx files in your home directory and if that does not work also files like linplot.sdf in the /home/you/adam subdirectory.

Related Applications :

SURF: dspbol, rlinplot;
KAPPA: linplot, cursor

Bugs:

Freezes when asked to plot a bad bolometer.

POINTSUM
Produce one-line summary of SCUBA pointing observations

Description:

Pointsum goes through all the sdf files in the current directory and, optionally, DATADIR (defined in an environment variable) and summarizes files containing pointing observations.

In the absence of the −all flag, a numeric range is requested. This range only has an effect on raw data or reduced files which have the run number embedded into the file name. Filenames with no numbers are treated as scan 0.

Usage:

```
pointsum [-h] [-demod] [-reduced] [-all|[-begin nn -end nn]]
```

Parameters:

−**h[elp]**
: Return a help message only. More help can be obtained by using 'showme sun216' or 'scuhelp pointsum'.

−**all**
: List all pointing files in the current directory and $DATADIR

−**demod**
: Only list demodulated data files (signified by _dem_ file name)

−**reduced**
: Only list reduced data files (signified by _red_ file name)

−**begin nn**
: First scan number to be considered (same as −−begin==nn)

−**end nn**
: Final scan number to be considered (same as −−end=nn)

Examples:

```
pointsum
```

Ask for a range of scan numbers and then give a summary of every pointing file matching this criterion in DATADIR and the current directory.

```
pointsum −all
```

Generate a summary of all pointing files in the current and DATADIR directory.

```
pointsum −−begin=5 −−end=100
```

Generate a summary of all pointing data from scans 5 to 100 inclusive.

```
pointsum −all −reduced
```

Produce a one line summary of all reduced pointing (_red_) files.

```
pointsum −all −reduced > log.txt
```

Produce a one line summary of all the reduced pointing files and store the output in the text file log.txt (note this example is shell specific).

```
pointsum −all −reduced −demod
```

Produce a summary of all reduced (_red_) and demodulated (_dem_) pointing files (ie not files produced during off-line data reduction).

Notes:

- pointsum only displays pointing data.
- Files are drawn from the current working directory and the directory indicated by the $DATADIR environment variable.
- Data reduced by the off-line system will all be treated as run 0 for the purposes of listing unless numbers are present in the filename.
- The output can be stored in a file by using unix redirection as long as the search range is fully specified (either as '−all' or with '−begin' and '−end').
- Command line options can be abbreviated.
- Options that take values can be used either as '−flag option' or as '−−flag=option'

Related Applications :

SURF: sculog, photsum, mapsum, obssum, skysum

QDRAW
Draw a data set with plus or minus 5 sigma range

Description:

This program uses KAPPA routines to calculate mean and standard deviation of an NDF. It then uses linplot to display the data with a range of plus or minus 5 sigma. Optionally, drawsig can be used to overlay 3 sigma lines.

Usage:

```
qdraw [-noline] NDF [Linplot/Stats/Drawsig parameters]
```

Parameters:

-noline
A Unix-type switch which controls whether the 3 sigma lines are displayed or not.

NDF (Given)
The required dataset

ADAM parameters = Any
Any parameters accepted by the individual routines as long as they use PARAM=VALUE format.

Examples:

```
qdraw test
```

Draws test.sdf with a scale of ± 5 sigma and draws lines at ± 3 sigma.

```
qdraw -noline test
```

Same as above but without the 3 sigma lines

```
qdraw mode=2 test
```

Plot the data using '+' symbols (linplot mode 2)

```
qdraw mode=2 sigcol=red test
```

Plot with '+' symbols and use red lines to show the ± 3 sigma lines.

Notes:

The $KAPPA_DIR environment variable must point to the location of the KAPPA binaries (this is usually done during a Starlink login).

Related Applications :

SURF: scucat, scuphot;
KAPPA: stats, linplot, drawsig

REBIN
Rebin demodulated SCUBA data onto output map

Description:

This routine rebins the demodulated data from SCUBA MAP observations onto a rectangular mesh by a variety of methods. Currently convolution by weighting functions, spline interpolation and median are supported.

- Weighting functions:
  Currently linear, Bessel and Gaussian weighting functions are supported. The width of the Bessel function is such that it should preserve all spatial information obtained by the telescope at the wavelength of observation, but suppress higher spatial frequencies. To minimise edge effects the Bessel function is truncated at a radius of 10 half-widths from the centre (although this is configurable), and apodized over its outer third by a cosine function. Viewed in frequency space the method consists of Fourier transforming the input dataset(s), multiplying the transform by a cylindrical top-hat (the F.T. of the Bessel function), then transforming back into image space. A linear weighting function is also available which works out to one half-width - this has the advantage that it is much faster to process and is much less susceptible to edge effects. The Gaussian weighting function is probably the best compromise between the Bessel (slow and prone to edge effects) and Linear (fast but the point spread function is non-trivial for modeling).
  The radius and size of 'footprint' for the weighting functions are configurable using the WTFNRAD and SCALE parameters.
- Splines:
  Additionally, spline interpolation and smoothing routines are also available. Note that the spline routines work on each integration in turn, whereas the weighting function routines work on all the input data in one go. At present the spline routines are experimental and comments are welcomed.
- Median:
  A regridding option derived from despike is available. This method simply puts all data points in an output grid and calculates the median of each output cell. Small pixel scales require large datasets (since not all cells in a 1 arcsecond grid will contain data points) although the KAPPA commands fillbad and glitch can be used to smooth over bad pixels.

Usage:

```
rebin ref
```

Parameters:

GUARD = LOGICAL (Read)

Controls whether the bolometer guard ring should be used during the regridding process. The guard ring enforces zero flux at the edge of the regridded image. Should be turned off if flux is present at the edge. Default is to use the guard ring for LINEAR, BESSEL and GAUSSIAN rebin modes.

IN = CHAR (Read)
The name of the input file to be rebinned. This parameter is requested repeatedly until a NULL value (!) is supplied. LOOP must be TRUE. IN can include a SCUBA section. Like the REF parameter this parameter accepts a text file.

LAT_OUT = CHAR (Read)
The latitude of the output map centre. The supplied default value is that of the map centre of the first map.

LONG_OUT = CHAR (Read)
The longitude of the output map centre. The supplied default value is that of the map centre of the first map.

LOOP = LOGICAL (Read)
Task will ask for multiple input files if true. Only REF is read if noloop.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)
This is the name of the NDF that will contain the rebinned map. A null value can be supplied to shut down rebin without error. This can be used to determine the size of the output map without creating it.

OUT_COORDS = CHAR (Read)
The coordinate system of the output map. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (e.g. Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)
- GA: Galactic coordinates (J2000)

For RD current epoch is taken from the first input file.

OUT_OBJECT = CHAR (Read)
The name of the object (ie the NDF title).

PIXSIZE_OUT = REAL (Read)
Size of pixels in the output map. Units are arcsec.

REBIN_METHOD = CHAR (Read)
The rebin method to be used. A number of regridding methods are available:

- LINEAR: Linear weighting function
- GAUSSIAN: Gaussian weighting function
- BESSEL: Bessel weighting function
- SPLINE1: Interpolating spline (PDA_IDBVIP)
- SPLINE2: Smoothing spline (PDA_SURFIT)
- SPLINE3: Interpolating spline (PDA_IDSFFT)
- MEDIAN: Median regridding

Please refer to the PDA documentation (SUN/194) for more information on the spline fitting algorithms.

REF = CHAR (Read)
The name of the first NDF to be rebinned. The name may also be the name of an ASCII text file containing NDF and parameter values. See the notes. REF can include a SCUBA section.

REFPIX (2) = INTEGER (Read)
The coordinate of the reference pixel in the output data array. This corresponds to the pixel associated with the specified RA/Dec centre. Default is to use the middle pixel if a size is specified or the optimal pixel if the default size is used (see the SIZE parameter).

TRIM = INTEGER (Read)
This parameter determines the amount of good data that should be trimmed from the final image to correct for edge effects. The supplied value should be in arcseconds. All pixels closer to a bad pixel than this distance will be set to bad in the output image (by setting bit 1 in the quality array). Default is 0.0.

SCALE = REAL (Read)
Radius of one scale size in arcsec. This effectively governs the size of the weighting function. For LINEAR one scale size corresponds to the zero of the cone, for BESSEL it is the first zero of the Bessel function (π) and for Gaussian it is the half-width half maximum (HWHM).

SIZE (2) = INTEGER (Read)
This array parameter sets the size of the output grid in pixels (nx, ny). The default values are the minimum dimensions required to display the entirety of the mapped area.

SHIFT_DX = REAL (Read)
The pointing shift (in X) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

SHIFT_DY = REAL (Read)
The pointing shift (in Y) to be applied that would bring the maps in line. This is a shift in the output coordinate frame.

TIMES = LOGICAL (Read)
Store an extra NDF in the output map containing the 2-D histogram of the data. This can be used to make an estimate of the actual number of samples responsible for each point in the output grid. Note that, in general, the number of pixels in the output grid exceeds the number of independent beams in the image. The data can be accessed as OUT.more.reds.times. Default is FALSE.

WEIGHT = REAL (Read)
The relative weight that should be assigned to each dataset.

WEIGHTS = LOGICAL (Read)
This parameter governs whether the convolution weights array will be stored in the output NDF. The default is FALSE (i.e. do not store the weights array).

WTFNRAD = INTEGER (Read)
Size of the weighting function in scale sizes. This parameter is irrelevant for LINEAR regridding. For Gaussian the default is 3 (i.e. a diameter of 3 FWHM for the footprint),

and for Bessel it is 10. The smaller the weighting function is (a combination of WTFNRAD and SCALE) the faster the regridding goes.

Examples:

```
rebin rebin_method=LINEAR out_coords=RJ
```

Rebin the maps with LINEAR weighting function in J2000 RA/Dec coordinates. You will be asked for input datasets until a null value is given.

```
rebin rebin_method=BESSEL out=map out_coords=NA
```

Rebin the maps with Bessel weighting function in Nasmyth coordinates.

```
rebin noloop accept ref=test.bat out=rebin
```

Rebin the files specified in test.bat onto a rectangular grid using linear interpolation, 3 arcsecond pixels and RJ coordinates.

Notes:

For each file name that is entered, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY are requested.

- The application can read in up to 256 separate input datasets.
- The output map will be large enough to include all data points.
- Spline regridding may have problems with SCAN/MAP (since integrations contain lots of overlapping data points).
- SCUBA sections can be given along with any input NDF
- The relative weights associated with each point in the output map are stored in a WEIGHTS NDF in the REDS extension of the output data (For WEIGHTS=TRUE). For spline rebinning each point is equivalent to the number of integrations added into the final data point. For weight function regridding the situation is more complicated. The actual number of points contributing to each cell can be stored using the TIMES parameter.
- Bolometer weights will be used if a BOLWT extension is found in the input data file (usually set with setbolwt).
- Astrometry information is stored in the WCS component and not the FITS extension.

ASCII input files :

The REF and IN parameters accept ASCII text files as input. These text files may contain comments (signified by a #), NDF names, values for the parameters WEIGHT, SHIFT_DX and SHIFT_DY, and names of other ASCII files. There is one data file per line. An example file is:

```
file1{b5}   1.0  0.5  0.0  # Read bolometer 5 from file1.sdf
file2                     # Read file 2 but you will still be
                          # prompted for WEIGHT, and shifts.
file3{i3}-  1.0  0.0  0.0  # Use everything except int 3
test.bat                  # Read in another text file
```

Note that the parameters are position dependent and are not necessary. Missing parameters are requested. This means it is not possible to specify SHIFT_DX (position 3) without specifying the WEIGHT. If the file has the .txt extension the NDF system will attempt to convert it to NDF format before processing – this is probably not what you want.

Related Applications :

SURF: bolrebin, intrebin, scuquick, extract_data

REDUCE_NOISE
Process demodulated noise data

Description:

This routine takes raw demodulated noise data and processes it. NDF and ASCII results files are generated.

The output NDF file is a 2-D dataset with a chop signal and calibrator signal per bolometer. The text file is similar to the file generated by the real-time system.

Parameters:

IN = NDF (Read)
The name of the raw noise data file. A single number can be supplied if SCUBA_PREFIX is set. DATADIR is recognised.

OUT = NDF (Write)
Output NDF. This file is 2-dimensional. The first dimension is bolometer number. The second dimension is chop signal and calibrator signal (along with variances and quality). If no output NDF is required a null value can be given.

FILE = FILENAME (Write)
Output text file. Format is almost identical to that generated by the real-time system. A null value can be supplied to prevent a text file from being written. The default output name is the same name as generated by the on-line system (noise_YYMMDD_nr.dat)

MSG_FILTER = CHAR (Read)
Message output level. Default is NORM. Allowed values are QUIET, NORMAL and VERBOSE.

Examples:

```
reduce_noise 19981113_dem_0001 out_noise !
```

Read in observation 1 and write the output to an NDF names out_noise.sdf. Do not write a text file.

```
reduce_noise '3' !  accept
```

Process observation 3 but do not write an NDF output file. Use the default file name for the text file.

Notes:

Noise observations containing multiple measurements are condensed into a single measurement.

REDUCE_SWITCH
reduce the switch sequence for a SCUBA observation

Description:

This application takes a SCUBA demodulated data file and splits the data array up into its various 'planes'; data, variance and quality. In addition, the application reduces the component switches of an exposure to give the exposure result. Optionally, the routine will divide the internal calibrator signal into the data before doing either of these things. It is also possible to select a single switch from the input data.

For skydip data, this routine calculates the sky temperature for each integration and sub-instrument.

Usage:

```
reduce_switch in out
```

Parameters:

IN = NDF (Read)
The name of the demodulated data file. If SCUBA_PREFIX is set this can be the number of the observation rather than the full filename.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Read)
The name of the file to contain the output data.

SPIKE_LEVEL = INTEGER (Read)
Number of spikes tolerated before marking data point bad. The default is that the sample should be marked bad if the transputers detected more than 5 spikes during a 1 second sample.

SWITCH = INTEGER (Read)
Parameter to indicate which switch to extract. A value of 0 means that all switches should be reduced. Default is 0.

TARRAY = LOGICAL (Read)
Controls whether the T_COLD parameters are read as an array of values (true) or read as a sequence of scalars (false) . This parameter is useful if the command is to be run in batch mode. Default is false.

T_COLD = REAL (Read)
Temperature of the cold load when processing skydip data. The default value is taken from the input file.

T_HOT = REAL (Read)
Temperature of the hot load when processing skydip data. The default value is taken from the input file.

USE_CALIBRATOR = LOGICAL (Read)
Yes, if you want the data for each bolometer measurement divided by the corresponding internal calibrator signal. The default is not to use the calibrator.

Examples:

```
reduce_switch
```

All parameters will be requested.

```
reduce_switch test nosw
```

This will reduce the switch from input file test.sdf without dividing by the calibrator signal and tolerating up to 5 spikes in a 1 second sample. The output data will be written to nosw.sdf.

```
reduce_switch test nosw SWITCH=2
```

This will select switch 2 from test.sdf and write it to nosw.sdf

Notes:

If the input file is not found in the current directory, the directory specified by the DATADIR environment variable is searched. This means that the raw data does not have to be in the working directory. In addition `IN` accepts a number. This number is converted to a demodulated data filename by prepending it with information specified in the SCUBA_PREFIX environment variable. This filename expansion only works for demodulated data (ie data containing `'_dem_'`). The `'_dem_'` is assumed and should not be present in SCUBA_PREFIX.

REMDBM
Remove dual beam signature from scan maps

Description:

This program should be used to reduce SCAN/MAP data taken using the technique described by Emerson (1995, ASP Conf Ser 75, 309). The deconvolution is performed using Fast Fourier techniques.

Usage:

```
remdbm [-h] [-v] [-out=] [-noams] [-filter] files
```

Parameters:

−h
Help message

−v
Version number. Also indicates whether ADAM communication is enabled.

−out=file
Filename of output image. Default is '`final.sdf`'

−noams
Turn off ADAM messaging if available. Default is false. Ignored if ADAM messaging is not available.

−filter
Turns on high frequency filtering. When used, data at frequencies greater than that to which the telescope is sensitive are set to zero.

files
List of input files to be processed. Shell wildcards are allowed. See notes for restrictions.

Examples:

```
remdbm *_reb.sdf
```

Process all files matching the pattern and write the result to `final.sdf`.

```
remdbm -out=m82 o66_lon_reb o67_lon_reb o68_lon_reb o69_lon_reb
```

Process the four input images. The output filename is set to `m82.sdf`.

```
remdbm -filter -noams *_reb.sdf
```

Process the supplied files with high frequency filtering. Do not use the messaging system.

Notes:

The following restrictions apply:

- Each image should contain a single chop configuration.
- Each image must have identical dimensions and pixel size (they do not need to be square)
- The images must be rebinned in the same coordinate system as the chop throw.

Related Applications :

SURF: scumakewt add_dbm
KAPPA: fourier

REMIP
Remove instrumental polarisation from SCUBA pol data

Description:

This task calculates and removes the instrumental polarisation signal from SCUBA polarimeter data.

For a fractional instrumental polarisation $P_I(e)$ at angle $\theta(e)$ and elevation e (the instrumental polarisation is elevation dependent) the correction to the measured flux at waveplate angle W is:

$$S_{Actual} = S_{Measured} - S_{Mean} P_I(e)(1 + \cos(4W - 2\theta(e))) \quad (1)$$

For SCUBA, we can not trivially measure the mean flux level (since each bolometer is jiggling to different areas on the sky) so this task uses an approximate form of the above equation to correct for instrumental polarisation that is valid for IPs of a few percent:

$$S_{Actual} \approx S_{Measured} * (1 - P_I(e)(1 + \cos(4W - 2\theta(e)))) \quad (2)$$

where we have made the approximation that $S_{Mean} \approx S_{Measured}$.

Usage:

```
remip in ipfile out
```

Parameters:

IN = NDF (Read)
Input data file.

IPFILE = FILE (Read)
File containing the IP 'flatfield'

MSG_FILTER = CHAR (Read)
Message filter level. Options are QUIET, NORMAL and VERBOSE. Default is NORM.

OUT = NDF (Write)
Output file containing IP removed data. Default output filename is '_ip' ('i' for short form).

Examples:

```
remip file1 ipfile.dat \\
```

Correct file1.sdf using ipfile.dat and write IP corrected data to the default output file (eg file1_ip).

Notes:

- Variance is propagated correctly.

- This task writes out the waveplate angles and rotation angles. The waveplate angle per integration is written to .MORE.REDS.WPLATE. The rotation angle (waveplate 0 to X pixel axis) is written to .MORE.REDS.ANGROT (angle per integration). The angle between nasmyth and the ra/dec frame (ie ANGROT - 90 degrees) is stored in .MORE.REDS.NASMYTH_ANG (angle per sample). These are written as NDFs and so can be displayed in the normal way. The angles are in degrees.
- An array containing the fast axis angle is also written to the REDS extension (FAST_AXIS). The size of this array matches the number of sub-instruments in the file.

REMSKY
Remove sky noise and constant offsets from SCUBA jiggle data

Description:

This task removes sky noise and constant offsets from SCUBA jiggle data. It does this by requesting 'sky' bolometers, calculating an average value for each jiggle and then subtracting this off the jiggle. Each jiggle is analysed in turn. The average value can be calculated in two ways: either MEDIAN or MEAN.

After the calculation, the mean value removed from each jiggle can be added back onto the data – this should protect against removing flux from MAP data.

If a SKY NDF is found in the REDS extension, it is assumed that the sky variation has already been determined (eg by calcsky) and this sky signature is removed. The 'ADD' parameter is ignored in this case.

Usage:

```
remsky in out
```

Parameters:

ADD = LOGICAL (Read)

This parameter governs whether the average value removed from the data should be added back after sky removal. The default is for ADD to be true for MAPs and false for other modes (the assumption being that sky bolometers in PHOTOM observations are guaranteed to be on sky)

BOLOMETERS() = CHAR (Read)

List of sky bolometers. The following options are now recognised for the BOLOMETERS parameter:

Code	Description	Example
nn	A number	5 or 19
id	Bolometer id	h7 or c14
r*n*	Ring number	r1 (for the first ring)
		r5 (for the outer ring of the SHORT array)
		r-1 (for the outer ring)
		r-2 (one ring in from outer ring)
all	All bolometers	all (select the entire array)

Each value must be comma separated but can be preceded by a minus sign to remove the bolometer(s) from the list. The definitions of ring number and 'all' are dependent on the selected sub-instrument.

Here are some example values for BOLOMETERS:

[17,18,19,20]	Bolometers 17, 18, 19 and 20
[h6,h7,h8,h9]	Bolometers H6, H7, H8, H9
[all]	Whole array
[r0]	Ring zero (central pixel)
[r0,-19]	No bolometers (bol 19 of LONG is R0/H7)
[h7,r1]	inner ring and H7
[r1,-h8]	inner ring without H8
[r1,-18]	inner ring without bolometer 18
[all,-r1,-h7]	all pixels except the inner ring/H7
[all,-r3,g1]	all pixels except ring 3 but with G1 (which happens to be in r3)
[all,-r1,-r2,-r3,-r4,-r5]	Selects the central pixel
[all,-r-1]	Selects all except outer ring

Note that the bolometer sum is calculated sequentially so that [all,-all,h7] would leave you with bolometer H7.

IN = NDF (Read)
This is the name of the input demodulated data file.

ITER_SIGMA = REAL (Read)
When using MEAN to calculate the average, this is the sigma clipping level used. This is an iterative value - points will be removed from the mean until the spread of data points is smaller than this value. Supplying a negative value will turn off clipping.

MODE = CHAR (Read)
Method to be used for calculating the average sky. There are two methods available:

- Median – the median value for all the sky bolometers is taken from each bolometer signal.
- Mean – the mean of the sky bolometers is used as the average. This mean value is iterative – i.e. The mean and standard deviation are calculated, any points greater than the given distance from the mean are removed and the mean and standard deviation are calculated. This process is repeated until no bolometers are dropped from the mean.

MSG_FILTER = CHAR (Read)
Message output level. Allowed values are QUIET, NORM and VERB. Default is NORM. In VERBOSE mode a list of the selected bolometers is returned along with the value of the sky offset removed for each jiggle.

OUT = NDF (Write)
Output data file.

Examples:

```
remsky ndf sky_removed bolometers='[g1,g2,g3,g4,g5]' mode=median \
```

Use the median of bolometers g1,g2,g3,g4,g5 (not necessarily the best choice) to calculate the sky signal and write the output to sky_removed.sdf.

```
remsky o12_lon_ext bolometers=[all] mode=median \
```

Use the median of all the bolometers for each jiggle and write the output to the default output file (e.g. o12_lon_sky).

```
remsky o25_sho_ext bolometers=[r5] mode=mean iter_sigma=4 \
```

Use the outer ring of the short-wave array as the sky bolometers. Calculate the sky contribution by using a clipped mean of each jiggle and remove any points from the calculation of the mean that are more than 4 sigma from the mean. Write the output to the default output file.

Notes:

- Source rotation is not accounted for so use only those bolometers that always observe sky. This can be checked by using scuover to overlay the bolometer positions on a NAsmyth regridded image (since NA shows the signal measured by each bolometer throughout the observation without source rotation).
- For weak sources (ie sources that are not obvious in a single integration) it is probably sufficient to choose BOLOMETERS=[all] and MODE=median.

Related Applications :

SURF: scuquick, rebin, scuphot, scuover

RESTORE
remove the chopped beam response from SCAN/MAP observations

Description:

This routine removes the chopped beam response from SCAN/MAP observations.

Usage:

```
restore in out chop
```

Parameters:

CHOP = INTEGER (Read)
Chop throw in arcseconds. The default chop throw is read from the FITS header of the input file.

IN = NDF (Read)
The name of the input file containing demodulated SCUBA data.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)
The name of the output file to contain the processed data.

Examples:

```
restore input output \
```

Restore input.sdf to output.sdf using the default chop throw.

```
restore resw restore 40.2
```

Restore resw.sdf to restore.sdf using a chop throw of 40.2 arcseconds.

Notes:

Uses the Emerson, Klein and Haslam algorithm (1979, A&A, 76, 92).

This routine can only be used on SCAN/MAP data taken whilst chopping along the scan direction (CHOP_COORDS=SC).

Related Applications :

SURF: despike2, rebin
JCMTDR: restore

RLINPLOT
Interactive display

Description:

rlinplot (or any r∗ link to scuplot) is a wrapper around the KAPPA utility mlinplot and facilitates data inspection. It provides plots of sets of bolometers in a single window with optionally data from a second file in a second window. Obvious files are despiked and non-despiked data or data from different exposures to check the noise.

The menu items are:

[M. H]	Redisplay menu
[Q]	Quit
[N]	Next bolometer(s)
[Y min max], [Y lim]	Y-axis from min:max or -lim:+lim
[U]	Reset Y-axis

Option >

Usage:

```
rlinplot [-f sdf_file] [-d sdf_file2] [-s min max] [-l #] [bol [bol [bol] ...]]
```

Parameters:

-h[elp]
Print the help information.

-f file
name of NDF file (.sdf may be included in the name).

-d file2
name of a second file: e.g. the despiked version of the NDF file. The same bolometers will be plotted in a second window or overlaid for comparison.

-s min max
Y-axis scales for plot (can be changed via menu).

-l #
number of bolometers per window

bol
list of bolometers to plot. Type 'all' for 1..37 and 'alls' for 1..91. Can be added via menu if mode = 'r'.

Examples:

```
rlinplot
```

The user will be asked for an input file before proceeding to the menu.

```
rlinplot -f o39_lon_ext
```

Plot bolometers from o39_lon_ext.sdf and ask for a bolometer list.

```
rlinplot -f o39_lon_ext -l 5
```

Plot 5 bolometers at a time.

```
rlinplot -f o39_lon_ext 6 5 8 20
```

Plot bolometers 5 6 8 and 20.

Notes:

- If the overlay comes up scrambled, delete the agi_xxx files in your home directory and if that does not work also files like linplot.sdf in the /home/you/adam subdirectory.

Related Applications :

SURF: pltbol, dspbol;
KAPPA: mlinplot, cursor

Bugs:

Freezes when asked to plot a bad bolometer.

SCAN_RLB
Remove baselines from SCAN/MAP data

Description:

This routine removes a baseline from each scan. The baseline is determined in a number of ways. For removal of a linear baseline, a fit is made to the scan ends before removing this from the entire scan.

Usage:

```
scan_rlb in out
```

Parameters:

CHOP = INTEGER (Read)

The linear baseline fit is calculated over regions CHOP arcseconds from the scan ends. This region should be as large as possible but should only include baseline regions – any scan that includes a source detection within CHOP arcseconds of the scan ends will be rendered useless. The default value is the chop throw.

IN = NDF (Read)

The name of the input file containing demodulated SCUBA data.

METHOD = CHAR (Read)

Governs the method to be used for calculating the baseline. Options are MEDIAN: Remove the median from each scan, MEAN: remove the mean level from each scan, LINEAR: fit a linear baseline to the ends of the scan.SECTION: Use a SCUBA section to specify regions of each integration that are thought to be flux free. Remove the median of the specified section from the associated integration. Default is LINEAR.

MSG_FILTER = CHAR (Read)

The messaging level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = NDF (Write)

The name of the output file to contain the processed data.

RLB = INTEGER (Read)

This parameter governs whether the baseline fit is removed from the input data or stored instead of the data. If RLB is .TRUE. the corrected data are returned. If RLB is .FALSE. the fit is returned.

SECTION = CHAR (Read)

This array parameter can be used to specify SCUBA sections to be used for baseline calculation. It is requested when METHOD=SECTION. In general the SCUBA section should include scan (exposure) or position (p) specifiers which will be applied to each bolometer and integration. It is possible to be more specific and to provide multiple sections singling out certain bolometers or integrations. If entire integrations are selected no baseline removal will occur on unselected integrations (this will be stated). The median of the section supplied for each integration is subtracted from every exposure in that integration (remember that if no integration is specified, all integrations are assumed).

Curly brackets must still be given. Since this is an array parameter square brackets must be used to specify more than one component:

SECTION > [{e1} , {e4;b2}]

would select exposure one from each integration along with exposure 4 for bolometer 2. be used if the square brackets are not used.

Care must also be taken when using commas in SCUBA sections - the parameter system will split multiple entries on commas unless the entire section is quoted:

SECTION > "{e1,4}"

If necessary the negation character should come after a section (ie after the closing curly bracket) and that negation applies to the combined section and not just the string containing the negation character:

SECTION > {e3}-

implies that the section consists of everything except exposure 3.

Examples:

```
scan_rlb infile method=linear \
```

Remove linear baselines from each scan using baseline regions the same size as the chop. Write the results to the default output file.

```
scan_rlb infile rlb method=linear chop=30 \
```

Calculate the linear baseline for each scan using the specified baseline region. Write the results to the default output file.

```
scan_rlb infile norlb method=median \
```

Calculate the fit using the median of each scan but do not remove the baseline from the data. Store the baseline determination for later analysis.

```
scan_rlb method=section rlb section=e1,4
```

Calculate the baseline using the first and 4th exposures of each integration.

Notes:

The KAPPA sub command can be used to subtract the baseline from the input data at a later stage (if RLB is true).

Related Applications :

SURF: restore
KAPPA: sub

SCUBA2MEM
Calculate bolometer positions as tangent plane offsets

Description:

This routine reads in SCUBA demodulated data and writes it out along with the positions of the bolometers on the sky for each sample. The positions of the chop beams can be requested as well as the positions of the tracking centre. Returns tangent plane offsets from the map centre in arcseconds. Additionally, the LST of each sample is stored as axis information.

Usage:

```
scuba2mem in out
```

Parameters:

IN = CHAR (Read)

The name ofthe input files to be processed. This is a demodulated data file. RESTORE should not have been run on it. Multiple file names can be specified (see the documentation on GRP). All the input files are referenced to the same output coordinate frame.

LAT = CHAR (Read)

The latitude of the output map centre. The supplied default value is that of the map centre of the observation in the output coordinates.

LONG = CHAR (Read)

The longitude of the output map centre. The supplied default value is that of the map centre of the observation in the output coordinates.

MSG_FILTER = CHAR (Read)

Message filter level. Default is NORM.

NBEAMS = INTEGER (Read)

Number of output beams to be written to file. NBEAMS=1 just writes the Middle beam, NBEAMS=2 writes the Left (negative) and Right beams, NBEAMS=3 writes Middle, Left and Right beams.

OUT = NDF (Write)

This parameter specifies the name of the output file to be used to store the positional information. The file format is described below.

OUT_COORDS = CHAR (Read)

The coordinate system of the output map. Available coordinate systems are:

- AZ: Azimuth/elevation offsets
- NA: Nasmyth offsets
- PL: RA/Dec Offsets from moving centre (eg Planets)
- RB: RA/Dec (B1950)
- RJ: RA/Dec (J2000)
- RD: RA/Dec (epoch of observation)

- GA: Galactic coordinates (J2000)

SHIFT = REAL(2) (Read)

The pointing shift [X,Y] to be applied that would bring the map into the correct position. This is a shift in the output coordinate frame. CHANGE_POINTING should be used to add Az/El pointing offsets.

Examples:

```
scuba2mem out_coords=GA o34_lon_ext o34_mem nbeams=1 \\
```

Calculate the coordinates of all bolometer positions in tangent plane offsets from the GA map centre.

```
scuba2mem o34_lon_ext nbeams=3 \\
```

Calculate all chop positions for o34_lon_ext. Use RJ coordinates.

Notes:

- Can be used on JIGGLE and SCAN data.
- The coordinates of the selected output frame are written to the output FITS extension in keywords OUT_CRDS, OUTLONG and OUTLAT. The full FITS header of the observation itself is still available.

Format of output file :

SCUBA DBMEM requires the data, positions of every beam and the LST for every point. This information (along with a standard FITS header) is stored as a standard NDF. The data array is constructed as follows:

3 dimensional: N_BOL $*$ N_POS $*$ ((N_BEAM $*$ 2) $+$ 1)

where N_BOL is the number of bolometers, N_POS is the number of samples for each bolometer (time axis), N_BEAM is the number of beams.

The 3rd dimension contains the actual data value plus positions of every beam associated with the data point. Each beam has two positions (X offset and Y offset) Axis components store bolometer number, LST and beam weight.

Related Applications :

SURF: extract_data, rebin
DBMEM, PIXON

Copyright :

SCUCAT
Concatenate photometry datasets for further processing

Description:

This routine reads in a list of user specified files and concatenates their data, variance and quality arrays so that KAPPA routines like stats and kstest can analyse a complete set of photometry observations. scucat can be configured so that either all data are concatenated into one file regardless of bolometer (METHOD=catall) or data for each bolometer is kept separate (METHOD=separate). In the latter case, if a file contained data for H7 and H9 then two output files would be created (e.g. test_h7 and test_h9 - if the OUT parameter was set to 'test') and for each new bolometer a new file is created (existing files are overwritten) and data is appended to these files when more data for these bolometers is supplied.

Usage:

```
scucat out in
```

Parameters:

BOL = CHAR (Read)

If the input file is an NDF (and not an HDS container as expected) then this parameter should be given to tell the software the bolometer that should be associated with this data.

IN = NDF (Read)

The input dataset(s). This parameter is requested repeatedly until a NULL (!) value is given. The input dataset can either be output from scuphot or an NDF file. A comma-separated list of files is allowed. A text file containing a list of files can be specified using the up-carat symbol (^) in front of the text file name.

LOOP = LOGICAL (Read)

Turns the looping on (default is true) or off (false)

METHOD = CHAR (Read)

Governs whether data from different bolometers are combined regardless (CATALL) or written to separate files (SEPARATE). Default is 'SEPARATE'. The choice of this parameter governs the behaviour of the OUT parameter.

MSG_FILTER = CHAR (Read)

Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = CHAR (Write)

If METHOD=separate this parameter governs the root name of the output NDF (i.e. <OUT>_bol). If METHOD=catall this parameter can be used to specify the actual output file name.

Examples:

```
scucat test phot
```

This routine will copy the data from phot to test_<bol>, reducing multiple bolometers

to individual files. If the input set contained data for bolometer H7 the output file will be test_h7.sdf. The program will then ask for another data set.

```
scucat test ext_long noloop
```

This will copy all the data from ext_long.sdf to test_<bol>.sdf and will then exit without asking further questions.

```
scucat outfile 'file1,file2,file3' noloop method=separate
```

Concatenate the data from file1, file2 and file3 into output files containing the rootname of 'outfile'.

```
scucat outfile in=^input.lis noloop method=catall
```

This will copy all the data contained in the files listed in `input.lis` and write it to a file called `outfile.sdf`.

Notes:

- SCUCAT can process output data from scuphot (e.g. file.sdf as an HDS container containing NDF files with the names <bol>_peak) or NDF files.
- If given an NDF the data array is vectorized so that the output is 1-dimensional regardless of the shape of the input file.
- This task can also be used to simplify further processing of the photometry data even if no data is to be concatenated (in this case the task would be identical to the KAPPA task ndfcopy).

Related Applications :

SURF: scuphot;
KAPPA: ndfcopy, kstest

Implementation Status:

- NDF sections can not be used
- All input pixels are propagated to the output file
- See the GRP documentation [34] for more information on specifying multiple input files for the 'IN' parameter.

SCUCLIP
Simple sigma clipping for each bolometer

Description:

Each bolometer is analysed independently, the mean and standard deviation are calculated, any points greater than NSIGMA sigma from the mean are treated as spikes and removed. Note that for mapping this despiking algorithm is only useful for very weak sources; bright sources will be removed (since a bolometer jiggles on and off bright sources). Photometry observations do not suffer from this problem as the bolometers are always on source.

Usage:

```
scuclip in out nsigma
```

Parameters:

IN = NDF (Read)
This is the name of the input demodulated data file

MSG_FILTER = CHAR (Read)
Message output level. Allowed values are QUIET, NORM and VERB. Default is NORM. If MSG_FILTER is set to VERBOSE the number of spikes removed from each bolometer is reported.

NSIGMA = DOUBLE (Read)
Number of sigma beyond which data are thought to be spikes. If this number is positive an iterative clip will be performed (ie the standard deviation is recalculated after clipping and points lying outside the new range are removed). If it is negative then iterative clipping is switched off.

OUT = NDF (Write)
Output data file.

Examples:

```
scuclip infile outfile 5
```

Clip any data points that are further than 5 sigma from the mean. The clipping is done on a per bolometer basis and is iterative.

```
scuclip infile outfile -5
```

Clip any data points that are further than 5 sigma from the mean. The clipping is done on a per bolometer basis and only one pass of clipping is performed.

Notes:

- The despiking routine is very primitive and should not be used with jiggle map data of bright sources. It can be used on PHOTOM data since the jiggle pattern never moves off source (although sigclip can be used once the data has been processed by scuphot).

Related Applications :

SURF: scuquick, rebin, scuphot, sigclip, despike;
KAPPA: setbb

Implementation Status:

The despiking routine sets QUALITY bit 5 to bad. It does not affect the data. The effects of despiking can be removed by using the KAPPA task setbb to unset quality bit 5.

SCUCLKERR
Determine the possible error in the times stored in the data header

Description:

This routine calculates the error in the times stored in the data header. It performs a self-consistency check to determine the local sidereal time from the Azimuth and elevation information (that comes directly from the telescope) and compares this to the LST stored in the header.

Usage:

```
scuclkerr filename
```

Parameters:

CLOCKERR = REAL (Write)
On exit, the clock error, in seconds, determined from the header.

DANG = REAL (Write)
Error in the array rotation angle due to the clock error (degrees)

DR = REAL (Write)
Positional error at the edge of the array for this particular observation. In arcseconds. Edge is defined as a radius of 70 arcseconds.

IN = NDF (Read)
The name of the NDF containing to be tested.

MSG_FILTER = CHAR (Read)
Message filter level. Default is NORM.

LAG = REAL (Write).
The discrepancy between the LST stored in the FITS header and the LST when data acquisition begins. This provides a measure of the lag in starting up the observation (including slew times). The value is stored in seconds.

MJD = DOUBLE (Write)
Modified Julian Date of start of observation corrected for the lag time and the clock error.

Notes:

- The calculated clock error is only accurate to about 15 seconds.

References :

Jenness, T., 2000, JCMT Technical Report TR/001/84

SCUHELP
Gives help about SCUBA software

Description:

Displays help about SCUBA software. The help information has classified and alphabetical lists of commands, general information about SCUBA and related material; it describes individual commands in detail.

Usage:

```
scuhelp [topic] [subtopic] [subsubtopic] [subsubsubtopic]
```

Parameters:

TOPIC = LITERAL (Read)
Topic for which help is to be given.

SUBTOPIC = LITERAL (Read)
Subtopic for which help is to be given.

SUBSUBTOPIC = LITERAL (Read)
Subsubtopic for which help is to be given.

SUBSUBSUBTOPIC = LITERAL (Read)
Subsubsubtopic for which help is to be given.

Examples:

```
scuhelp
```

No parameter is given so the introduction and the top-level help index is displayed.

```
scuhelp application/topic
```

This gives help about the specified application or topic.

```
scuhelp application/topic subtopic
```

This lists help about a subtopic of the specified application or topic. The hierarchy of topics has a maximum of four levels.

```
scuhelp Hints
```

This gives hints for new and intermediate users.

```
scuhelp summary
```

This shows a one-line summary of each application.

```
scuhelp classified classification
```

This lists a one-line summary of each application in the given functionality classification.

Notes:

The environment variable SURF_HELP should be set to point to the help file. This variable is usually set as part of the Starlink login.

Navigating the Help Library :

The help information is arranged hierarchically. You can move around the help information whenever SCUHELP prompts. This occurs when it has either presented a screen's worth of text or has completed displaying the previously requested help. The information displayed by SCUHELP on a particular topic includes a description of the topic and a list of subtopics that further describe the topic.

At a prompt you may enter:

- a topic and/or subtopic name(s) to display the help for that topic or subtopic, so for example, "block parameters box" gives help on BOX, which is a subtopic of Parameters, which in turn is a subtopic of BLOCK;
- a <CR> to see more text at a "Press RETURN to continue ..." request;
- a <CR> at topic and subtopic prompts to move up one level in the hierarchy, and if you are at the top level it will terminate the help session;
- a CTRL/D (pressing the CTRL and D keys simultaneously) in response to any prompt will terminate the help session;
- a question mark "?" to redisplay the text for the current topic, including the list of topic or subtopic names; or
- an ellipsis "..." to display all the text below the current point in the hierarchy. For example, "BLOCK..." displays information on the BLOCK topic as well as information on all the subtopics under BLOCK.

You can abbreviate any topic or subtopic using the following rules.

- Just give the first few characters, e.g. "PARA" for Parameters.
- Some topics are composed of several words separated by underscores. Each word of the keyword may be abbreviated, e.g. "Colour_Set" can be shortened to "C_S".
- The characters "%" and "$*$" act as wildcards, where the percent sign matches any single character, and asterisk matches any sequence of characters. Thus to display information on all available topics, type an asterisk in reply to a prompt.
- If a word contains, but does end with an asterisk wildcard, it must not be truncated.
- The entered string must not contain leading or embedded spaces.

Ambiguous abbreviations result in all matches being displayed.

Implementation Status:

- Uses the portable help system.

SCULOG
Produce summary of SCUBA observations

Description:

Sculog goes through all the sdf files in the current directory and, optionally, DATADIR (defined in an environment variable) and extracts information from any FITS entries that may be present. If a HISTORY record is present (i.e. the data have been partially reduced) the most recent application to manipulate the data is reported.

In the absence of the −all flag, a numeric range is requested. This range only has an effect on raw data or reduced files which have the run number embedded into the file name. Filenames with no numbers are treated as scan 0.

Usage:

```
sculog [-h] [-summary] [-demod] [-reduced] [-mode ??]  [-all|[-begin nn -end nn]]
```

Parameters:

−**h[elp]**
Return a help message only. More help can be obtained by using 'showme sun216' or 'scuhelp sculog'.

−**summary**
Return a one line summary of each observation file. No HISTORY information is reported.

−**all**
List all files in the current directory and $DATADIR

−**demod**
Only list demodulated data files (signified by _dem_ file name)

−**reduced**
Only list reduced data files (signified by _red_ file name)

−**begin nn**
First scan number to be considered (same as −−begin==nn)

−**end nn**
Final scan number to be considered (same as −−end=nn)

−**mode obs**
Select only specified observation modes for listing. The list should be comma separated. (same as −−mode=obs)

Examples:

```
sculog
```

Ask for a range of scan numbers and then give a full listing of every sdf file matching this criterion in DATADIR and the current directory.

```
sculog −all
```

Generate a full listing of all sdf files in the current and DATADIR directory.

```
sculog ——begin=5 ——end=100
```

Generate a detailed log of all data from scans 5 to 100 inclusive.

```
sculog —summary —all
```

Produce a one line summary of all files (see also obssum).

```
sculog —summary —all —reduced
```

Produce a one line summary of all reduced (_red_) files.

```
sculog —summary —all —reduced > log.txt
```

Produce a one line summary of all the reduced files and store the output in the text file log.txt (note this example is shell specific).

```
sculog —summary —all —reduced —demod
```

Produce a summary of all reduced (_red_) and demodulated (_dem_) data files (ie not files produced during off-line data reduction).

```
sculog —summary —all —mode pointing
```

Produce a one line summary of all pointing observations

```
sculog —summary —reduced —begin 100 —end 200 ——mode=photom,skydip
```

Produce a one line summary of the photom and skydip observations of reduced files with scan numbers 100 to 200. This is similar to photsum except that the signal and signal-to-noise will not be displayed even if reduced files are being listed.

Notes:

- sculog only uses information stored in the FITS header of reduced and raw data files and does not provide summaries of reduced (RO) data such as photometry results (essentially for reasons of clarity). 'photsum' must be used to generate a summary of photometry observations that includes reduced data.
- Files are drawn from the current working directory and the directory indicated by the $DATADIR environment variable.
- Data reduced by the off-line system will all be treated as run 0 for the purposes of listing unless numbers are present in the filename.

- The output can be stored in a file by using unix redirection as long as the search range is fully specified (either as '−all' or with '−begin' and '−end').
- Command line options can be abbreviated.
- Options that take values can be used either as '−flag option' or as '−−flag=option'

Related Applications :

SURF: obssum, photsum, pointsum, mapsum, skysum

SCUMAKEWT
Create weights array for dual beam deconvolution

Description:

Construct an NDF holding the weights array for a particular chop throw and the Fourier Transform (FT) of the chop function (a sine wave).

Usage:

```
scumakewt chop pa pixsize size ftchop wtchop
```

Parameters:

CHOP = REAL (Read)
Chop throw in arcseconds. There is no default

FTCHOP = NDF (Write)
Output NDF containing fourier transform of the chop function. The size of the output array matches the dimensions supplied by parameter SIZE

LIKE = NDF (Read)
This parameter may be used to supply an NDF which is to be used as a template. If such a template is supplied, then its origin (its lower pixel-index bounds) and extent will be read used for the output NDFs. By default no template will be used and the size information will be read from the SIZE parameter. Additionally, the PA, PIXSIZE and CHOP parameters are searched for in the FITS extension if one is present (using keywords of CHOP_PA, SCUPIXSZ and CHOP_THR respectively). These parameters values are requested if not found in the FITS extension.

MSG_FILTER = CHAR (Read)
Message filter level. Default is NORM.

OUTCHOP = REAL (Write)
Chop throw angle actually used.

OUTPA = REAL (Write)
Position angle actually used.

OUTPIXSZ = REAL (Write)
Actual pixel size used (arcsec)

PA = REAL (Read)
Position angle of chop throw. Positive is anti-clockwise starting from North. The angle should be specified in degrees.

PIXSIZE = REAL (Read)
Pixel size to be used for output images. Should be in arcseconds (ie same units as used for the CHOP parameter)

SIZE(2) = INTEGER (Read)
Array parameter containing the number of pixels (X, Y) in the output images.

WTCHOP = NDF (Write)
Output NDF containing the weights contributed by this chop configuration. This is FTCHOP squared. The size of the output array matches the dimensions supplied by parameter SIZE

Examples:

```
scumakewt 20 90 3 '[256,256]' ft wt
```

Generate the FT and weight of a 20 arcsec RA chop using 3 arcsec pixels and a 256 square output image. The weight is written to wt.sdf and the FT to ft.sdf.

```
scumakewt chop=20 size=[256,512] ftchop=fft wtchop=weights
```

Generate the weight and ft of a chop of size 20 arcseconds on a 256 x 512 image. The pixel scale will be requested.

Related Applications :

SURF: remdbm

SCUNOISE
Display SCUBA noise data

Description:

Scunoise can read in a directory of noise summaries (the .dat files produced by the real-time system) and plot them. A date must be supplied so that SCUNOISE can pick up the correct file associated with a given run number. Once the noise data are displayed the pointer can be moved over a point to determine the associated bolometer name. Double on the window will bring up a diagram of the array with all bolometers above the specified noise level (specified by the position of the pointer for the double click) highlighted in a different colour.

Usage:

```
scunoise [-h | -v | -d] [obsdate] [runnr]
```

Parameters:

−h
Return a help message only.

−v
Return the version number of scunoise

−d
Switch on debug output

obsdate
Observation directory/date (e.g. 19980210)

runnr
SCUBA observation number of noise measurement.

Examples:

```
scunoise
```

Prompt for date and run number

```
scunoise 19980210 5
```

Display the noise data for observation 5 on 19980210

```
scunoise 19980315
```

Prompt user for observation number, using data from 19980315.

Notes:

SCUNOISE has been developed for use at the JAC and therefore knows where to find the archived data. The current directory and $DATADIR are searched for files when the program is run outside of JAC.

SCUOVER
Routine to overlay the bolometer names onto a rebinned image

Description:

This routine is used to overlay the array layout onto a rebinned SCUBA image. The displayed image is read from the graphics database unless a command line value is given. In order to calculate the bolometer positions it is also necessary to read in the extinction corrected data file that was used to regrid the data (in fact any extinction corrected file can be used, possibly with strange results). By default the position of the bolometers at the start of the first integration and zero jiggle offset is plotted. Optionally, it is possible to plot the bolometer positions at any point during the observation (still with zero jiggle offset).

Usage:

`scuover`

Parameters:

DEVICE = DEVICE (Read)
The graphics device on which the bolometers are to be drawn. The global default (set with KAPPA gdset) will be used unless specified otherwise.

EXPOSURE = INTEGER (Read)
Ues the bolometer positions at the specified exposure within the specified INTEGRATION and MEASUREMENT. For SCAN/MAP data the middle of an exposure (ie scan) is used. Default is exposure 1.

EXT = NDF (Read)
The name of the extinction corrected data from which the bolometer positions should be taken.

INTEGRATION = INTEGER (Read)
Use the bolometer positions at the specified integration. Default is measurement 1.

MEASUREMENT = INTEGER (Read)
Use the bolometer positions at the specified exposure. Default is measurement 1.

MSG_FILTER = CHAR (Read)
Message filter level. Default is NORM.

NDF = NDF (Read)
The name of the regridded data set (taken from the AGI graphics database).

NAME = LOGICAL (Read)
Label with bolometer name if true, else bolometer number. The default is true. If a null response is given the bolometer label is not drawn.

STYLE = LITERAL (Read)
Plotting style to be used for the bolometers. The relevant key to use for adjusting the plotting style is '`bolometer`'. This is a synonym for curve and can be abbreviated to '`bol`'. The most useful attribute to change is the colour. Explicit control of the style of the text labels is provided using the 'text' attribute. If this attribute is not supplied all plotting styles are inherited from the '`bol`' style.

Examples:

```
scuover
```

The bolometer names will be overlaid using the default colour.

```
scuover style='colour(bol)=red' noname
```

This command will overlay bolometer numbers over the image in red.

```
scuover style='colour(bol)=yellow,font(text)=3,colour(text)=cyan'
```

Draw yellow circles but draw the labels in cyan using font 3 (italics).

```
scuover integration=2 name=!
```

Overlay the bolometer positions at the start of the second integration but do not label them

Notes:

- An image must have already been displayed before using SCUOVER.
- The image must have been displayed using an AST aware application (such as KAPPA display). Otherwise the alignment will not occur.
- The array position is always shown with zero jiggle offset.
- This routine does not take into account the use of SHIFT_DX or SHIFT_DY in rebin. (the relevant information is not stored in the rebinned image).
- Pointing shifts are taken into account.
- It is assumed that the displayed image id regridded to the default map centre. scuover aligns the image using AXIS coordinates and not SKY coordinates therefore there will be an error if incorrect sky coordinates are assumed.

Related Applications :

SURF: rebin, scupa;
KAPPA: display, gdset;
FIGARO: image

SCUPA
Show position angle of array

Description:

This script reduces the specified demodulated data file, displays the image using Az/El coordinates, and overlays the array in order to show the position angle of the array during the observation.

Usage:

`scupa [NDF]`

Parameters:

NDF = NDF (Read)

Name of raw data file. Can be located in $DATADIR. The filename will be requested if not specified on the command line.

Examples:

`scupa 19970623_dem_0012`

Reduce the data with scuquick, displays the image and overlays the array using scuover.

Notes:

Only JIGGLE/MAP, POINTING and PHOTOM observations can be used.

Related Applications :

SURF: scuquick, scuover;
KAPPA: display

Implementation Status:

- Requires KAPPA.
- All files created by this task are removed.

SCUPHOT
Reduce SCUBA PHOTOM data

Description:

This routine reduces the data for a single sub-instrument from a PHOTOM observation. For each bolometer used to look at the source the data will be analysed as follows:-

- An ndf called <bolname>_map (e.g. h7_map) will be created in the OUT file to hold the coadded data from all the integrations. If the jiggle pattern points fit a 2-d rectangular pattern then these data will be arranged as a 2-d map suitable for plotting as an image. A 2-d parabola will be fitted to the coadded image and the results written in ASCII form to FILE. If an irregular jiggle pattern is used the map will take the form of a 1-D strip.
- Second, an ndf called <bolname>_peak (e.g. h7_peak) will be created in the OUT file to hold the fitted results to the data for each integration. The results stored are the fit peak, its variance and quality and they are held as a 1-d array suitable for plotting as a graph. The fit results are also written in ASCII form to FILE, as is the coadd of all the individual fits to the data.

Usage:

```
scuphot in analysis out file
```

Parameters:

ALLBOLS = LOGICAL (Read)

By default only the observed bolometers are processed (i.e. if you observed with H7 only H7 data will be stored). If ALLBOLS is set to true then all middle beam data is processed. This is useful for examining sky noise. Note that for 2 and 3 bolometer photometry ALLBOLS must be false to avoid weighting problems for the bolometers that were observed in the left or right beams.

ANALYSIS = CHAR (Read)

The method used to determine the peak for each integration. Either average or parabola. Parabola is not recommended at this time. Alternatively, all the samples can be propagated without processing ('samples') – this will give the same result for the signal as 'average' (since 'average' returns a smoothing of all the data) but for small datasets may give a more accurate measure of the error. The discrepancy is especially noticeable for calibration measurements where N_INTEGRATIONS may only be 6 – the noise statistics on 6 averaged numbers are less reliable than those of 6 $\times$ 9 numbers (assuming 9 samples per integration).

FILE = FILENAME (Write)

The name of the ASCII output file.

IN = NDF (Read)

The name of the input file containing demodulated (extinction corrected) SCUBA data.

MSG_FILTER = CHAR (Read)
Message output level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = CHAR (Write)
The name of the HDS output file to contain the NDFs described above. This file will have the extension .sdf but this should not be specified in the name.

Examples:

```
scuphot o56_lon_ext average o56_lon_pht !
```

Process o56_lon_ext by averaging integrations. Do not write a text file containing the results.

Notes:

- ALLBOLS must be false for 2 and 3 bolometer photometry unless you know what you are doing.
- SCUPHOT can process JIGGLE/MAP data. The output is the signal for each integration for each bolometer. This is useful for checking sky removal and should not be used for performing on-source photometry on map data! This method can not be used for SCAN/MAP data.

Related Applications :

SURF: scucat

Implementation Status:
Ideally scuphot should process MAP data on a per exposure basis. Currently only per integration is supported.

SCUPLOT
Interactive display and despiking

Description:

Scuplot is a wrapper script around a number of KAPPA utilities. Since it understands the Scuba NDF file format, it hides most of the complicated syntax from the user. Mode = 'p' and 'r' are wrappers around plotting utilities and facilitate the inspection of the data of each bolometer. The utility allows change to the plot scales via the menu but will keep the scales the same for all bolometers which makes is easy to compare bolometers. Mode = 'd' allows for interactive despiking. Please read the note below the description of the menu on the use of the mouse.

Mode = 'p' or pltbol (or any p∗ link to scuplot) is a wrapper around the KAPPA utility linplot. It allows plots of a whole series of bolometers one by one, optionally overlaying them with the same bolometer from a second file. Obvious overlays are despiked on non-despiked data or data from different exposures to check the noise.

Mode = 'r' or rlinplot (or any r∗ link to scuplot) is a wrapper around the KAPPA utility mlinplot. It provides plots of sets of bolometers in a single window with optionally data from a second file in a second window. Obvious files are despiked and non-despiked data or data from different exposures to check the noise.

Mode = 'd' or dspbol (or any d∗ link to scuplot) can be used to interactively despike bolometers. While it is not as fast as a completely integrated routine would be, it makes interactive despiking much easier by hiding the cycle between linplot and change_quality for the user. The most common use is to zoom in on the region with the spike via the 'X' menu option (either typing the input or using the cursor) and subsequently to flag the offending point (just type the coordinate of the point, a range, or use the cursor; *in general the coordinate is to the right of the plotted point*). The routine will overlay the despiked data, prompt the user to accept the new set and de-zoom to the original scale. To reset a previously flagged point, flag the point again but do *not* accept it: the point will be set to GOOD again. Please read the note below the description of the menu on the use of the mouse.

For each mode the menu items are a subset of:

[M. H]	Redisplay menu
[Q]	Quit
[N]	Next bolometer
[B#]	Switch to bol #
[X min max], [X cen]	X-axis from min:max or cen+/-10
	Just 'x' activates the cursor.
[R]	Reset X-axis
[Y min max], [Y lim]	Y-axis from min:max or -lim:+lim
[U]	Reset Y-axis
[#], [#:#], [#-#]	Despike point or range of points;
	Just 'p' activates the cursor.

Option >

Note that a X center defined with the cursor or [X cen] defaults to a 20 points window around cen, the position of the spike. Using the CURSOR, the Left Mouse button always defines the point, the Right Mouse button exits the cursor task while accepting the last point clicked.

Usage:

```
scuplot [-m mode ] [-f sdf_file] [-d sdf_file2] [-s min max] [-l #] [bol [bol
[bol] ...  ]]
```

Parameters:

-h[elp]
Print the help information.

-m mode:
Select usage mode: p: plot bolometers one by one, optionally overlaid with data from the second input file (equivalent to pltbol) d: interactively despike the data for the bolometers in specified file (equivalent to dspbol). r: same as 'p' except that a whole set of bolometers is plotted in a window (equivalent to rlinplot).

-f file
name of NDF file (.sdf may be included in the name).

-d file2
name of a second file: e.g. the despiked version of the NDF file. The same bolometers will be plotted in a second window or overlaid for comparison.

-s min max
Y-axis scales for plot (can be changed via menu).

-l #
number of bolometers per window

bol
list of bolometers to plot. Type 'all' for 1..37 and 'alls' for 1..91. Can be added via menu if mode = 'r'.

Examples:

```
scuplot
```

The user will be asked for a mode and input file before proceeding.

```
scuplot -m d -f o39_lon_ext
```

Interactive despiking on o39_lon_ext.sdf (see also dspbol)

```
scuplot -m p -f s14_lon_ext 12 13 18 20 25 26 19
```

Enter p mode and use file s14_lon_ext.sdf. Plot bolometers 12,13, 18, 20, 25, 26 and 19.

Notes:

- If the overlay comes up scrambled, delete the agi_xxx files in your home directory and if that does not work also files like linplot.sdf in the /home/you/adam subdirectory.

Related Applications :

SURF: pltbol, dspbol, rlinplot, change_quality, despike;
KAPPA: linplot, mlinplot, cursor

Bugs:

Freezes when asked to plot a bad bolometer.

SCUQUICK
automate the basic SCUBA data reduction

Description:

This script attempts to automate the first 3 steps of scuba data reduction. This script runs reduce_switch, change_flat (if requested), flatfield on the data. Then for each sub-instrument extinction, scuphot (if a photometry observation), remsky (if requested) and rebin (if requested) are used. The output name for each task is related to the task and current sub-instrument (see Notes).

Usage:

```
scuquick [-quick] [-tau|notau] NDF [PARAM=value]
```

Parameters:

−**help**
Print the help message.

−**quick**
This flag makes all of the SURF tasks run with the 'accept' flag (see SUN/95) so that default values are accepted for all parameters unless specified on the command line.

−**quiet**
Hide all messages generated by the script (note this is not the same as using MSG_FILTER=quiet which hides messages from the tasks)

−**tau value**
Run extinction with a tau of 'value'. (the LST range is set automatically since we are using a constant tau) Note that this is dangerous when processing multiple sub-instruments. (Same as −−tau=value).

−**notau**
Run extinction with a zero value of tau (the LST range is set for you). This is equivalent to using the −−tau=0.0 option.

−**sub sub_instrument**
Only process the specified sub instrument. This is equivalent to setting the SUB_INSTRUMENT parameter explicitly. (same as −−sub=sub_instrument)

−**change_flat**
Invoke the change_flat task after reduce_switch.

−**clip**
Invoke the scuclip task after extinction.

−**remsky**
Invoke the remsky task after extinction (or scuclip).

−**rebin**
Invoke the rebin package after extinction (or remsky)

NDF
The required dataset. This parameter is optional – reduce_switch will ask for an input file if no value is given.

ADAM parameters = Any

Any parameters accepted by the individual routines as long as they use PARAM=VALUE format.

Examples:

```
scuquick
```

When run this way, reduce_switch will ask for the input file name and for the output root name. flatfield will then run followed by extinction on each sub-instrument. Each task will ask questions as needed.

```
scuquick −quick
```

Same as scuquick except that defaults will be assumed for all parameters that have defaults.

```
scuquick −rebin
```

Process as for scuquick except that rebin is run on each sub-instrument.

```
scuquick −quick jun02_dem_0002
```

Process the input file jun02_dem_0002.sdf, accepting all defaults.

```
scuquick −quick jun02_dem_0003 MSG_FILTER=QUIET
```

Process jun02_dem_0003.sdf, accepting all defaults and turning off all but the most important messages from the SURF tasks.

```
scuquick −quick −notau −rebin temp OUT=root
```

Process temp.sdf with zero extinction correction, accept all defaults, use 'root' as the default filename and regrid.

```
scuquick −remsky −change_flat −−sub=long
```

Run the remsky and change_flat tasks in addition to the standard tasks but only process the LONG sub-instrument.

```
scuquick −rebin −quick MSG_FILTER=QUIET PIXSIZE_OUT=1 test OUT=temp
```

Process test.sdf. Accept all defaults. Use 'temp' as the filename root. Regrid all data onto a 1 arcsecond grid. Hide all messages from the SURF tasks.

Notes:

Given a rootname (specified with OUT=root or by accepting the default value offered by reduce_switch) SCUQUICK produces the following files (identical to the files produced

with SCUBA_SUFFIX=long):

- root.sdf from reduce_switch
- root_flat.sdf from flatfield
- root_<*sub*>_ext.sdf from extinction (one for each sub)
- root_<*sub*>_sky.sdf from remsky (with the –remsky switch)
- root_<*sub*>_reb.sdf from rebin (with the –rebin switch)
- root_<*sub*>_pht.sdf from scuphot (if processing a PHOTOM observation)
- root_<*sub*>_pht.dat from scuphot (if processing a PHOTOM observation)

Where <*sub*> is the first three letters of the sub-instrument name. Using the −tau switch is dangerous when processing multiple sub-instruments since the extinction changes with wavelength.

- Command line options can be abbreviated.
- Skydip observations are recognised.
- Options that take values can be used either as '−flag option' or as '−−flag=option'

Prior requirements :

- The NDF perl module must exist (this should be installed by your system administrator if it is missing).

Related Applications :

SURF: reduce_switch, change_flat, flatfield, extinction, remsky, rebin, scuphot, scuclip

SCUSETENV
Set the startup environment variables for SURF

Description:

This script sets the standard DATADIR and SCUBA_PREFIX environment variables given a UT date.

Usage:

```
scusetenv [UTdate]
```

Examples:

```
scusetenv
```

Set DATADIR and SCUBA_PREFIX for the current UT date

```
scusetenv 19980201
```

Set DATADIR and SCUBA_PREFIX for the data observed on date 19980201

Notes:

- Currently this routine only works for the JAC and JCMT systems. This is because the data are stored in standard directories and indexed by YYYYMMDD UT date.
- ORAC_DATA_IN environment variable is also set (only relevant for users of the ORAC-DR pipeline)
- If this routine is run from a non-JAC/JCMT site DATADIR will not be set but SCUBA_PREFIX will be set.

Parameters :

UTdate = YYYYMMDD format string (Optional) The UT date of the data to be processed (in YYYYMMDD format). The default value is to use the current UT date

Implementation Status:

This script should be sourced (not executed) since the environment variables should be set after the script has been read.

SCUSHIFT
Correct for data shift error in demodulated data files

Description:

This script corrects for the DAQ communications error and shifts the data from ADC cards along by a specified amount. Since all channels are read from a particular ADC card but only some of them are actually stored in the demodulated data file, the shift may result in fewer bolometers being stored for a given sub-instrument.

Usage:

```
scushift [-h] NDF card shift
```

Parameters:

-h Help information

NDF (Given)
The input files to be modified.

card
The letter identifying the A-to-D card (allowed values are A to I)

shift
The number of bolometers to shift by. A negative shift moves D1 to D16 (for example) and a positive shift D1 to D2. In most cases a negative shift is required (usually -1).

Examples:

```
scushift test i -2
```

Move the I card data of test.sdf by minus 2 bolometers

```
scushift test2 h 1
```

Move the H-card data by plus 1 bolometer.

Notes:

- extinction must not have been run on the input NDF.
- Arguments are requested if they are missing from the command line
- If the system stores channels 1,2,3,6,7,8,10 but we know that we have a shift of -1 in the system (ie an extra byte is present). This implies that we have actually stored channels 16,1,2,5,6,7,9 and if only bolometers 1,2,6,7 are from the required sub-instrument we have to throw away data from channels 15,5 and 9.
- The DAQ hardware fault always introduced extra bytes and therefore a negative shift should be used in scushift.
- Currently photometry data is not corrected properly (the PHOT_BB extension is not modified so the correct bolometer will not be extracted by scuphot). This can be overcome by using the ALLBOLS parameter in scuphot.

SDIP
Reduces and displays skydip data

Description:

This script first runs the skydip task in order to fit the sky parameters to the data. The sky data and model are written to files and are then displayed using KAPPA's linplot.

Usage:

```
sdip [NDF]
```

Parameters:

NDF = NDF (Read)

The name of the skydip data file, or, if SCUBA_PREFIX is set, the number of the observation (raw demodulated data only). The input data file can be the output from reduce_switch or the raw skydip data. Can be located in $DATADIR. The filename will be requested if not specified on the command line.

Examples:

```
sdip 19970623_dem_0008
```

Reduce the skydip data in 19970623_dem_008.sdf and plots the result.

Related Applications :

SURF: skysum, skydip;
KAPPA: linplot

Implementation Status:

- Requires KAPPA.
- All files created by this task are removed.

SETBOLWT
Calculate or set bolometer weights

Description:

This routine sets the bolometer weights. It can do this in two ways:

1. Calculate the statistics for each bolometer then generate the weights relative to the central pixel. Should not be used when a strong source is present. The weights are calculated by using KAPPA stats to calculate the standard deviation of each bolometer in turn. The weight is defined as the relative variance between this bolometer and the reference bolometer.

2. Read the weights from a text file using the -wtfile option.

Writes to the BOLWT extension. This extension is then read by rebin.

Multiple files can be referenced to the first file by specifying multiple files on the command line or by using a rebin-style input file and the -filelist option. In conjunction with the `-wtfile` option all input files are given the same weights.

Usage:

```
setbolwt [-h] [-wtfile=] [-filelist=] filenames...
```

Parameters:

−h
Return a usage message.

−wtfile=file
An ASCII text file containing the weights, one weight per line corresponding to the order of bolometers stored in the file.

−filelist=file
An ASCII text file containing a list of files to be processed. There must be one file per line and it must be in a form acceptable to rebin (ie comments can be included).

filenames
List of filenames to be processed. Wild cards can be used. eg ∗_lon_ext.sdf.

Examples:

```
setbolwt
```

The user will be prompted for a list of input NDFs. The weights will be calculated by setbolwt.

```
setbolwt -wtfile=weights.dat file1
```

Set the weights in file1.sdf from the list contained in weights.dat

```
setbolwt file1 file2 file3 file4
```

Calculate the weights of each bolometer in all four files relative to the central pixel in file1.sdf.

```
setbolwt -wtfile=wt.dat -filelist=rebin.inp
```

Set the weights of the files listed in rebin.inp to those stored in wt.dat (same weights for each file).

Notes:

- Input files must have been extinction corrected so that only one sub-instrument is present per file.
- When multiple files are used bolometers are compared to the central bolometer of the first file.
- If source signal is present in any bolometer at a level significantly above the noise, the automatic weighting will be skewed (in fact the bolometer with the source signal will be down-weighted relative to all the others since the standard deviation on the bolometer will be much higher.). The weights must be set via an external file in this case.

Related Applications :

SURF: rebin
KAPPA: stats

SIGCLIP
Clip a dataset at n-sigma

Description:

This program uses KAPPA stats to calculate mean and standard deviation of an NDF. It then uses KAPPA thresh to set the values at ±n-sigma to BAD. The clipped data are written to NDF_clip.sdf.

Usage:

```
sigclip NDF SIGMA
```

Parameters:

NDF (Given)
The required dataset

SIGMA = REAL (Given)
The clipping level

Examples:

```
sigclip test 3.0
```

Clips test.sdf at ±3.0 sigma and writes the data to test_clip.sdf.

Notes:

The $KAPPA_DIR environment variable must point to the location of the KAPPA binaries (this is usually done during a Starlink login).

Related Applications :

SURF: scucat, scuphot;
KAPPA: stats, thresh

Implementation Status:

- The program must have two arguments. Parameters are not requested if an argument is omitted from the command line.

SKYDIP
calculate sky properties from SCUBA skydip data

Description:

This application takes raw SKYDIP data and calculates tau, eta_tel and B by fitting. Sky brightness temperatures are calculated for different airmasses and then fitted with a model of the sky.

Usage:

```
skydip in sub_instrument t_cold eta_tel b_fit out model_out
```

Parameters:

IN = NDF (Read)
The name of the skydip data file, or, if SCUBA_PREFIX is set, the number of the observation (raw demodulated data only). The input data file can be the output from reduce_switch or the raw skydip data. The file can be located in $DATADIR.

B_ERR = REAL (Write)
Error in the fitted value of B. Set to bad if the fit has failed.

B_FIT = REAL (Write)
The fitted value of the B parameter (Filter transmission). Set to bad if the fit has failed.

B_VAL = REAL (Read)
The B parameter (filter transmission). This efficiency factor must be between 0 and 1. A negative value allows this parameter to be free.

CVAR = LOGICAL (Read)
This parameter governs whether the points are fitted with a constant variance for all points (true) or the variance derived from the scatter in the individual integrations (false). The value used for the fixed variance is the mean of all the calculated variances.

ETA_TEL = REAL (Read)
The telescope efficiency. If available the current telescope value is used as the default. Values must be between 0 and 1.0. A negative value allows this parameter to be free. For data taken before 26 April 2000, the default values supplied for 850 and 450 are provided by the routine rather than being read from the FITS header.

ETA_TEL_ERR = REAL (Write)
Error in the fitted value of ETA_TEL. Set to bad if the fit has failed.

ETA_TEL_FIT = REAL (Write)
The fitted value of ETA_TEL. Set to bad if the fit has failed.

GOODFIT = LOGICAL (Write)
Flag to indicate whether the fit was good (TRUE) or bad (FALSE).

MODEL_OUT = CHAR (Write)
The name of the output file that contains the fitted sky temperatures.

MSG_FILTER = CHAR (Read)
Message filter level. Allowed values are QUIET, NORM and VERB. Default is NORM. There are no verbose messages.

OUT = CHAR (Write)
The name of the output file that contains the measured sky temperatures.

RESIDUAL = REAL (Write)
Absolute difference between the model and the data (in Kelvin). i.e. $\sum abs(Data - Model)$

SIGMA = REAL (Write)
Standard deviation of the residuals of the fit (Kelvin).

SUB_INSTRUMENT = CHAR (Read)
The name of the sub-instrument whose data are to be selected from the input file and fitted. Permitted values are SHORT, LONG, P1100, P1350 and P2000

TAUZ_ERR = REAL (Write)
Error in the fitted value of TAUZ. Set to bad if the fit has failed.

TAUZ_FIT = REAL (Write)
The fitted sky opacity for the selected sub instrument.

T_COLD = REAL (Read)
Temperature of the cold load. The default value is taken from the input file. (This parameter is not required for data that has been processed by reduce_switch.)

T_HOT = REAL (Read)
Temperature of the hot load. The default value is taken from the input file. (This parameter is not required for data that has been processed by reduce_switch.)

WAVELENGTH = REAL (Write)
The wavelength of the selected sub instrument.

XISQ = REAL (Write)
The reduced χ^2 of the fit. The nature of the error determination forces the reduced χ^2 to be approximately 1. The SIGMA parameter provides a better guide to the goodness of fit.

Examples:

```
skydip jun10_dem_0002 short \
```

Process the short sub-instrument using the default value for T_COLD and allowing ETA_TEL and B to be free parameters. No output files are written.

```
skydip 19970610_dem_0003 long eta_tel=0.9 out=sky model_out=model \
```

Process the long wave sub-instrument with ETA_TEL fixed at 0.9 and B free. Write the sky temperature to sky.sdf and the fitted model to model.sdf.

Notes:

If the input file is not found in the current directory, the directory specified by the DATADIR environment variable is searched. This means that the raw data does not have to be in the working directory. In addition `IN` accepts a number. This number is converted to a demodulated data filename by prepending it with information specified in the SCUBA_PREFIX environment variable. This filename expansion only works for demodulated data (ie data containing `'_dem_'`). The `'_dem_'` is assumed and should not be present in SCUBA_PREFIX.

If the `CVAR` parameter is true the reduced χ^2 value can not be used to compare the goodness of fit between datasets.

Both RASTER and DISCRETE skydips are supported.

See Appendix I for more information on skydips.

Related Applications :

SURF: extinction, sdip, skysum

SKYSUM
Produce one-line summary of SCUBA skydip observations

Description:

Skysum goes through all the sdf files in the current directory and, optionally, DATADIR (defined in an environment variable) and summarizes files containing skydip observations.

In the absence of the −all flag, a numeric range is requested. This range only has an effect on raw data or reduced files which have the run number embedded into the file name. Filenames with no numbers are treated as scan 0.

Usage:

```
skysum [-h] [-demod] [-reduced] [-all|[-begin nn -end nn]]
```

Parameters:

−**h[elp]**
: Return a help message only. More help can be obtained by using 'showme sun216' or 'scuhelp skysum'.

−**all**
: List all skydip files in the current directory and $DATADIR

−**demod**
: Only list demodulated data files (signified by _dem_ file name)

−**reduced**
: Only list reduced data files (signified by _red_ file name)

−**begin nn**
: First scan number to be considered (same as −−begin==nn)

−**end nn**
: Final scan number to be considered (same as −−end=nn)

Examples:

```
skysum
```

Ask for a range of scan numbers and then give a summary of every skydip file matching this criterion in DATADIR and the current directory.

```
skysum −all
```

Generate a summary of all skydip files in the current and DATADIR directory.

```
skysum −−begin=5 −−end=100
```

Generate a summary of all skydip data from scans 5 to 100 inclusive.

```
skysum −all −reduced
```

Produce a one line summary of all reduced skydip (_red_) files.

```
skysum −all −reduced > log.txt
```

Produce a one line summary of all the reduced skydip files and store the output in the text file log.txt (note this example is shell specific).

```
skysum −all −reduced −demod
```

Produce a summary of all reduced (_red_) and demodulated (_dem_) skydip files (ie not files produced during off-line data reduction).

Notes:

- skysum only displays skydip data.
- Files are drawn from the current working directory and the directory indicated by the $DATADIR environment variable.
- Data reduced by the off-line system will all be treated as run 0 for the purposes of listing unless numbers are present in the filename.
- The output can be stored in a file by using unix redirection as long as the search range is fully specified (either as '−all' or with '−begin' and '−end').
- Command line options can be abbreviated.
- Options that take values can be used either as '−flag option' or as '−−flag=option'

Related Applications :

SURF: sculog, photsum, mapsum, obssum, pointsum, skydip

D Reducing data at the Joint Astronomy Centre

This section describes the location of SCUBA data at the Joint Astronomy Centre.

D.1 During Observing

At the JCMT the SCUBA data is written to a unix disk upon completion of each observation. Both the demodulated and reduced data are written to a directory in `/jcmtarchive`. Usually the directory name is constructed from the UT date in YYYYMMDD format. i.e. on June 27th 1997 the directory will be called 19970627. The data should not be copied into the working directory (primarily to save disk space) and can be accessed by setting $DATADIR:

```
% setenv DATADIR /jcmtarchive/19970627
```

This can be automated by using the scusetenv command:

```
% scusetenv
Setting up SURF for UT date 19990618
SCUBA_PREFIX set to 19990618
DATADIR has been set to /jcmtarchive/19990618
ORAC_DATA_IN has also been set to this value
```

D.2 Hilo

SCUBA data is transferred to Hilo every afternoon. This data is stored in `/scuba/` in semester directories (eg `/scuba/m99a` for data taken during semester M99A) containing a UT directory and an `ro/UT` directory. Data can be accessed by setting $DATADIR:

```
% setenv DATADIR /scuba/m99a/19990615/
```

or

```
% setenv DATADIR /scuba/m98b/ro/19980927/
```

Note that, unlike at the summit, the demodulated and reduced data are in separate directories. The directories containing the demodulated data also contain index and log files which summarise the observations.

This can be automated by using the scusetenv command:

```
% scusetenv 19990205
Setting up SURF for UT date 19990205
SCUBA_PREFIX set to 19990205
DATADIR has been set to /scuba/m99a/19990205
ORAC_DATA_IN has also been set to this value
```

E File naming and data structures

Unless instructed otherwise in the observation definition file (ODF) the SCUBA software writes a demodulated data file (essentially the raw data) and a reduced observation (RO) file to disk.

E.1 Naming Conventions

SCUBA data files have the following naming convention: *string_obs type_run number*.sdf. Where string is either the UT date of the observation in YYYYMMDD format or the PATT ID for the observation.

Therefore the first data from 23rd June 1997 will be in files

```
% ls
19970623_dem_0001.sdf
19970623_red_0001.sdf
```

for the demodulated and reduced data respectively.

The RO file contains the reduced data calculated by the telescope during the observation and supplies a first look at the data. At present the on-line system does not produce calibrated publishable quality images – the data should be re-processed using the demodulated data and SURF.

E.2 Structure of RO files

Since SCUBA can produce data from more than one sub-instrument simultaneously and yet only one file is wanted for each observation, the RO files are in fact HDS container files containing NDFs. In general there is one NDF for each sub-instrument used plus one NDF containing all the observation parameters (it is a blank NDF containing a FITS extension).

For example, a map observation with the LONG and SHORT wave array would produce an RO file with the following structure:

```
% hdstrace m97az98_red_0001
M_970308_50  <SCUDR_MAP>

    LONG  <NDF>
        ....image from long-wave array

    SHORT <NDF>
        ....image from short-wave array

    HEADER <NDF>
        ....Observation parameters in FITS extension
```

The image from the long wave array would be displayed in KAPPA with:

```
% display clear axes m97az98_red_0001.long
```

and the FITS information would be displayed with:

```
% fitslist m97az98_red_0001.header
```

In addition to one NDF per sub-instrument, there is also one NDF per measurement. For example, the RO file from a FOCUS observation would contain an NDF for each FOCUS position names MEAS_1, MEAS_2 etc. – this is the case for FOCUS and ALIGN observations. Skydip data is slightly different since the names of the NDFs are of the form SUB_WAVELENGTH (i.e. SHORT_450 and LONG_850).

If an observation is only using a particular bolometer (eg a FLATFIELD or PHASE observation) there will be an NDF for the bolometer (eg H7) rather than for the array as a whole.

E.3 Structure of demodulated files

Demodulated data files are much more complicated as they have to contain a full description of the state of SCUBA for each observation. Here is an example trace (the map of 3C279 used in the example):

```
% hdstrace apr8_dem_0059

STRUCT  < >

   MORE           <EXT>           {structure}
      FIGARO         <FIGARO_EXT>    {structure}
         {structure is empty}

      SCUCD          <SCUCD_ST>      {structure}
         JIGL_X(64)     <_REAL>         5.3457,0,-5.3457,-8.033999,
                                        ... 0,-5.3457,-8.033999,-2.6883,2.6883
         JIGL_Y(64)     <_REAL>         12.36,12.36,12.36,10.815,10.815,
                                        ... -9.27,-10.815,-10.815,-10.815
         DEC1           <_REAL>         0
         DEC2           <_REAL>         0
         LST_STRT(2,4,3,1)  <_DOUBLE>   3.23079147492436,3.2322998582771,
                                        ... 3.26511400298336,3.26350802081885
         RA1            <_REAL>         0
         RA2            <_REAL>         0

      SCUBA          <SCUBA_ST>      {structure}
         BOL_CALB(16,9)  <_REAL>        0.858,0.9311,0.9499,1.002,0.9585,
                                        ... 1.213,0.928,1.304,1,1,1,1,1,1,0
         BOL_DU3(16,9)  <_REAL>         57.08,45.9,36.15,24.64,14.55,3.62,
                                        ... -15.78,9.047,-54.65,0,0,0,0,0,0
         BOL_DU4(16,9)  <_REAL>         -28.14,-35.91,-41.46,-49.62,
                                        ... 63.89,77.76,71.16,0,0,0,0,0,0
         BOL_QUAL(16,9)  <_INTEGER>     0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
                                        ... 0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,1,1
         BOL_TYPE(16,9)  <_CHAR*20>     'SHORT','SHORT','SHORT','SHORT',
                                        ... 'P...','P1350_DC','P1100_DC','BAD'
         BOL_ADC(128)   <_INTEGER>      1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,
                                        ... 8,8,8,8,8,8,8,8,9,9,9,9,9,9,9,9
```

```
      BOL_CHAN(128)  <_INTEGER>      1,2,3,4,5,6,7,8,9,10,11,12,13,14,
                                     ... 12,13,14,15,16,1,2,3,4,5,6,7,8,9
      FLAT_ADC       <_INTEGER>      0
      FLAT_CHN       <_INTEGER>      0
      FLAT_IND       <_INTEGER>      0
      PHOT_BB        <_INTEGER>      0
      DEM_PNTR(2,4,3,1)  <_INTEGER>   1,17,49,33,65,81,113,97,129,145,
                                      ... 257,273,305,289,321,337,369,353
      ISTART(62,2,4,3,1)  <_INTEGER>   20,19,18,18,18,18,18,15,14,13,
                                       ... 14,13,14,16,22,23,31,41,0,0,0,0
      NPIX(62,2,4,3,1)  <_INTEGER>   2,5,12,13,28,29,29,32,33,34,34,35,
                                     ... 37,36,34,32,30,24,23,14,3,0,0,0,0
      POINTER(62,2,4,3,1)  <_INTEGER>   2,4,9,21,34,62,91,120,152,185,
                                        ... 52804,52807,52807,52807,52807

   FITS(164)      <_CHAR*80>      'ACCEPT  = 'not used'           / ac...'
                                  ... 'WAVE_5  =                 ...','END'

 DATA_ARRAY(5,128,384)  <_REAL>   0.011504,0.000014,0.029308,0.000015,0,
                                 ... 0.006727,0.000003,0.022551,0.000003,0
                                     ... 0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,1,1

End of Trace.
```

From this we can see that there is a 3 dimensional data array and 4 NDF extensions. Each will be described in turn:

DATA_ARRAY

The data array contains three dimensions. The first dimension is a vector of size 5 and relates to the chop data, the chop error, the calibrator data the calibrator error and the quality respectively. The second dimension is the bolometers and the third is the number of measurements (ie number of jiggle positions $\times$ number of integrations $\times$ 2 (number of nods)). These data can be displayed to examine each component in turn (for example checking whether the OFF position contains a source) by using NDF sections.

FIGARO extension

The FIGARO extension is not used by the SURF package.

SCUCD extension

The SCUCD extension contains information on the position of the telescope for each sample along with the local sidereal time of each sample.

SCUBA extension

The SCUBA extension contains the flatfield information (position of the bolometers, subintrument of bolometers, quality of bolometers and A-to-D card). There are also arrays to aid in the location of each jiggle in the data array (DEM_PNTR).

FITS extension

The FITS Extension is described in the next appendix.

In addition a new extension is created by the SURF package itself. This extension (called REDS for historical reasons) contains beam weights for chopping, and pointing corrections. In general this extension is created for PHOTOMetry observations and by the change_pointing task.

A more detailed description of the file format can be found in Starlink System Note 72.

F FITS keywords

FITS information is stored in the NDF FITS extension of all SCUBA NDFs. This information can be accessed by using the KAPPA fitslist command (or, less conveniently, with hdstrace). This appendix gives a full listing of all the information stored in the FITS header.

F.1 Demodulated data

All observation parameters are stored in the NDF FITS extension. They can be accessed using the KAPPA task fitslist. The same information is stored in the reduced files but in the HEADER component.

```
% fitslist apr8_dem_0059
ACCEPT  = 'not used'           / accept update; PROMPT, YES or NO
ALIGN_AX= 'not used'           / Alignment measurements in X or Y axis
ALIGN_SH=                   -1 / Distance between successive alignment offsets(
ALT-OBS =                 4092 / Height of observatory above sea level (metres)
AMEND   =             1.117139 / Airmass at end of observation
AMSTART =             1.123245 / Airmass at start of observation
APEND   =             625.0427 / Air pressure at end of observation (mbar)
APSTART =             624.7985 / Air pressure at start of observation (mbar)
ATEND   =             0.158733 / Air temp. at end of observation (C)
ATSTART =             0.305252 / Air temp. at start of observation (C)
BOLOMS  = 'SHORT,LONG'         / Names of bolometers measured
CALIBRTR=                    T / Internal calibrator is on or off
CAL_FRQ =                1.984 / Calibrator frequency (Hz)
CENT_CRD= 'RB      '           / Centre coordinate system
CHOP_CRD= 'AZ      '           / Chopper coordinate system
CHOP_FRQ=              6.94444 / Chopper frequency (Hz)
CHOP_FUN= 'SCUBAWAVE'          / Chopper waveform
CHOP_PA =                   90 / Chopper P.A., 0 = in lat, 90 = in long
CHOP_THR=                   60 / Chopper throw (arcsec)
DATA_DIR= 'apr8    '           / Sub-directory where datafile was stored
DATA_KPT= 'DEMOD + RESAMPLED'  / The type of data stored to disk
END_AZD =              165.715 / Azimuth at end of observation (deg)
END_EL  =                   -1 / Elevation of last SKYDIP point (deg)
END_ELD =              63.6382 / Elevation at end of observation
EQUINOX =                 2000 / Equinox of mean coordinate system
EXPOSED =             3.022848 / Exposure per pixel (seconds)
EXP_NO  =                    4 / Exposure number at end of observation
EXP_TIME=             1.007616 / Exposure time for each basic measurement (sec)
E_PER_I =                    4 / Number of exposures per integration
FILTER  = '450N:850N'          / Filters used
FOCUS_SH=                   -1 / Shift between focus measurements (mm)
```

```
GAIN    =                   10 / Programmable gain
HSTEND  = '23:43:50.003365'    / HST at end of observation
HSTSTART= '23:35:09.999847'    / HST at start of observation
HUMEND  =                   22 / Humidity (%) at end of observation
HUMSTART=                   23 / Humidity (%) at start of observation
INSTRUME= 'SCUBA   '           / Name of instrument used
INT_NO  =                    3 / Integration number at end of observation
JIGL_CNT=                   64 / Number of offsets in jiggle pattern
JIGL_NAM= 'JCMTDATA_DIR:tile_64_3p09.JIG' / File containing jiggle offsets
J_PER_S =                   16 / Number of jiggles per switch position
J_REPEAT=                    1 / No. jiggle pattern repeats in a switch
LAT     = '-005:31:08.40'      / Object latitude
LAT-OBS =        19.8258323669 / Latitude of observatory (degrees)
LAT2    = 'not used'           / Object latitude at MJD2
LOCL_CRD= 'RB      '           / Local offset coordinate system
LONG    = '+012:53:35.84'      / Object longitude
LONG-OBS=        204.520278931 / East longitude of observatory (degrees)
LONG2   = 'not used'           / Object Longitude at MJD2
MAP_HGHT=                  180 / Height of rectangle to be mapped (arcsec)
MAP_PA  =                    0 / P.A. of map vertical, +ve towards +ve long
MAP_WDTH=                  180 / Width of rectangle to be mapped (arcsec)
MAP_X   =                    0 / Map X offset from telescope centre (arcsec)
MAP_Y   =                    0 / Map Y offset from telescope centre (arcsec)
MAX_EL  =                   -1 / Max elevation of sky-dip (deg)
MEANDEC =            -5.790909 / -5:47:27.27173 = approx. mean Dec. (deg)
MEANRA  =             194.0517 / 194:03:06.053467 = approx. mean R.A. (deg)
MEAS_NO =                    1 / Measurement number at end of observation
MIN_EL  =                   -1 / Min elevation of sky-dip (deg)
MJD1    =                   -1 / Modified Julian day planet at RA,DEC
MJD2    =                   -1 / Modified Julian day planet at RA2,DEC2
MODE    = 'MAP     '           / The type of observation
N_INT   =                    3 / No. integrations in the observation
N_MEASUR=                    1 / No. measurements in the observation
OBJECT  = '3c279   '           / Name of object
OBJ_TYPE= 'PLANET  '           / Type of object
OBSDEF  = '3c279_map.obs'      / The observation definition file
OBSERVER= 'Captain Nemo'       / The name of the observer
PROJ_ID = 'scuba   '           / The project identification
RUN     =                   59 / Run number of observation
SAM_CRDS= 'NA      '           / Coordinatesystem of sampling mesh
SAM_DX  =                   -1 / Sample spacing along scan direction (arcsec)
SAM_DY  =                   -1 / Sample spacing perp. to scan (arcsec)
SAM_MODE= 'JIGGLE  '           / Sampling method
SAM_PA  =                   -1 / Scan P.A. rel. to lat. line; 0=lat, 90=long
SPK_NSIG=                    0 / N sigmas from fit of spike threshold
SPK_RMVL=                    T / Automatic spike removal
SPK_WDTH=                    0 / Assumed width of spike
START_EL=                   -1 / Elevation of first SKYDIP point (deg)
STATE   = 'Terminating         :   RECORD_DATA RESET_DATA_SIZE RECORD_DATA' /SC
STEND   = '12:28:40.78857'     / ST at end of observation
STRT_AZD=              161.247 / Azimuth at observation start (deg)
STRT_ELD=               63.081 / Elevation at observation start (deg)
STSTART = '12:19:59.36714'     / ST at start of observation
SWTCH_MD= 'BMSW    '           / Switch mode of observation
```

```
SWTCH_NO=                    1 / Switch number at end of observation
S_PER_E =                    2 / Number of switch positions per exposure
TELESCOP= 'JCMT    '           / Name of telescope
TEL_OPER= 'Ned Land'           / Telescope operator
UTDATE  = '1997:4:8'           / UT date of observation
UTEND   = '9:43:49.99992'      / UT at end of observation
UTSTART = '9:35:09.999847'     / UT at start of observation
VERSION =                    0 / SCUCD version
ALIGN_DX=           -0.414241 / SMU tables X axis alignment offset
ALIGN_DY=            0.556058 / SMU tables Y axis alignment offset
ALIGN_X =             -4.0787 / SMU tables X axis
ALIGN_Y =             4.16459 / SMU tables Y axis
AZ_ERR  =                    0 / Error in the telescope azimuth
CHOPPING=                    T / SMU Chopper chopping state
EL_ERR  =                    0 / Error in the telescope elevation
FOCUS_DZ=           -0.113297 / SMU tables Z axis focus offset
FOCUS_Z =                 -16 / SMU tables Z axis
SEEING  =               0.316 / SAO atmospheric seeing
SEE_DATE= '9704072245'         / Date and time of SAO seeing
TAU_225 =               0.096 / CSO tau
TAU_DATE= '9704080210'         / Date and time of CSO tau
TAU_RMS =             3.0E-03 / CSO tau rms
UAZ     =             3.35413 / User azimuth pointing offset
UEL     =             2.04832 / User elevation pointing offset
UT_DATE = ' 8 Apr 1997'        / UT date at start of observation
BAD_LIM =                   32 / No. spikes before quality set bad
CALIB_LG=                    5 / Lag of internal calibrator in samples
CALIB_PD=            64.02849 / Period of internal calibrator in samples
CHOP_LG =                    4 / Chop lag in samples
CHOP_PD =             18.2927 / Chop period in samples
CNTR_DU3=                    0 / Nasmyth dU3 coord of instrument centre
CNTR_DU4=                    0 / Nasmyth dU4 coord of instrument centre
FILT_1  = '450     '           / Filter name
FILT_2  = '850     '           / Filter name
FILT_3  = 'not used'           / Filter name
FILT_4  = 'not used'           / Filter name
FILT_5  = 'not used'           / Filter name
FLAT    = 'noiseflat.dat'      / Name of flat-field file
JIG_DSCD=                   -1 / No. samples discarded after jiggle movement
L_GD_BOL= 'H7      '           / Bol. to whose value LW guard ring is set
L_GUARD =                    F / Long wave guard ring on or off
MEAS_BOL= 'not used'           / Bolometers  actually measured in observation
N_BOLS  =                  128 / Number of bolometers selected
N_SUBS  =                    2 / Number of sub-instruments used
PRE_DSCD=                    0 / No. of samples discarded before chop movement
PST_DSCD=                    0 / No. samples discarded after chop movement
REBIN   = 'LINEAR  '           / Rebinning method used by SCUIP
REF_ADC =                   -1 / A/D card of FLATFIELD reference bolometer
REF_CHAN=                   -1 / Channel of FLATFIELD reference bolometer
SAM_TIME=                  123 / A/D sample period in ticks (64musec)
SIMULATE=                    F / True if data is simulated
SKY     = 'skydip_startup.dat' / Name of sky opacities file
SUB_1   = 'SHORT   '           / SCUBA instrument being used
SUB_2   = 'LONG    '           / SCUBA instrument being used
```

```
SUB_3   = 'not used'           / SCUBA instrument being used
SUB_4   = 'not used'           / SCUBA instrument being used
SUB_5   = 'not used'           / SCUBA instrument being used
S_GD_BOL= 'D9      '           / Bol. to whose value SW guard ring is set
S_GUARD =                    F / Short wave guard ring on or off
TAUZ_1  =                    0 / Zenith sky optical depth
TAUZ_2  =                    0 / Zenith sky optical depth
TAUZ_3  =                    0 / Zenith sky optical depth
TAUZ_4  =                    0 / Zenith sky optical depth
TAUZ_5  =                    0 / Zenith sky optical depth
T_AMB   =                   -1 / The ambient air temperature (K)
T_COLD_1=                   -1 / Effective temperature of cold load (K)
T_COLD_2=                   -1 / Effective temperature of cold load (K)
T_COLD_3=                   -1 / Effective temperature of cold load (K)
T_COLD_4=                   -1 / Effective temperature of cold load (K)
T_COLD_5=                   -1 / Effective temperature of cold load (K)
T_HOT   =                   -1 / The temperature of the hot load (K)
T_TEL   =                   -1 / The temperature of the telescope
USE_CAL =                    F / .TRUE. if dividing chop by cal before rebin
WAVE_1  =                  442 / Wavelength of map (microns)
WAVE_2  =                  862 / Wavelength of map (microns)
WAVE_3  =                    0 / Wavelength of map (microns)
WAVE_4  =                    0 / Wavelength of map (microns)
WAVE_5  =                    0 / Wavelength of map (microns)
END
```

F.2 Rebinned data

The rebinned data files contain the following. Note that the astrometry information is not stored in the FITS extension.

```
% fitslist n59_reb_lon
OBJECT  = '3c279   '           / name of object
FILE_1  = 'n59_sky_lon'        / name of input datafile
SYSTEM  = 'EQUATORIAL(2000.0)' / sky coordinate system
LONG    =      3.3867510541917 / centre longitude (radians)
LAT     =    -0.10104535223053 / centre latitude (radians)
TELESCOP= 'JCMT-Hawaii'        / name of telescope
INSTRUME= 'SCUBA   '           / name of instrument
WAVELEN =             0.000862 / Wavelength of the observation (metres)
FREQ    =      347787074245.94 / Frequency of observation (Hz)
FILTER  = '450     '           / Filter name
SCUPROJ = 'RJ      '           / SCUBA output coordinate system
SCUPIXSZ=                    1 / Pixel size (arcsec)
DATE-OBS= '08/04/97'           / Date of first observation
DATE    = '2000-07-06T02:35:49'/ file creation date (YYYY-MM-DDThh:mm:ss UTC)
ORIGIN  = 'SCUBA User Reduction Facility (SURF)'/  Origin of the FITS file
OBSRA   =      194.04654166665 / RA of map centre (degrees; deprecated)
OBSDEC  =     -5.7894722222218 / Dec. of map centre (degrees; deprecated)
```

G Description of despiking method used by despike

The despike routine works in the following way:

- Create an output grid with a cell of size one quarter of the beamwidth ($\lambda/4D$).
- Calculate the position of every data point in the output coordinate frame and place it in the corresponding cell of the output grid.
- For each cell/bin calculate statistics (mean, median and standard deviation).
- If neither smoothing nor a plot are required simply remove spikes from each cell. Spikes are found if a point in a given cell is further than NSIGMA from the mean of the data in the cell. Spikes are marked bad.
- Write the despiked data to disk (one output file for each input file).

Displaying the data in 3 dimensions (x, y grid and n data points for each bin) would be far too cluttered so the 2-dimensional grid is transformed to a 1-dimensional strip before plotting. The plot shows data value against bin number for all the bins. The transformation from 1- to 2-dimensions can be achieved in many ways but only 5 methods have been implemented in despike. The supported methods, presented graphically in figure 13 and with reference to the bin numbers used in the figure, are:

- SPIRAL: A Spiral outwards from the reference bin (the pointing centre of the map). Using the example presented in the figure the bin order used by the plotting task becomes 28, 20, 21, 29, 37, 36, 35, 27 etc. This means that data from the centre of the array is displayed before the (sparse) data at the edges of the array.
- XLINEAR: unfold each X strip in turn for each Y. In this case the bin order becomes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, etc. A source in the centre of the array will be displayed in the middle of the default range provided.
- YLINEAR: unfold each Y strip in turn for each X. In this case the bin order becomes 1, 9, 17, 25, 33, 41, 49, 2, 10 etc.
- DIAG1: diagonal strips starting at position (1,1). The bin order in the example becomes 1, 2, 9, 3, 10, 17, 4, 11, 18, 25, 5 etc.
- DIAG2: diagonal strips starting at positions (nx,1). The bin order in the example becomes 8, 7, 16, 6, 15, 24, 5, etc.

In general this means that in the case where the source lies in the centre of the array, the spiral display mode will show the source in the first few bins whereas the other modes will display the source in the middle of the range.

Sometimes spikes skew the statistics of an individual bin to such an extent that a spike lies within the NSIGMA cutoff region (i.e. the spike makes the standard deviation so large that it lies within NSIGMA of the mean). In an effort to overcome this problem a smoothing option

Figure 13: A schematic of the different display modes for despike. The start of each scan is represented by the letter **S** and the end by the letter **E**.

Table 4: Quality bits used by SURF

Bit#	Value	Meaning
0	1	Infinity (eg division by zero)
1	2	Set by flatfield.
2	4	Set by reduce_switch if the transputers detected more spikes than specified by the SPIKE_LEVEL parameter.
3	8	Set by change_quality.
4	16	Set by despiking (scuclip and despike)

is provided. This option smooths the clipping envelope (the region that determines whether a point is a spike or not) across adjacent bins so that fluctuations in the statistics of adjacent bins are reduced. This smooth works in one dimension only and the definition of *adjacent* depends on the method used for transforming the data to 1-D (parameter DMODE).

Figure 14 shows an example of the different modes with and without smoothing. Points lying outside the high and low lines are treated as spikes. In this example the smoothing has resulted in the detection of two spikes (probably too faint on this figure but the spikes are in bins 120 (spiral) and 2370 (x)).

H Quality flags

The SURF software conforms to the NDF standard concerning the processing of quality or bad-pixel masks. Each method of setting a pixel bad is associated with a bit in the quality masking flag (the NDF.QUALITY.BADBITS component). The bad bits and their meaning in SURF are described in table 4.

In order to remove the effect of a particular bit (i.e. to ignore a despiking), the KAPPA task setbb can be used to change the bad-bits mask in the NDF. Simply calculate the value related to the bits you are interested in keeping and use this value in setbb. Note that care must be taken in deciding which bits are to be used for masking bad data. Bits zero and one must always be set whereas the other three bits are optional. change_quality is the only task that acts on a file rather than producing a processed copy and it is probably better if change_quality is used directly if you wish to manipulate the mask associated with bit three.

Additionally, regridded images also use quality flags. Bit 0 is used to represent areas where no data were available and bit 1 is used to mask data at the edge of the regridded area via the TRIM parameter.

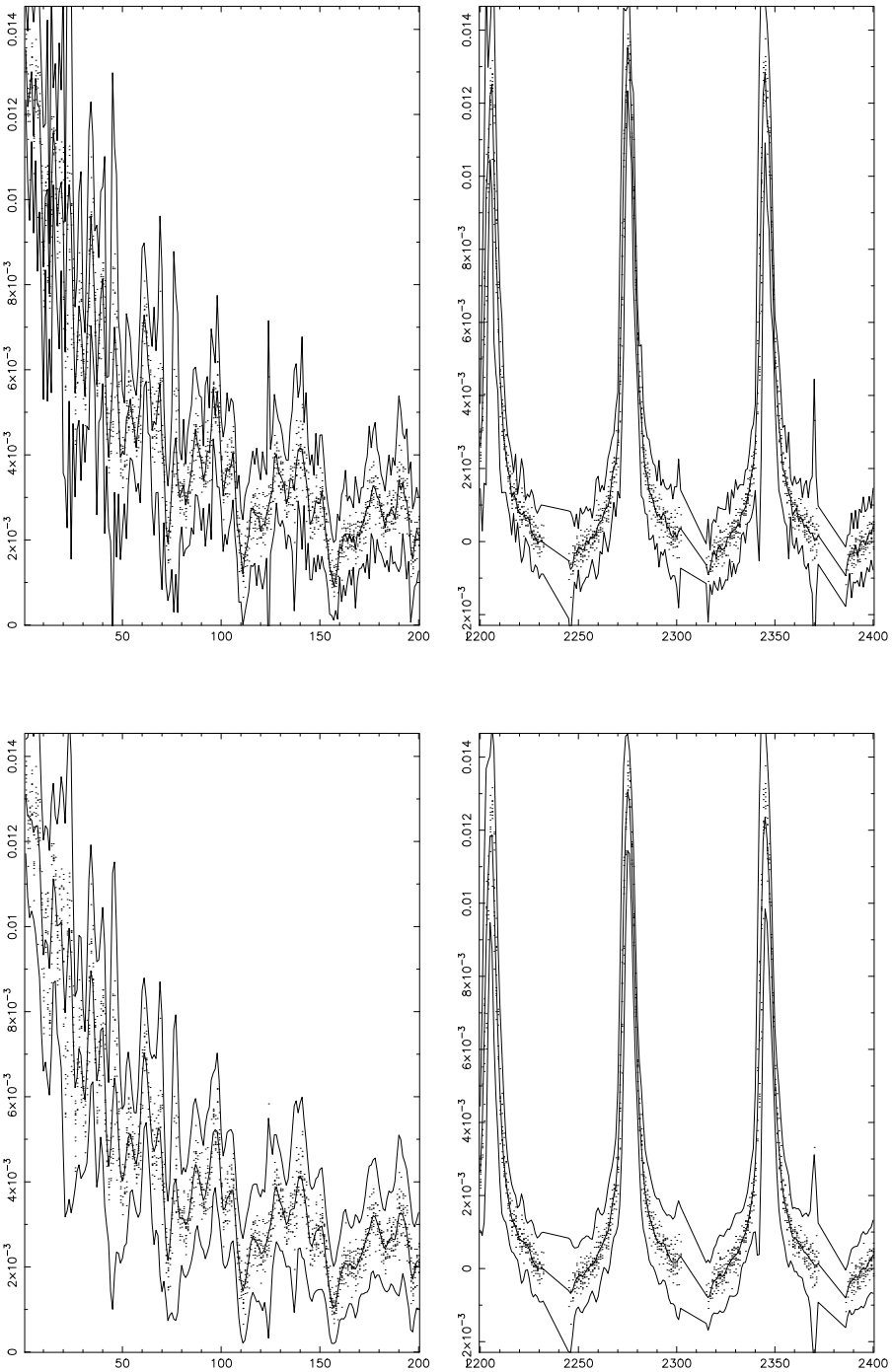

Figure 14: Example despiking of a point source. The two outside lines on each diagram indicate the region outside which a spike would be found (the clipping envelope). The middle line indicates the median of the data in each cell. The top two diagrams show the data displayed using Spiral (left) and Xlinear (right) modes. The x-axis indicates that the source is visible for small bin number in spiral mode and for a much larger bin number in xlinear mode. The lower two diagrams show the same thing except that hanning smoothing has been applied to the clipping envelope in each case.

I Skydips

The skydip observing mode measures the sky brightness at a range of elevations and uses that data to calculate the zenith sky opacity. The absolute value of the sky brightness is required and this values is calculated by interpolating its measured signal from that measured with ambient and cold loads.

In order to calculate the zenith sky opacity to the sky brightnesses the skydip task fits a theoretical curve to the data. The theoretical curve at each wavelength takes the form:

$$J_{\rm meas} = (1-\eta_{\rm tel})J_{\rm tel} + \eta_{\rm tel}J_{\rm atm} - b\eta_{\rm tel}J_{\rm atm}e^{-A\tau}, \tag{3}$$

where $J_{\rm meas}$ is the measured brightness temperature of the sky, $\eta_{\rm tel}$ is the transmission of the telescope, $J_{\rm tel}$ is the brightness temperature of a black-body at the temperature of the telescope, $J_{\rm atm}$ is the brightness temperature of the atmosphere, b is the bandwidth factor of the filter being used ($1-b$ is the fraction of the filter bandwidth that is opaque due to atmospheric absorption and, like τ, it is a function of water vapour content), τ is the zenith sky optical depth and A is the airmass of the measurement.

Of these parameters, $J_{\rm meas}$, $J_{\rm tel}$ and A are known. $J_{\rm atm}$ can be estimated from the ambient air temperature at ground level using a model for the behaviour of the observing layer above the telescope, as described below. $\eta_{\rm tel}$ may be fitted to the data for every skydip and, because it does not vary with atmospheric conditions, a reliable 'average' value can be derived from many observations. Thus, there are two remaining free parameters, τ and b, that must be derived from the fit (three if fitting $\eta_{\rm tel}$).

$J_{\rm atm}$ is calculated from $T_{\rm amb}$, the ambient air temperature, by assuming that the sky emission is dominated by a single absorber/emitter whose density falls exponentially and temperature linearly with height. In this case it can be shown that

$$J_{\rm atm} = J_{\rm amb}\int_0^{40} A\left[k\exp\left(-\frac{h}{h_2}\right)\exp\left[Akh_2\left(\exp\left(-\frac{h}{h_2}\right)-1\right)\right]\left(1-\frac{h}{h_1}\right)\right]{\rm d}h, \tag{4}$$

where h_1 is $J_{\rm amb/6.5}$ to give a 6.5 K fall in temperature per km height, h_2 is the scale height of the absorbers (2 km), A is the airmass and k the extinction per km.

If we approximate the result of the integral by

$$J_{\rm atm} = J_{\rm amb}X_{\rm g}\left[1-\exp\left(-Akh_2\right)\right], \tag{5}$$

it can be shown that $X_{\rm g}$ has the form

$$X_{\rm g} = 1 + \frac{h_2T_{\rm lapse}}{T_{\rm amb}}\exp\left(-\frac{A\tau}{X_{\rm gconst}}\right) \tag{6}$$

where $T_{\rm lapse}$ is the temperature drop per kilometre altitude (-6.5 K/km) and $X_{\rm gconst}$ is a constant determined empirically and has a value of 3.669383.

For more information see [35].

I.1 Calibration

The choice for T_HOT and T_COLD critically affects the result of the skydip fit. The default values for the hot and cold temperatures are usually stored in the data header but occasionally these values are redetermined and the header values must be over-ruled. As of version 1.6 of SURF the cold load temperature (as well as the default telescope efficiency, $\eta_{\rm tel}$) for the 850 and 450-μm filters is suggested from a lookup table rather than the data headers. Also, the hot load temperature is now known to be wavelength dependent and an adjustment of -1K (at 850 microns) and -3K (at 450 microns) is now automatically applied to the value stored in the header. More details on skydip calibration can be found in Archibald et al [36].

I.2 Removing bad skydip data from the fit

Occasionally it is necessary to remove bad points from skydip data prior to fitting. This is implemented in the same way as it is implemented for other SCUBA data by using change_quality. The following extra steps are required:

(1) Run reduce_switch to calculate the sky brightness temperature for each integration at each airmass (measurement). The cold load temperature for each sub instrument will be requested.

```
% reduce_switch 70
SURF: Opening 19971115_dem_0070 in /scuba/observe/19971115/dem
SURF: run 70 was a SKYDIP observation
SURF: file contains data for 1 switch(es) in 1 exposure(s) in 10 integration(s)
in 10 measurement(s)
OUT - Name of output file to contain reduced switch data /'o70'/ >
T_COLD - Temperature of cold load for SHORT_DC /95/ >
T_COLD - Temperature of cold load for LONG_DC /55/ >
```

(2) The resulting output file looks just like a file produced by reduce_switch on map data: it contains a 2 dimensional data array of sub-instrument (bolometer) number along the first axis and sample number (number of integrations times number of measurements) along the second axis. You can find the sub-instrument corresponding to each 'bolometer' number either by running skydip and noting the order of the listed sub-instruments or by using the KAPPA fitslist command:

```
% fitslist o70 | grep SUB_
SUB_1   = 'SHORT   '           / SCUBA instrument being used
SUB_2   = 'LONG    '           / SCUBA instrument being used
SUB_3   = 'not used'           / SCUBA instrument being used
SUB_4   = 'not used'           / SCUBA instrument being used
SUB_5   = 'not used'           / SCUBA instrument being used
```

For example, the data for the second sub-instrument (in this case the LONG array) can be plotted by using:

```
% linplot mode=2 device=xwindows 'o70(2,)'
```

Fig. 15 shows an example. Note that, in contrast with other observing modes, the second axis is labelled in measurements rather than integrations.

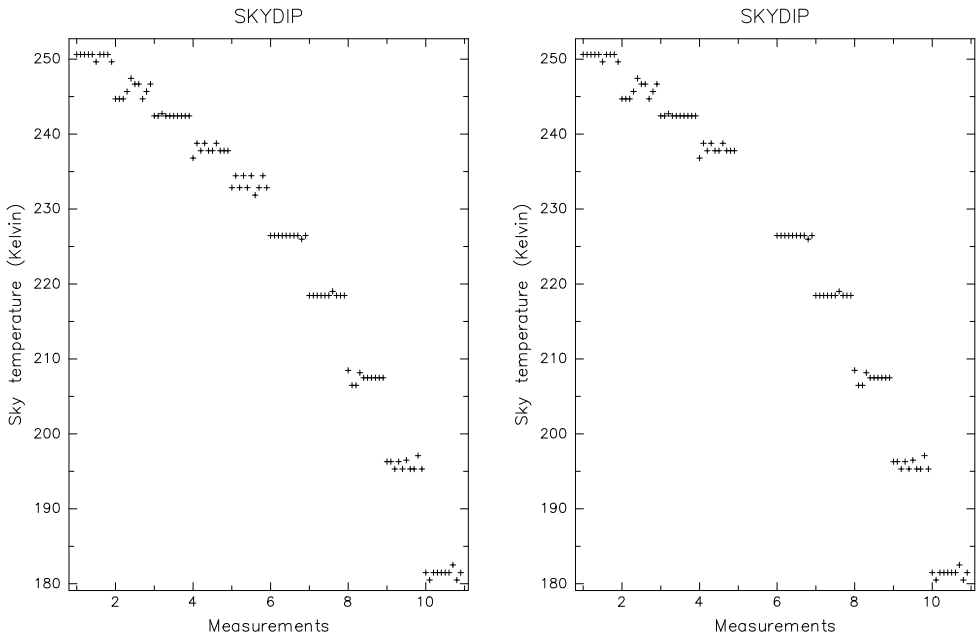

Figure 15: Skydip data after processing with reduce_switch (left) and after measurement 5 has been removed with change_quality (right).

(3) Once a bad measurement has been identified, it can be switched off using change_quality:

```
% change_quality 'o70{b2;m5}' yes
SURF: run 70 was a SKYDIP observation of not used
SURF: file has data for 2 bolometers, measured at 100 positions.
 - there are data for 1 exposure(s) in 10 integration(s) in 10 measurements.
```

The main thing here is that the `m` identifier should be used to specify measurements[15] and that only bolometer (i.e. sub-instrument) 2 should be affected.

(4) Now skydip(or sdip) can be run on the file:

```
% skydip o70
SURF: run 70 was a SKYDIP observation
SURF: observation started at sidereal time 1 10 41 and ended at 1 16 38
SURF: file contains data for the following sub-instrument(s)
 - SHORT with filter 350
 - LONG with filter 750
SUB_INSTRUMENT - Name of sub-instrument to be analysed /'SHORT'/ > long
SURF: file contains data for 10 integration(s) in 10 measurement(s)
ETA_TEL - Telescope efficiency /0.87/ >
B_VAL - B parameter /-1/ >
SCULIB: fit for filter 750 and sub-instrument LONG_DC
```

[15]Of course it is still possible to specify an integration to be marked bad but remember to specify also the measurement otherwise the 'nth' integration for each measurement will be marked bad rather than the 'nth' integration of the 'mth' measurement.

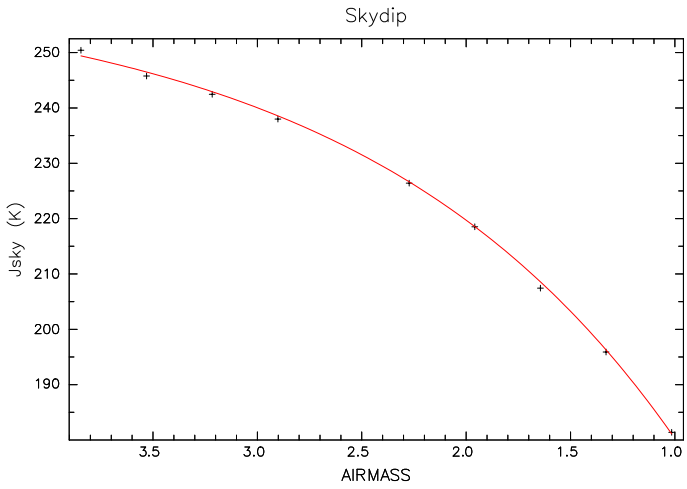

Figure 16: Skydip plus model without measurement 5

```
eta =  0.87 +/-  0.00  b =  0.86 +/-  0.01  tau =   0.667 +/- 0.007
Standard Deviation of fit residual =   0.81 K (X=     0.9 N=    7)
```

The fit is shown in Fig. 16. skydip is the only task that can process raw demodulated data and data processed with reduce_switch.

J Correcting 'shifted' data

Between early 1997 and 15th September 1997 there was an intermittent fault with the SCUBA data acquisition system (DAQ) that led to a particular form of data corruption. The problem is most serious in MAP/JIGGLE observations but can also affect PHOTOM. The DAQ fault was identified and fixed on 15th September 1997 and checking routines were added to the data-taking software to warn of any such data synch problems that occur in the future. Observers with data taken after that date need read no further.

Those with data taken in the problem period may remember that the SCUBA bolometer channels are collected into 9 groups of 16, with each 16 channel group being handled by a different A/D card in the DAQ. The name of each bolometer reflects the A/D card and channel number on that card which handles the signal; for example, B12 will be routed through channel 12 on card B. The 9 A/D cards have single letter identifiers running from A to I, the channel numbers on each run from 1 to 16.

Roughly once or twice a night the fault would insert a spurious number into the data stream from one or more of the A/D cards to the transputer system that does the digital demodulation. The system design is such that until the system was reloaded a spurious shift would be applied to the data. Thus if the fault occurred in the B card then after that point the system would see the data from that card as shifted up by one channel number; data for channel B5 would appear in channel B6, B7 in B8, etc. The end channels wrap around so that channel B16 would appear in

channel B1 of the next dataset. The effect is cumulative, so that if 2 faults occurred on the B card then the data would then be shifted by 2 channels.

If the fault occurs for a card whose bolometers are measuring source signal then the image of the source will be reconstructed incorrectly by both the real-time display and the SURF package. In fact, the problem was first noticed when jiggle map images of Uranus showed an apparent double source.

Faulty data can be patched up using the scushift utility. The difficulty is in finding when and where in your data the problem has occurred since, without a high signal-to-noise signal to judge by, you cannot go on the appearance of the final image.

The situation is saved by SCUBA's internal calibrator. During all jiggle-type observations a sinusoidal signal from a source inside the cryostat is superimposed on the astronomical data. The digital demodulation recovers the amplitudes of both the calibrator and astronomical signals. The pattern of the calibrator signal from the SCUBA bolometers forms a signature that is constant over long periods and can be used to detect shifts in the data.

To illustrate this point there are four data files distributed with this package.[16] These files contain the calibrator signal for this period for the 450- and 850 μm filters[17]. The files are:

- calsig_850_map.sdf

  Calibrator signal for the long-wave array with the 850 micron filter.

- calsig_450_map.sdf

  Calibrator signal for the short-wave array with the 450 micron filter.

- calsig_450_850_map.sdf

  Calibrator signal for the short and long-wave arrays at 450 and 850 microns.

- calsig_450_850_photom.sdf

  Calibrator signal for the short and long-wave arrays at 450 and 850 microns but for a photom observation.

The '_map' files are intended for comparison with JIGGLE/MAP data whereas the '_photom' file is intended for use with PHOTOM data (there are two extra bolometers in this case). In addition, there is also a file containing shifted data, calsig_450_850_bp2.sdf, where the signal from the B card has been shifted by 2 channels. Fig. 17 shows this file overlaid on the correct, unshifted, calibrator signal.

Demodulated data can be checked as follows:

(1) Extract the calibrator signal from the raw demodulated data (i.e. before running reduce_switch). The simplest way to extract the signal is to use the KAPPA command manic:

[16] The files can be found in $SURF_DIR/

[17] for the calibrator signal prior to April 1997 or for different filters please contact your SCUBA support scientist for more advice

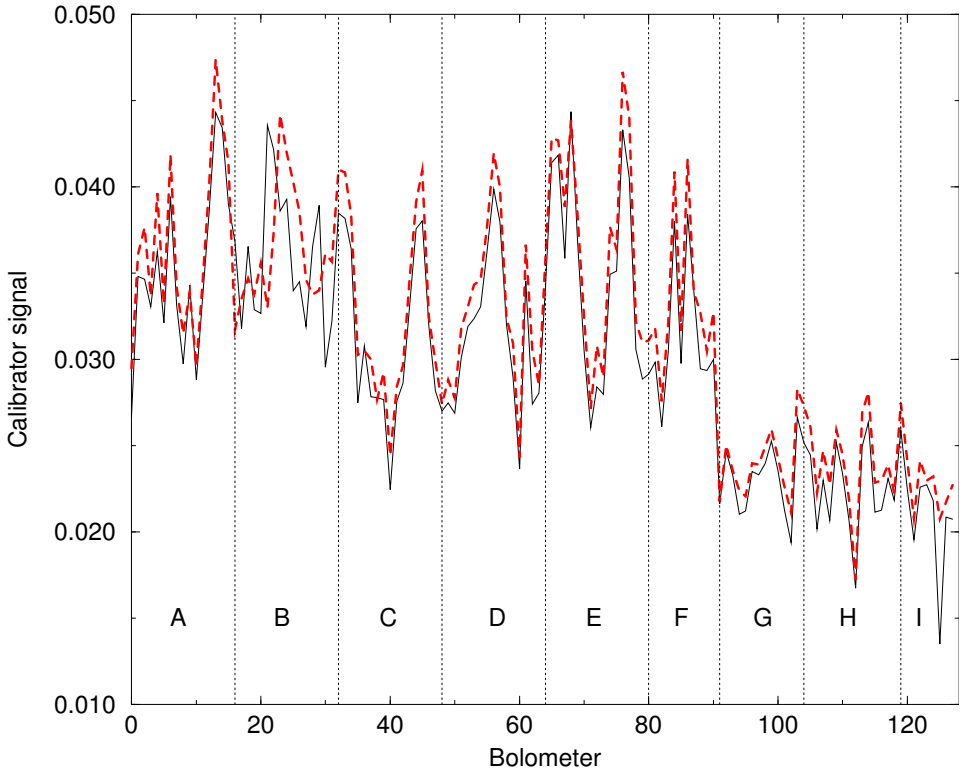

Figure 17: The standard calibrator signal (solid line) with an overlay of a shifted calibrator signal (dashed). The A/D cards are indicated and a shift is clearly seen on card B.

```
% manic
INPUT - Input image /@calsig_450_850_map/ > 19971008_dem_0039
Array is 3 -dimensional
Dimensions are ( 5, 128, 384 )
ONDIM - Dimensionality of output image /3/ > 1
ELINE2 - Axis of the input data array that will be used to form the
 output data array /'Y'/ > Y
YLIMITS - Window limits for the Y-axis of the input data array /[1,37]/ >
XRANGE - Range for summation over the X-axis of the input data array /[1,5]/ > [3,3]
ZRANGE - Range for summation over the Z-axis of the input data array /[1,384]/ >
OUTPUT - Output image > calsig
LOOP - Produce another output IMAGE structure and data array? /NO/ >
```

The dimensions of the data array in the demodulated file should be [5, *n_bols*, *n_jiggles*] (§E.3), where *n_bols* is the total number of bolometers measured (128 for both short and long arrays), and *n_jiggles* is the total number of jiggle positions measured in the observation.

In summary, manic should be given the following parameters: ONDIM=1, ELINE2='Y', YLIMITS=*default*, XRANGE=[3,3] and ZRANGE=*default* (where *default* is the default value suggested for the parameter)

Alternatively, it should be possible to use ndfcopy to extract the NDF section, using the TRIM parameter to reduce the resultant section to 2 dimensions.

```
% ndfcopy '19971008_dem_0039(3,,)'  TRIM TRIMWCS
```

(2) Normalise the calibrator signal by using cdiv to divide the result from manic by *n_jiggles* (384 in this example):

```
% cdiv
IN - Input NDF data structure /@calsig/ >
SCALAR - Division constant /1280/ > 384
OUT - Output NDF > calsig_div
```

(3) Plot the standard calibrator and overlay the calibrator signal derived above.

```
% linplot ${SURF_DIR}/calsig_450_850_map
% linplot calsig_div noclear lincol=(some colour)
```

where '*some colour*' is a different colour to that used to display the first calibrator signal.

(4) Once you have identified a data shift this must be corrected with the scushift command. Since the shift is usually caused by adding extra bytes to the data stream, a negative shift must be applied to correct the problem.

```
% scushift
Input NDF (no .sdf): r95
Which A to D card (a single letter): B
Using the NDF r95...
Card 2 starts and ends at positions 16 and 31
Enter required shift (<14): -2
Before: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 1 2 3 4 5 6 7 8 9 10 11 12 13
```

```
14 15 16 1...<cut>
Bolchan: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 15 16 1 2 3 4 5 6 7 8 9 10
11 12 13 14 1...<cut>
```

scushift is very verbose! The 'before' and 'bolchan' entries simply tell the user the form of the correction used. If you look carefully you will see that the 17th number in the list has changed from a 1 to a 15 indicating that the shift was successful.

This command works 'inplace' and, in fact, will not run on the raw data file; instead it should be run on the file produced by reduce_switch or flatfield.

(5) The data should now be corrected (but note that PHOTOM data will still need more work; see the note in the scushift documentation for more details).

There is one last wrinkle to the process of extracting calibrator data.. PHOTOM observations after 3rd June 1997 store signals from 2 channels in addition to the arrays, if the arrays were being used. Thus *n_bols* for a PHOTOM demodulated data array will be 130 rather then 128. In this case you should compare the calibrator signature with that in the file calsig_450_850_photom.sdf.

K Notes on scripts

sculog, scushift and the scripts scuquick, qdraw, remdbm, change_nacentre, setbolwt and sigclip do not form part of the SURF monolith and are all written in perl [37]. They all use the Perl NDF module [38] and therefore require at least version 5.003 of perl. The perl NDF binary will be installed as `/star/Perl/bin/perl` on Starlink sites.

The sdip, scuplot and scupa scripts are written in C-shell.

scunoise is written in perl/Tk (version 800.001 or newer, available from CPAN[18]).

Additionally, qdraw, sigclip, sdip, scuplot, setbolwt, remdbm and scupa require that KAPPA is installed.

[18] http://www.cpan.org/