

6 Cookbook

6.1 Preparation

Create the directory for the analysis

```
mkdir ibis_data_rep
cd ibis_data_rep
setenv REP_BASE_PROD $PWD
unsetenv AUXL_REF_DIR
```

Install there the test data, as it is explained in the Installation Guide for the INTEGRAL Data Analysis System [6]. The setting of the environment is explained in the Section “Working Environment” of the Introduction to the INTEGRAL Data Analysis [1].

To have log messages both at the screen and in the file (**common_log.txt** in the given example) give the command

```
setenv COMMONLOGFILE +common_log.txt
```

If you want to produce a script and do not want any graphical interface you should set **COMMONSCRIPT** variable.

```
setenv COMMONSCRIPT=1
```

6.2 Script launch

After setting up the environment you are ready to call the analysis script.

The first thing to do is to create a list of the Science Windows you want to analyze. Unfortunately PICsIT sensitivity is not enough to create a good image for a single Science Window, thus you should expect good results only if *INTEGRAL* was in staring mode. For ISGRI this constraint is not that important. To illustrate this we provide below two examples, based on dithering and staring Crab observations.

To follow the examples create ASCII file **dith.lst** with the following list of DOL's of the prepared Science Window Groups you want to analyze. (DOL (Data Object Locator) specifies the Data Structure in the FITS file you are interested in, see more details in the Introduction to the INTEGRAL Data Analysis [1].)

```
scw/0102/010200210010.000/swg.fits[1]
scw/0102/010200220010.000/swg.fits[1]
```

Warning! Please note that there is different naming scheme for revision 1 and revision 2 data. For the revision 1 data the name of the prepared Science Window Group is **swg_prp.fits**.

Also create file **staring.lst** with the following DOLs:

```
scw/0039/003900020020.000/swg.fits[1]
scw/0039/003900020030.000/swg.fits[1]
scw/0039/003900020040.000/swg.fits[1]
scw/0039/003900020050.000/swg.fits[1]
scw/0039/003900020060.000/swg.fits[1]
```

Create Observation Groups (see the description of the executable *og_create* in the Toolbox section of the Introduction to the INTEGRAL Data Analysis [1]):

```
og_create idxSwg=dith.lst ogid=dith baseDir="." instrument=IBIS
og_create idxSwg=staring.lst ogid=staring baseDir="." instrument=IBIS
cp -r obs/dith obs/dith_bkg
```

Now you are ready to change the directory and start the analysis. In the examples below we build an image of the sky region observed in the chosen Science Windows. The energy range of the desired images can be chosen with the parameters of the main script.

Warning! In OSA 4.2 the structure of the results slightly differs from the previous versions. Directories **ibis/** and **scw/RRRRPPPPSSSF.000/ibis** do not exist any more, see [1] for more details. Do not forget to update your scripts!

6.3 ISGRI

6.3.1 Image Reconstruction

For ISGRI seven default output energy bands are defined:

```
Number of Energy bands
IBIS_II_ChanNum = 7
```

```
List of low energy boundaries, keV
IBIS_II_E_band_min = "15 40 100 200 400 700 1200"
```

```
List of high energy boundaries
IBIS_II_E_band_max = "40 100 200 400 700 1200 2500"
```

During the BKG step the efficiency correction and instrument bkg subtraction is done. In the current OSA you have background maps provided by the ISGRI team. These maps are still preliminary and though in lots of cases the maps obtained after the background subtraction are smoother, there are also cases in which the effect is not seen, or even make the result worse. So in the course of your analysis you should try to analyze data with and without background subtraction, and then to decide which variant is better in your case. To do this you should use the parameter **SCW1_BKG_I_isgrBkgDo1**. If it is left empty then the background map is taken automatically from the IC files. If you set it to **SCW1_BKG_I_isgrBkgDo1='-'**, then no background subtraction is done.

During the CAT_I step the script selects the sources that are actually in the field of view among the sources given in the input catalog defined by the parameter **CAT_refCat**. The default value of this parameter is

```
CAT_refCat="$ISDC_REF_CAT"
```

If you would like to use among the sources in the general reference catalog only those that were previously detected by ISGRI (in public data) you give the following value of the parameter:

```
CAT_refCat=".../cat/hec/gnrl_refr_cat_0016.fits[1][ISGRI_FLAG==1]"
```

After the deconvolution the script is looking for a defined number of sources in the Field of View (FOV). The set of sources is chosen with the parameters **OBS1_SearchMode** and **ToSearch**. These parameters allow you the following possibilities:

```
OBS1_SearchMode = 0 -- search for all significant excesses

OBS1_SearchMode = 1 -- search for all catalog sources

OBS1_SearchMode = 2 -- search for K sources, where K = ToSearch

OBS1_SearchMode = 3 -- search for all catalog sources and plus for
                       K significant excesses, where K = ToSearch
```

SearchMode= 1,3 concerns only images at a Science Window level. In the mosaic image *ii_skyimage* always looks for **K = ToSearch** sources.

The default values are:

```
OBS1_SearchMode=2
OBS1_ToSearch=3
```

This means that if you are running analysis with the default values software will find 3 sources maximum, regardless the real number of the sources in the field of view. Thus if you are working with a sky region with lots of sources you should increase the **OBS1_ToSearch** number, as the ghost subtraction is done only for the found sources.

If you don't want the program to look for the source position, but to use a catalog one you should change the value of the parameter **OBS1_SouFit** from 0 to 1.

It is possible to run the analysis for ISGRI or for PICsIT only. You can select it with the following parameters (the default values are given):

```
Disable ISGRI analysis (YES/NO)
SWITCH_disableIsgr=no
```

```
Disable PICsIT analysis (YES/NO)
SWITCH_disablePICsIT=yes
```

Currently you may download from the ISDC Browser two types of data - revision 1 and revision 2. For the revision 2 data COR, DEAD and GTI steps were already processed, so that you can start directly from BIN_I level. In the current cookbook we discuss examples based on revision 2 data. For the revision 1 data do not forget to run COR – GTI steps.

The command given below launches the analysis of the data attached to the Observation Group. The analysis will pass all the stages from energy binning (BIN_I) to the ISGRI Image creation (IMA). With the help of the parameter **OBS1_DoPart2** you decide whether you want (**OBS1_DoPart2=1**) or not (**OBS1_DoPart2=0**) to produce the mosaic image. If you decide not to create the mosaic image at the moment you will have a possibility to produce it later, see the example below. To run the analysis with the instrument background subtraction the command is:

```
cd obs/dith_bkg
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="BIN_I" endLevel="IMA" \
OBS1_DoPart2=0 SCW1_BKG_I_isgrBkgDol=""
```

After this command the script launches the Graphic User Interface (GUI) and you have a chance to check the parameter settings. Only non hidden parameters appear. To see hidden parameters press button “**hidden**”, to close the window with hidden parameters you should press “**Ok**”. Don't

forget to press “Save” if you change something. When you are ready press “Run” to start the analysis.

In the Table 4 at the end of this Section we list all the parameters of the main script with a brief explanation. To indicate query parameters bold font has been used. The detailed description of the main script structure and algorithms is given in Section 7.

For the comparison you can also try to analyze the data without the background subtraction (with this command also the mosaic image will be created):

```
cd obs/dith
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="BIN_I" endLevel="IMA" \
OBS1_DoPart2=1 SCW1_BKG_I_isgrBkgDol="-"
```

ISGRI has two levels of results - it produces results for each Science Window, then (if `OBS1_DoPart2=1`) it combines the deconvolved images into one mosaic image and continues the analyses at the mosaic level. Here we discuss the results only briefly. For a more detailed discussion, see Appendix C.

The output source lists are in the following FITS files:

```
scw/RRRRPPPPSSSF.000/isgr_sky._res.fits List of sources found in single ScW
isgri_mosa_res.fits      List of sources found in the Mosaic Image
isgri_srcl_res.fits     The output catalog
```

Both at mosaic and Science Window levels the list of found sources is produced for each energy band. The output catalog is a copy of the input catalog with additional columns for the parameters found in the analysis (found position, flux, significance, ...) and with the new rows for the new sources.

The input catalog with the selected sources is in the file

```
isgri_catalog.fits
```

The output images are:

```
./scw/RRRRPPPPSSSF.000/sgr_sky._ima.fits
./isgri_mosa_ima.fits      (Mosaic Image)
```

For each energy bin four images are produced – intensity, variance, significance, and residual.

To make the mosaic image after you already run your pipeline till IMA level you should first clean the observation group from former mosaic results.

```
cd $REP_BASE_PROD/obs/dith_bkg
rm isgri_mosa_ima.fits
rm isgri_mosa_res.fits
fdelrow og_ibis.fits+1 4 2 N Y
```

If you want to make a mosaic image in case you have a set of observation groups you should clean one group in the manner shown above. Then create a list of DOLs `dols.txt` of science window groups you want to create a mosaic (**WARNING:** make sure that `isgri_mosa_ima.fits` files exist in all the science windows group you mention, otherwise `ii_skyimage` will crash), in our case list looks like:

```
scw/010200210010/swg_ibis.fits[1]
scw/010200220010/swg_ibis.fits[1]
```

In case of creating an index of the science window groups from the different observation groups give a full path!

To create an index:

```
txt2idx index="index_mosa.fits[1]" \
template="GNRL-SCWG-GRP-IDX.tpl" element="dols.txt"
```

Now create file **modfile** with one line in it:

```
1 index_mosa.fits
```

and replace with the help of the FTOOLS program `fmodtab` in the cleaned observation group the science window group index it is pointed to:

```
fmodtab og_ibis.fits+1 MEMBER_LOCATION modfile
```

To create a mosaic give the following command:

```
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="IMA" endLevel="IMA" OBS1_DoPart2=2
```

There is a nice way to locate the found sources on the sky image. To do it convert the output catalog to the ds9 format with the program **cat2ds9**:

```
cd $REP_BASE_PROD/obs/dith_bkg
cat2ds9 isgri_mosa_res.fits\[2] found.reg symbol=box color=green
cat2ds9 isgri_catalog.fits\[1] cat.reg symbol=box color=white
cd $REP_BASE_PROD/obs/dith
cat2ds9 isgri_mosa_res.fits\[2] found.reg symbol=box color=green
cat2ds9 isgri_catalog.fits\[1] cat.reg symbol=box color=white
```

To find more about this program look into the [1], or type

```
cat2ds9 --h
```

On the Figure 10 you see the resulted significance mosaic image in the 15 – 40 keV energy range with (left) and without (right) background subtraction. This image was created with a command

```
ds9 $REP_BASE_PROD/obs/dith_bkg/isgri_mosa_ima.fits\[4] \
  -region $REP_BASE_PROD/obs/dith_bkg/found.reg\
  -region $REP_BASE_PROD/obs/dith_bkg/cat.reg\
  -cmap b -scale sqrt -scale limits 0 60 -zoom 2\
  $REP_BASE_PROD/obs/dith/isgri_mosa_ima.fits\[4]\
  -region $REP_BASE_PROD/obs/dith/found.reg\
  -region $REP_BASE_PROD/obs/dith/cat.reg\
  -cmap b -scale sqrt -scale limits 0 60 -zoom 2
```

All the catalog sources in the field of view are shown with white boxes. Only Crab was found among them. This example also shows you that you should be careful with the new sources found by the software, and always make a detailed analysis to verify whether they are real, or spurious ones.

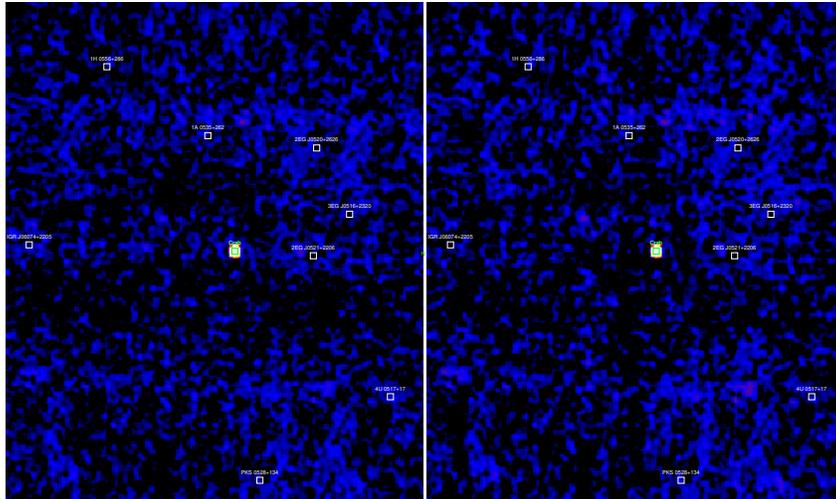


Figure 10: Crab significance image with (left) and without (right) background subtraction in the 15 – 40 keV energy band

6.3.2 Spectral Extraction

If you run the analysis until SPE level, then the spectra for all sources present in the output catalog ISGR-SRCL-RES will be produced. Be aware that spectral extraction is time consuming, so that you should carefully define the list of sources for the spectral extraction. To have meaningful results you should include in your analysis all bright sources in the field of view. To specify the list of sources you should either modify the output file (`isgri_srcl_res.fits`), or create a catalog with the ISGR-SRCL-RES structure (`isgri_srcl_res.fits="crab_specat.fits[1]`) To create such a catalog you can either use `dal_create` program (see [1] for the description)

```
cd $REP_BASE_PROD
dal_create obj_name=crab_specat.fits template=ISGR-SRCL-RES.tpl,
```

or copy and modify the existing output catalog `isgri_srcl_res.fits`. Crab is the brightest source of the region, thus in this case we can extract the spectrum of one source only. From the modified catalog you should remove all lines but the one with Crab. If you prefer to create a new file, then you should with the help of `fv` add to the table inside one line, and fill there `SOURCE_ID`, `NAME`, `RA_OBJ`, `DEC_OBJ` and `ERR_RAD` columns (all the information you can take from the general catalog). Put 0 to the column `NEW_SOURCE`. With the help of `FTOOLS` the `isgri_srcl_res.fits` can be modified within the script by the commands like:

```
cd $REP_BASE_PROD
cp obs/dith/isgri_srcl_res.fits dummy.fits
fcopy "dummy.fits[ISGR-SRCL-RES][DETSIG >= 10.0]" crab_specat.fits
rm dummy.fits
```

With the help of the parameter `IBIS_SI_inEnergyValues` you can specify the desired binning of the response matrix. File `$REP_BASE_PROD/ic/ibis/rsp/isgr_rmf_grp_0012.fits` contains the latest full response matrix with 2048 channels. With the help of the `FTOOLS` 5.3 program `rbinrmf` you can rebin this matrix in way optimal for your task. You should not waste you time having fine energy resolution in the energy range where only the background has an influence on the resulted spectrum, and you also should avoid to have too narrow energy channels for the weak sources, as in this case the rebinning the spectrum afterwards will lead to another, less accurate results, than if you run the spectral extraction with larger channels from the very beginning. To use the

rbrnrmf program you should create an ASCII file with three columns, with channel ranges and the compression factor. In the example below we use the following rebinning which is written to the file `crab_bin.txt`:

```
0 415 16
416 1017 602
1018 2047 1030
```

to rebin the matrix give a command:

```
rbrnrmf infile="$REP_BASE_PROD/ic/ibis/rsp/isgr_rmf_grp_0012.fits" \
outfile="crab-rmf.fits" binfile="crab_bin.txt"
```

As a result of this you now have the rebinned response matrix `crab-rmf.fits`

For the successful analysis you should make the just created files read-only:

```
chmod -w crab-rmf.fits
chmod -w crab_specat.fits
```

Within OSA 4 you have two alternative programs of spectral extraction *ii_spectra_extract* (method 1) and *ii_spectral* (method 2). Parameter `method` allows you to choose between this two possibilities. The scientific evaluation of these two methods can be found in [3], [4]. There is no differences between methods 1 and 2 before **BIN_S** level, so that we can just copy our **IMA**-level results and use it later with the method 2 pipeline.

```
cd $REP_BASE_PROD/obs
cp -r dith dith_2
```

Note that for method 2 the input catalog for spectral extraction can be of any format, not only of ISGR-SRCL-RES as in method 1.

In method 1, similar to the case of the image reconstruction, you can choose (with the help of the parameter `SCW2_ISPE_isgrBkgDol`) whether you want or not to subtract the instrumental background. In method 2 instrumental background is not subtracted regardless the `SCW2_ISPE_isgrBkgDol` value.

For the spectral extraction with the background subtraction and method 1 give a command:

```
cd $REP_BASE_PROD/obs/dith_bkg
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="BIN_S" endLevel="SPE" \
SCW2_ISPE_isgrBkgDol="" SCW2_cat_for_extract="../../crab_specat.fits[1]" \
IBIS_SI_inEnergyValues="../../crab-rmf.fits[3]" method=1
```

For the spectral extraction without background subtraction and method 1 give a command:

```
cd $REP_BASE_PROD/obs/dith
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="BIN_S" endLevel="SPE" \
SCW2_ISPE_isgrBkgDol="" SCW2_cat_for_extract="../../crab_specat.fits[1]" \
IBIS_SI_inEnergyValues="../../crab-rmf.fits[3]" method=1
```

For the spectral extraction without background subtraction and method 2 give a command:

```

cd $REP_BASE_PROD/obs/dith_2
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="BIN_S" endLevel="SPE" \
SCW2_ISPE_isgrBkgDol="-" SCW2_cat_for_extract="../../crab_specat.fits[1]" \
IBIS_SI_inEnergyValues="../../crab-rmf.fits[3]" method=2

```

The resulted spectra are produced for each science window:

```
scw/RRRRPPPPSSSF.000/isgri_spectrum.fits
```

In these files you find the spectra of the desired sources plus the background spectrum. In the header of each data structure the Name and ID of each source is given (for the case of Crab you find SOURCEID= 'J053432.0+220052').

To plot the spectra with XSPEC you should specify the location of response matrices. Note that these matrices are still preliminary and cannot be fully trusted. There is a known bug in OSA 4: if you have extracted spectrum with method 1 and background subtraction, then to avoid problems with XSPEC you should delete the BACKFILE keyword from the header of the spectrum you want to analyze with XSPEC. To do this create a file `templ.dat` with a single line in it:

```
- BACKFILE
```

and then use FTOOLS program `fmodhead`

```
fmodhead obs/dith_bkg/scw/010200210010/isgri_spectrum.fits\[2] templ.dat
```

To analyze your spectrum with XSPEC:

```

cd $REP_BASE_PROD
xspec
  cpd /xw
  data obs/dith_bkg/scw/010200210010/isgri_spectrum.fits
  resp crab-rmf.fits
  arf ic/ibis/rsp/isgr_arf_rsp_0006.fits
  setpl energy
  plot ldata
  ign **-20.
  ign 200.-**
  systematic 0.05
  plot ldata
  model powerlaw
  2
  10
  fit 100
  plot ldata del
  error 1. 1
  error 1. 2

```

On the Figure 11 the spectrum of the Crab observed in 004400540010 Science Window is given. In method 2 errors are known to be overestimated. The work is in process.

To sum up spectra from different science windows from the same Observation Group use `spe_pick`:

```

cd $REP_BASE_PROD/dith
spe_pick group="og_ibis.fits[1]" source="Crab" response="../../crab-rmf.fits\
ancrfile="../../ic/ibis/rsp/isgr_arf_rsp_0006.fits sumname=crab_sum.pha

```

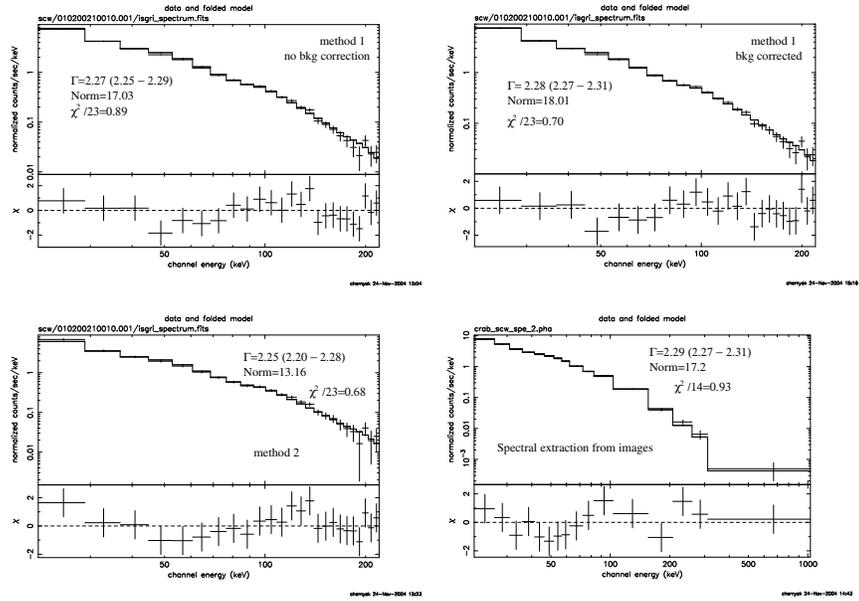


Figure 11: Crab spectrum extracted with different methods.

To use *spe_pick* for spectra created in different observation groups do the same trick, as for the mosaic creation in Section 6.3.1 – create with the help of *txt2idx* an index of the desired science window groups, and substitute it to *og_ibis.fits*.

6.3.3 Spectral Extraction from the Images

As it is said in the Known Issues (Section 8 “*ii_spectra_extract* runs per science window and in case of weak sources, addition of many spectra obtained for the different science windows may give a bad total spectrum. Spectral reconstruction is very sensitive to the background correction. In certain cases running the imaging procedure on several (large) energy bands can provide a better spectrum”. Thus in a case of a faint source it may be worth to produce the source spectrum from the set of images as an average of fluxes F_i observed in single science windows at a source position weighted with their variance V_i . The formula for the weighted average flux F and its error Err is

$$F = \frac{\sum F_i V_i^{-1}}{\sum V_i^{-1}} \quad Err = \sqrt{1/\sum(V_i^{-1})}$$

As for weaker objects or for higher energies the source is not detected in a single ScW it is recommended to use the catalog position, since ISGRI is known to be good in proper positioning of sources. See [4] for the tests that were done to compare this method with a standard spectral extraction described in the previous section.

Select the energy binning you would like to have and run the analysis till IMA level. Note that you can select more than 10 energy bins. To do this rebin response matrix in a way you like it, and set the `IBIS_II_inEnergyValues` to point to the ISGR-EBDS-MOD extension of your new matrix. Parameter `IBIS_II_ChanNum` should be set equal to -1.

```
cd $REP_BASE_PROD
og_create idxSwg=dith.lst ogid=dith_15 baseDir="." instrument=IBIS
```

In the example below we use the following rebinning which is written to the file `crab.15.txt`:

```
0 14 15
15 25 11
26 35 10
36 45 10
46 56 11
57 66 10
67 77 11
78 87 10
88 98 11
99 119 21
120 139 20
140 181 42
182 286 105
287 390 104
391 495 105
496 599 104
600 2047 1448
```

to rebin the matrix give a command:

```
rbnrnf infile="$REP_BASE_PROD/ic/ibis/rsp/isgr_rmf_grp_0012.fits" \
outfile="crab-15-rmf.fits" binfile="crab_15.txt"
```

Launch the analysis:

```
cd $REP_BASE_PROD/obs/dith_15
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="BIN_I" endLevel="IMA" \
OBS1_DoPart2=0 IBIS_II_ChanNum=-1 \
IBIS_II_inEnergyValues="../../crab-15-rmf.fits[3]"
```

To produce a spectrum download a perl script *spextract* from <http://isdc.unige.ch/index.cgi?Soft+scripts>

Create a list of images you want to use

```
scw/010200210010.001/isgri_sky_ima.fits
scw/010200220010.001/isgri_sky_ima.fits
```

and give a command:

```
perl spextract.pl -r 8.3633209E+01 -d 2.2014471E+01 -i crab_ima.lst -n 17 -o crab_scw_spe
-m ../../crab-15-rmf.fits -a ../../ic/ibis/rsp/isgr_arf_rsp_0006.fits
```

The result is shown on a Figure 11.

6.3.4 Lightcurve Production

To use the tool described in this section you should have ROOT installed!

After you have done the spectral extraction you may produce a lightcurve for the same sources. In the following example we build two Crab lightcurves in 20 – 40 keV and 40 – 60 keV energy bands with the 100 s resolution. Note that during the lightcurve extraction the background is assumed to be flat, so the the result would be the same in both **dith_bkg** and **dith** cases.

```
cd $REP_BASE_PROD/obs/dith
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel="LCR" endLevel="LCR" \
ILCR_num_e=2 ILCR_e_min="20 25" ILCR_e_max="25 30" \
ILCR_delta_t=100
```

The resulted lightcurves are produced for each science window:

```
scw/RRRRPPPPSSSF.000/isgri_lcr.fits
```

If after the end of the analysis you would like to produce lightcurves in other energy bands, simply rerun LCR level without any preliminary cleaning. New lightcurves will be simply added to the `isgri_lcr.fits` file.

To see the lightcurve of the source you should plot the column RATE with error ERROR versus column TIME, to see the lightcurve of the background you should plot column BACKV with error BACKE versus column TIME. To group the lightcurves from different science windows you can use either `lc_pick`, or FTOOLS program `lcurve`.

To create a merged lightcurve in 20 – 25 keV energy band with `lc_pick` give the command:

```
lc_pick source='Crab' attach=n merge=y \
        group=og_ibis.fits+1 lc=crab.fits lcselect='E_min==20'
```

The result is written to `crab.fits`. To use `lc_pick` for lightcurves created in different observation groups do the same trick, as for the mosaic creation in Section 6.3.1 – create with the help of `txt2dol` an index of the desired science window groups, and substitute it to `og_ibis.fits`.

To display the resulted lightcurve it is convenient to use `lcurve` program from FTOOLS package:

```
lcurve
Number of time series for this task[] 1
Ser. 1 filename +options (or @file of filenames +options)[] @crab.fits
Name of the window file ('-' for default window)[] -
Newbin Time or negative rebinning[] 100
Number of Newbins/Interval[] 46 (this number you take from the line above:
                                Maximum Newbin No. 46)
Name of output file[default]
Do you want to plot your results?[] yes
Enter PGPLOT device[] /XW
hardcopy crab_lc.ps/PS
```

As result the `crab_lc.ps` file was produced and is shown on Figure 12.

If you want to apply barycentrisation for the created lightcurve use `barycent` tool. Note that it will rewrite the input file, so it may be worth to copy the original file first.

```
cd $REP_BASE_PROD/obs/dith
cp scw/010200210010.000/isgri_lcr.fits isgri_lcr_010200210010_bar.fits
barycent inCOL=TIME outCOL=TIME \
outDOL="isgri_lcr_010200210010_bar.fits[2]" \
inDOL='' auxDOL="../../aux/adp/0102.000/orbit_historic.fits[1]" \
raOBJ=83.6332 decOBJ=22.0145
```

At the moment *ii_light* is not taking into account some important effects like:

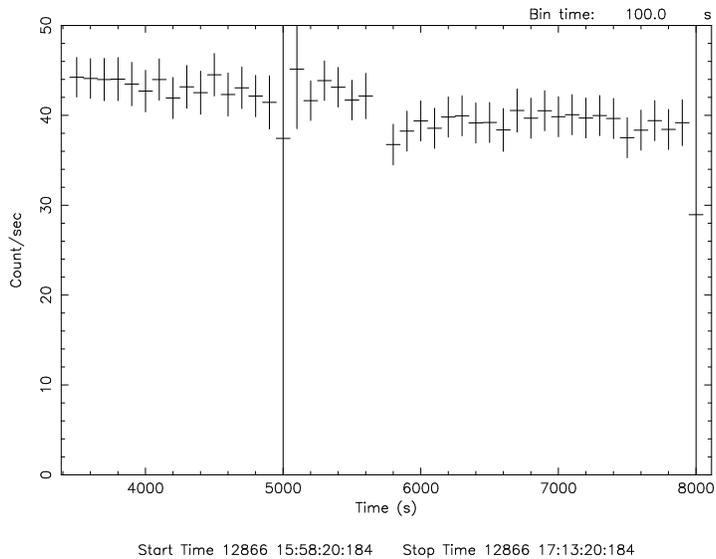


Figure 12: Crab lightcurves in 20 – 25 keV energy range with 100 sec binning.

- collimation by the NOMEX structure (support of the mask introducing additional absorption of photons depending on energy and angle). It is possible however to take care on this in some specific energy ranges, see Section 6.3.5 below.
- energy dependent efficiency of the detector

This mean that the absolute number given for the flux cannot be fully trusted. But the relative level inside one Science Window, or between the Science Windows of the same pointing direction can be trusted.

6.3.5 Lightcurve Production with the correction for the NOMEX structure

As it was said in previous Section for the correct lightcurve production it is necessary to take into account corrections due to the presence of the NOMEX structure. At the moment IBIS/ISGRI efficiency maps for NOMEX effect correction (data structure ISGR-EFFI-MOD) exist only in 20 – 25, 25 – 30, 30 – 35, 35 – 40, 40 – 60 and 60 – 120 keV energy ranges. If you want to create a lightcurve in one of the above energy bands specify the desired energy band and run CAT_S and LCR levels (you can also run all previous steps, but here we show you the fastest way to produce the lightcurve from scratch).

```
cd $REP_BASE_PROD
og_create idxSwg=dith.lst ogid=dith_lc baseDir="." instrument=IBIS
cd $REP_BASE_PROD/obs/dith_lc
ibis_science_analysis ogDOL="og_ibis.fits[1]" method=2\
GENERAL_levelList="CAT_S,LCR" startLevel="CAT_S" endLevel="LCR"\
SCW2_cat_for_extract="../crab_specat.fits[1]"\
ILCR_delta_t=100 ILCR_num_e=1 ILCR_e_min="20" ILCR_e_max="25"
```

Note that at the moment you can run analysis for only one energy bin at a time. To produce lightcurve in another energy band repeat previous command with new ILCR_e_min and ILCR_e_max.

The resulted 20-25 keV lightcurve merged over two science windows is shown on Figure 13.

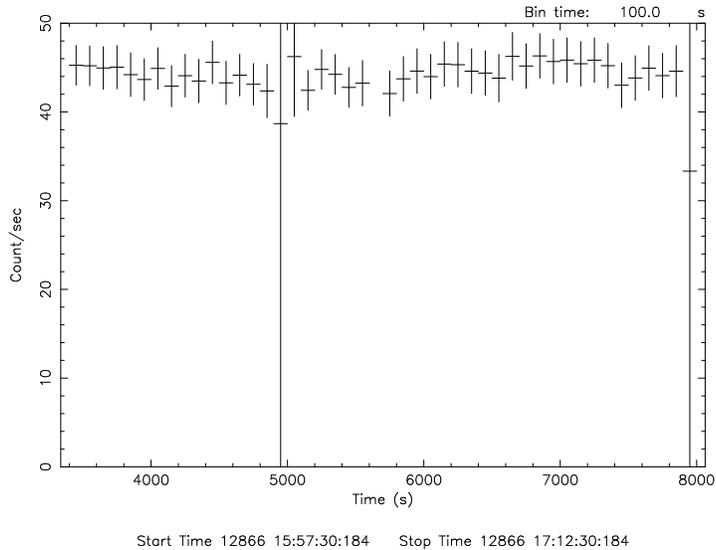


Figure 13: Crab lightcurves in 20 – 25 keV energy range with 100 sec binning.

6.3.6 Timing Analysis without the deconvolution

In this section we describe the alternative way of timing analysis, which is done by the creating and analyzing the list of the observed ISGRI events from a given Observation Group.

In general the events table are very big, so if you are interested in only part of the Science Window data (e.g. in the case of burst) it is better to define a user good time interval and work within it. To follow the example given below create the **usrgti.fits** file with `IJD_START=1322.67`, `IJD_END=1322.68` (the way to define GTIs is described in [1]).

```
cd $REP_BASE_PROD
og_create idxSwg=dith.lst ogid=nodeconv baseDir="." instrument=IBIS
cd obs/nodeconv
ibis_science_analysis ogDOL="og_ibis.fits[1]" \
startLevel=COR endLevel=DEAD \
SCW1_GTI_gtiUserI="../../usrgti.fits[1]" SCW1_GTI_TimeFormat=IJD
```

Now you should create PIFs for all the bright sources in the field of view, so that you would be later able to select photons that comes from the source you are interested in.

```
cd scw/010200210010/
ii_pif_build outGRP="swg_ibis.fits[1]" \
outPIF="crappif.fits(ISGR-PIF.-SHD-IDX.tpl)" \
srcDOL="../../../../crab_specat.fits[1]" filter="" \
racolumn=RA_OBJ deccolumn=DEC_OBJ E_MIN=0 E_MAX=2000 \
maskDOL="$ISDC_IC_TREE/ic/ibis/mod/isgr_mask_mod_0003.fits[1]"
```

Now you are ready to create lists of photons, the result is written to the **GNRL-EVTS-GTI** and **GNRL-EVTS-LST** data structures, (see Appendix C.9.3, Tables 58, 59)

```
cd ../../
evts_extract group="og_ibis.fits[1]" \
```

```

events="crabevts.fits" instrument=IBIS \
sources="../../../crab_specat.fits[1]" gtiname="MERGED_ISGRI" \
pif=yes deadc=yes attach=no barycenter=1 timeformat=0 instmod=""

```

To increase signal-to-noise ratio select only events with PIF=1:

```

fdelhdu crabevts.fits+1 confirm=no proceed=yes
fcopy "crabevts.fits[1][PIF_1==1]" crab_pif1.fits

```

For the compatibility of the output file with FTOOLS do the following:

```

fparkey EVENTS crab_pif1.fits+1 EXTNAME
fparkey GTI crab_pif1.fits+2 EXTNAME

```

Now you can for example produce the Crab power spectrum:

```

powspec
Ser. 1 filename +options (or @file of filenames +options) [] crab_pif1.fits
Name of the window file ('-' for default window) [] -
Newbin Time or negative rebinning [] 0.01
Number of Newbins/Interval [] INDEF
Number of Intervals/Frame [] INDEF
Rebin results? (>1 const rebin, <-1 geom. rebin, 0 none) [] 0
Name of output file[default]
Do you want to plot your results? [] yes
Enter PGPLOT device [] /XW
hardcopy crab_powerspec.ps/PS

```

As result the crab_powerspec.ps file was produced and is shown on Figure 14.

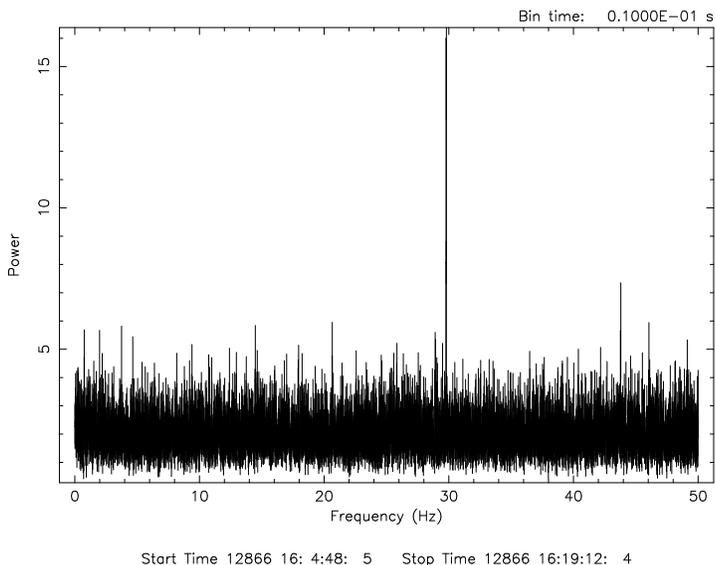


Figure 14: Crab power spectrum.

For the details on *INTEGRAL* absolute timing see Walter et al. 2003 [14]