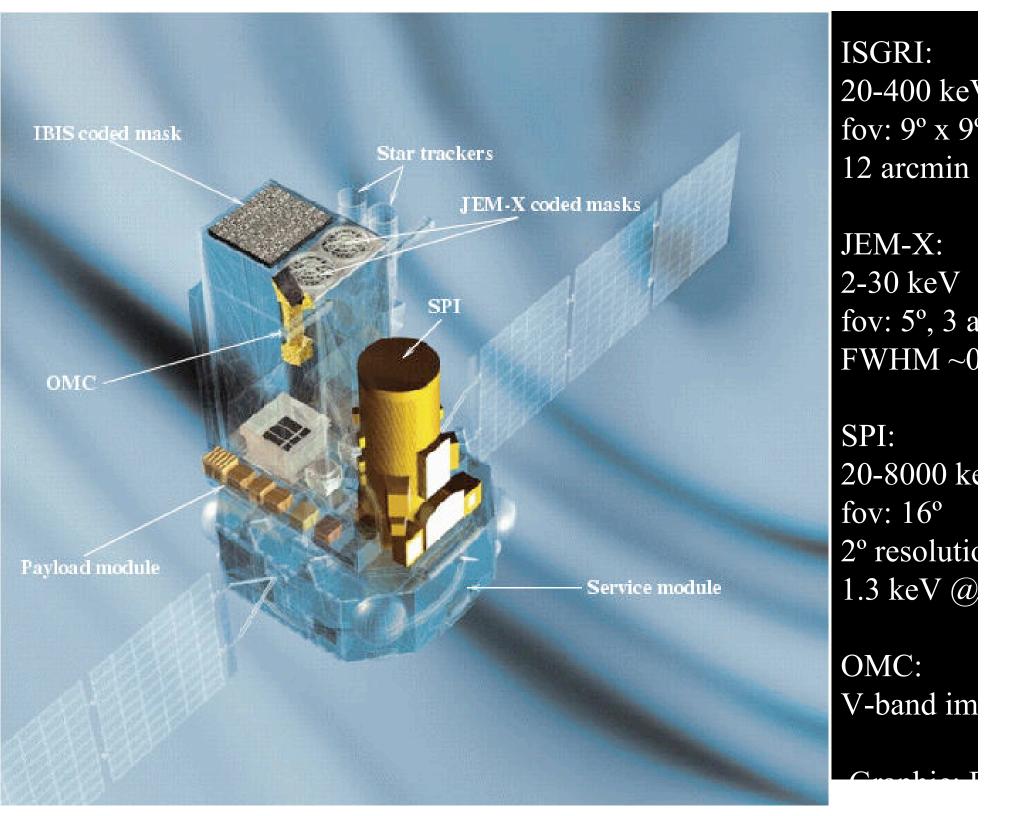


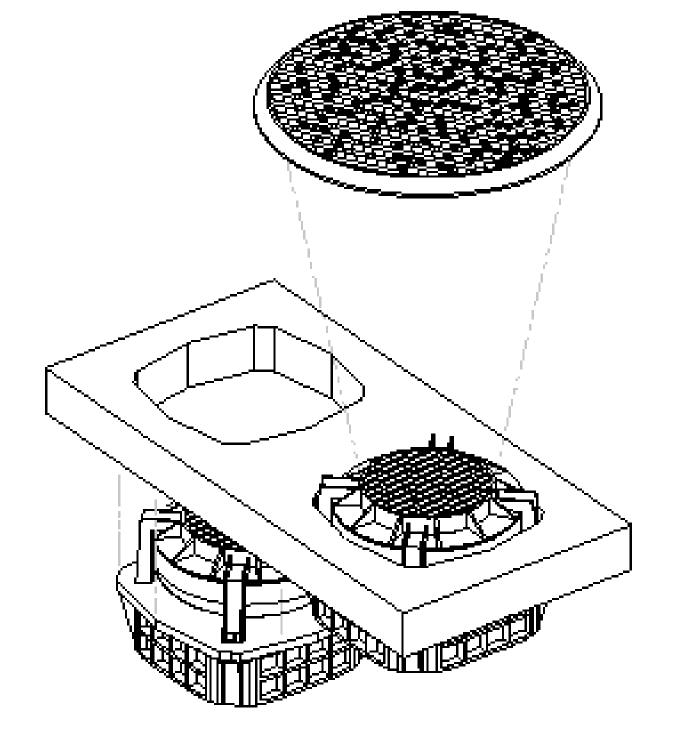




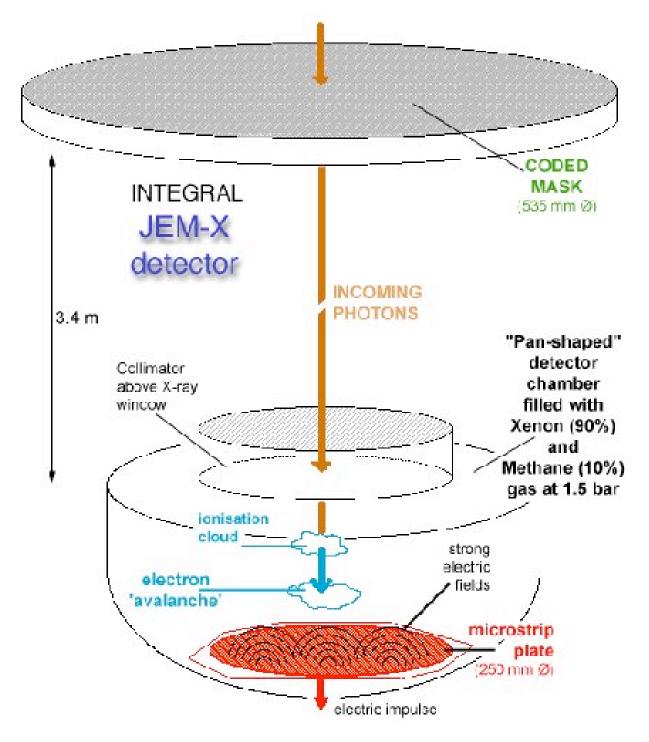
# JEM-X data analysis

- \_ JEM-X the X-ray monitor of INTEGRAL
- \_ What can we do with JEM-X?
- \_ Running the pipeline jemx\_science\_analysis
- \_ Data products images and spectra
- \_ JEM-X spectra in XSPEC
- \_ Summary





JEM-X consists of two identical detectors, JEM-X1 and JEMX2



Functional design of the JEM-X detector

(Graphic: ESA/JEM-X instrument team)

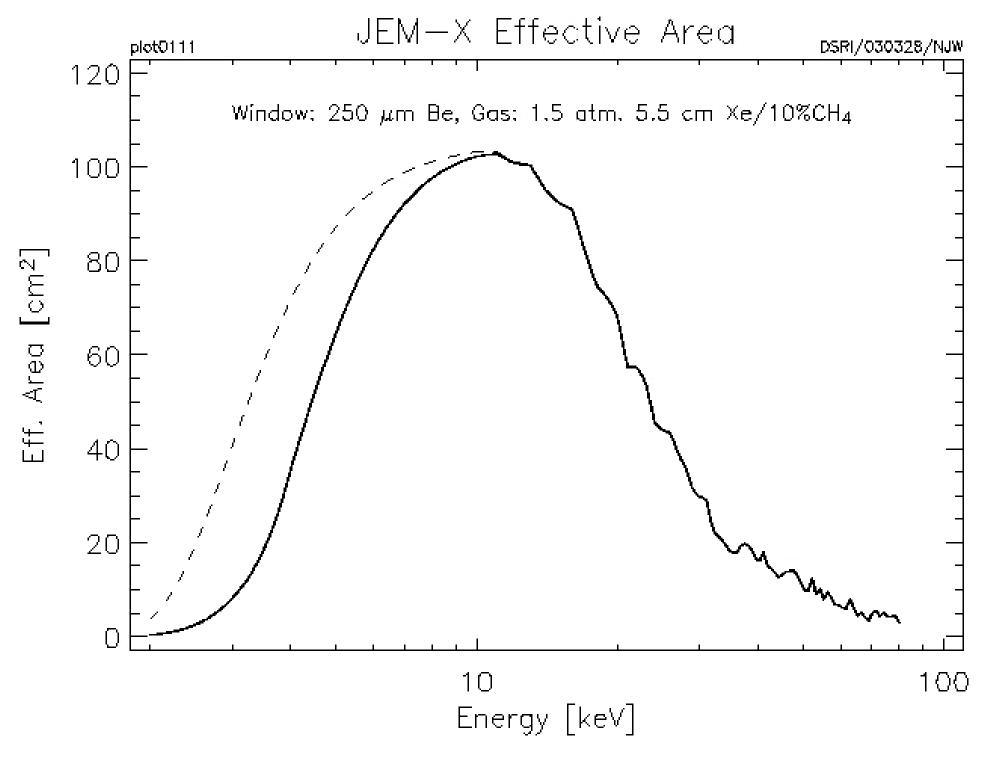
#### Some numbers...

Energy rangeFWHM3 – 35 keV0.40 E[ke]

 $\sqrt{\phantom{a}}$ 

 $\boldsymbol{\mathsf{Q}}$ 

μ



Graphic: DSRI

- Target position
- 7 point hexagonal pattern
- 25 point rectangular pattern

Graphic: ISDC

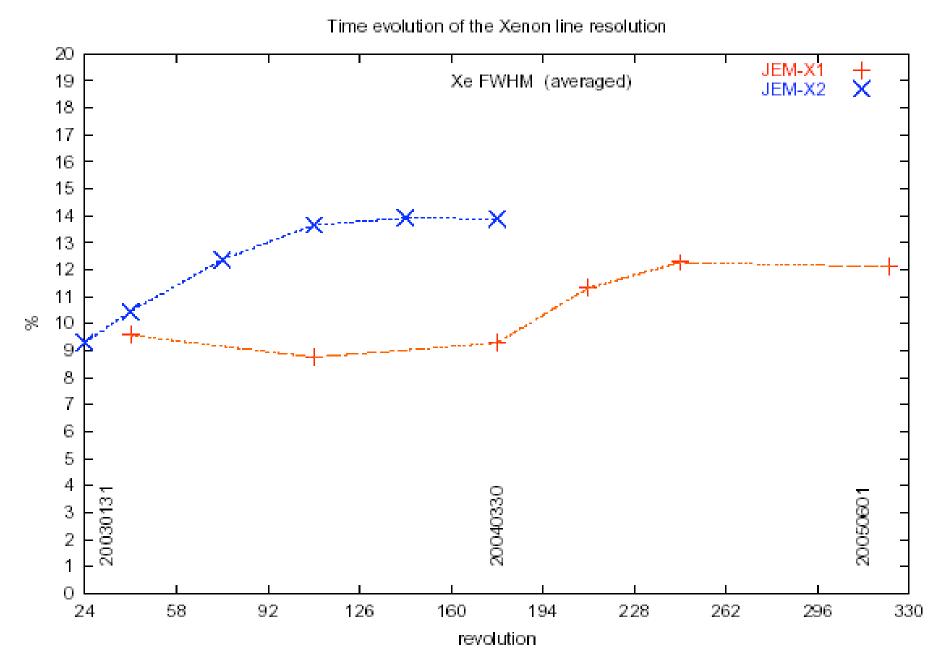
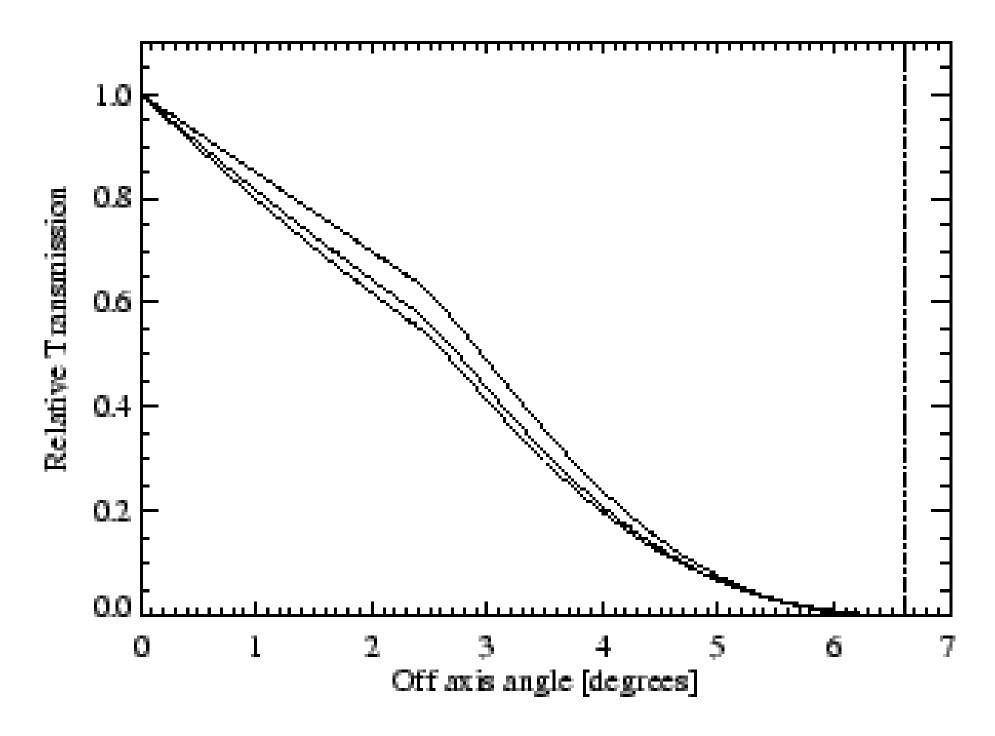
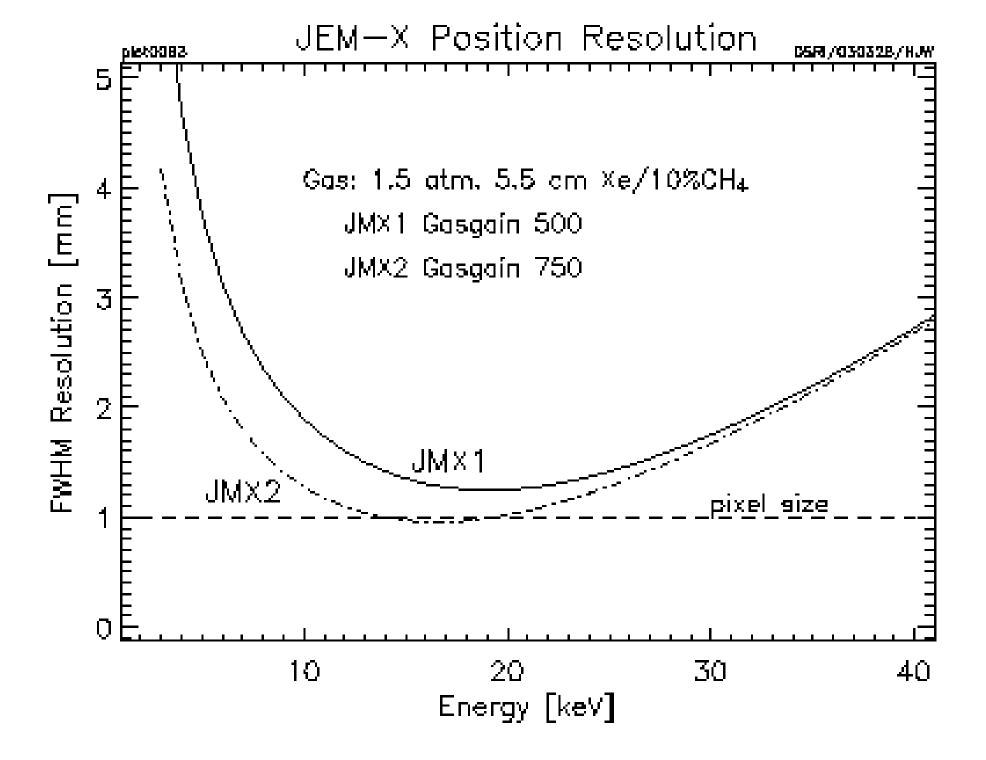


Figure 2.7: The energy resolution of the two JEM-X instruments determined from the 30 keV Xe line. To improve statistics results from several science windows are added.

Graphic: JEM-X Science Validation Report 5.0



Graphic: JEM-X user manual



Graphic: DSRI

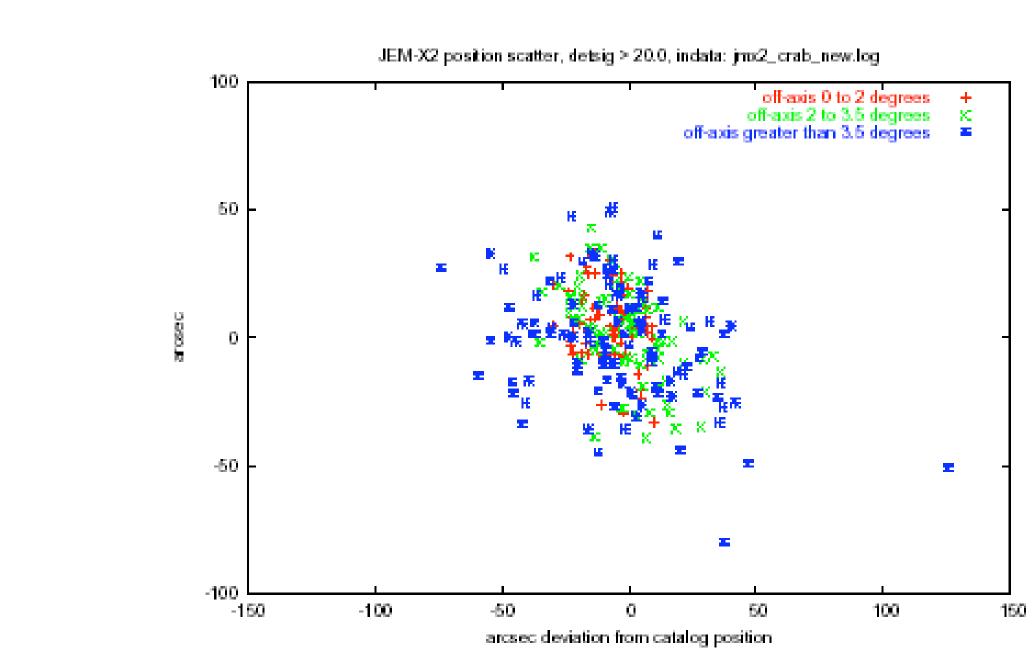
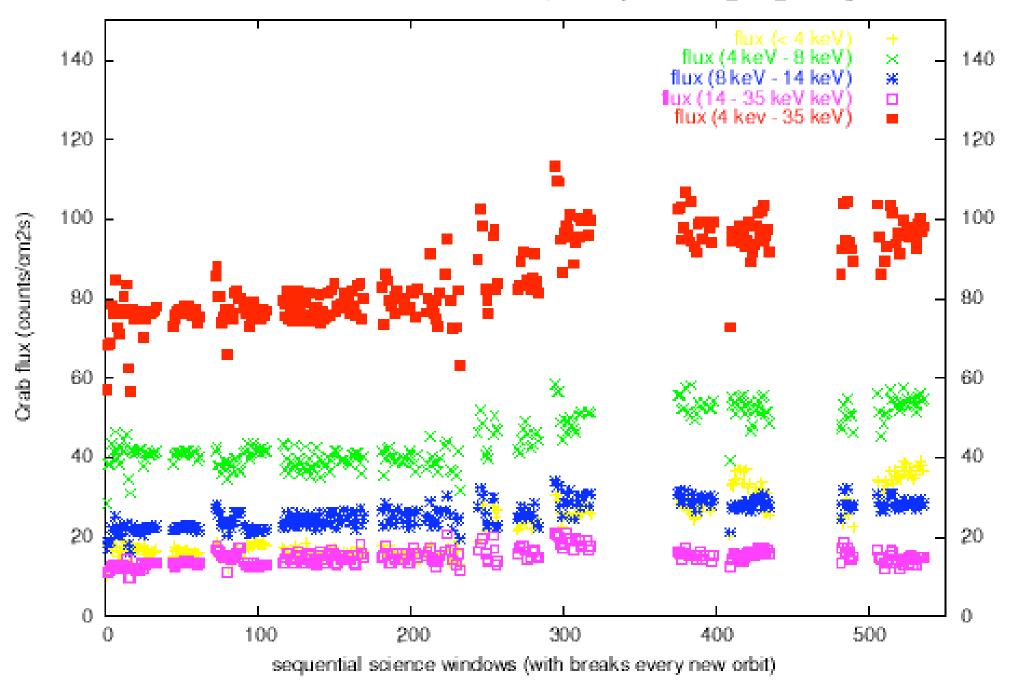


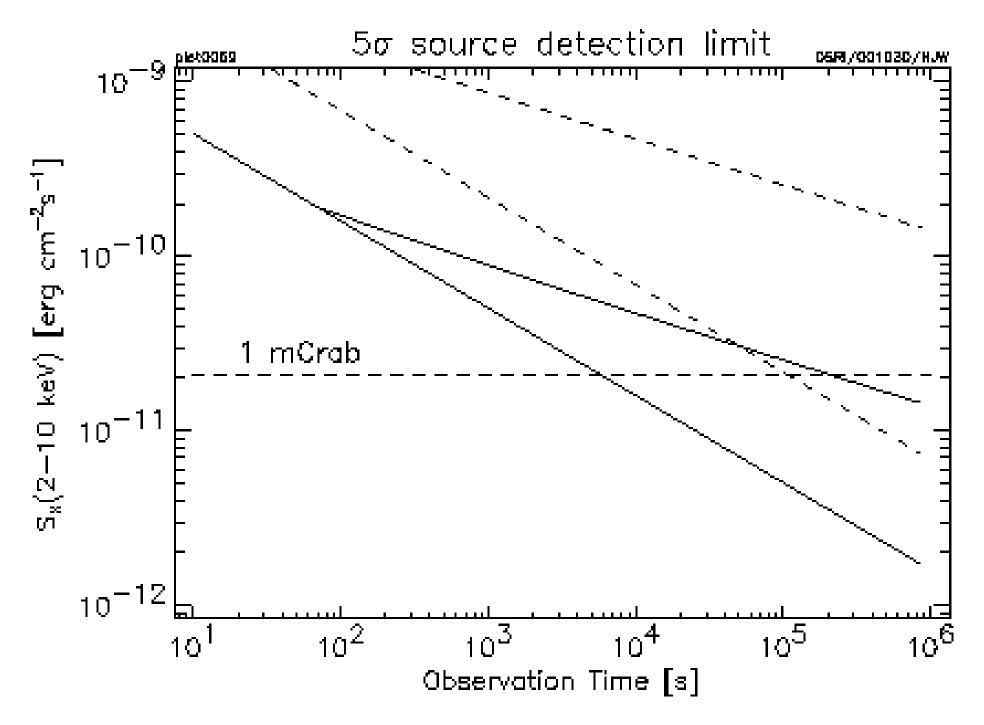
Figure 4.4: Position scatter of 350 detections of the Crab by JEM–X2. A detection significance limit of *detsig*> 20 has been used.

Graphic: JEM-X Science Validation Report 5.0

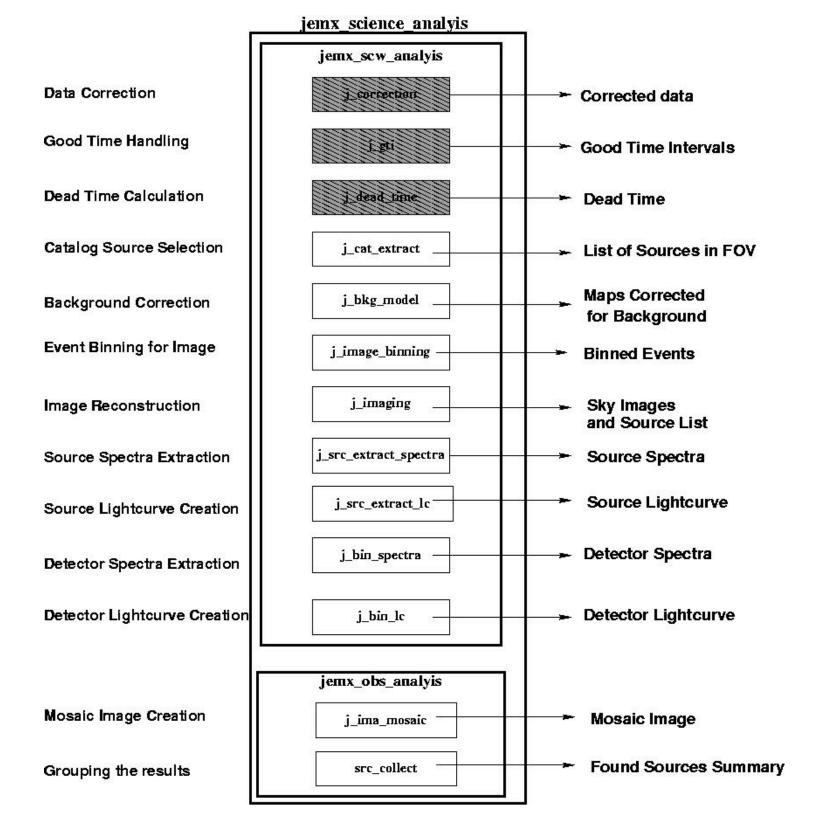
JEM-X1 and -2 flux values for Crab obs., indata: jmx1 and -2\_crab\_new.log.



Graphic: JEM-X Science Validation Report 5.0



Graphic: DSRI



jemx_science_analysis		
General ogDOL: jemxNum: startLevel: General Binning Tasks nChanBins:	CAT_I endLevel: IMA2	Save Save As Run Quit Help hidden
	46 83 129 160 82 128 159 223	
Good Time Intervals  GTI_gtiUser:  GTI_TimeFormat:	<u> </u>	
Catalog Extraction  CAT_I_refCat:  CAT_I_usrCat:	\${ISDC_REF_CAT} browse browse	
Event Binning for Imaging - BIN_I_backCorr	□ checked: yes	
Source Spectra Extraction SPE_timeStep:	0	
Source Lightcurve Extracti		

JEM-X science analysis GUI

- Which JEM-X was on? Set jemxNum
- Run from COR to IMA2
- \_ Select energy channels for the images you find the channel/energy correlation in the cookbook
- \_ use the general reference catalog or your personalized catalog
- \_ set the timing step
- \_ set IMA\_DetSigSingle to <12 for weak sources
- \_ jemx\_science\_analysis on GCDE revolution 175 (38 pointings) takes about 1 hour

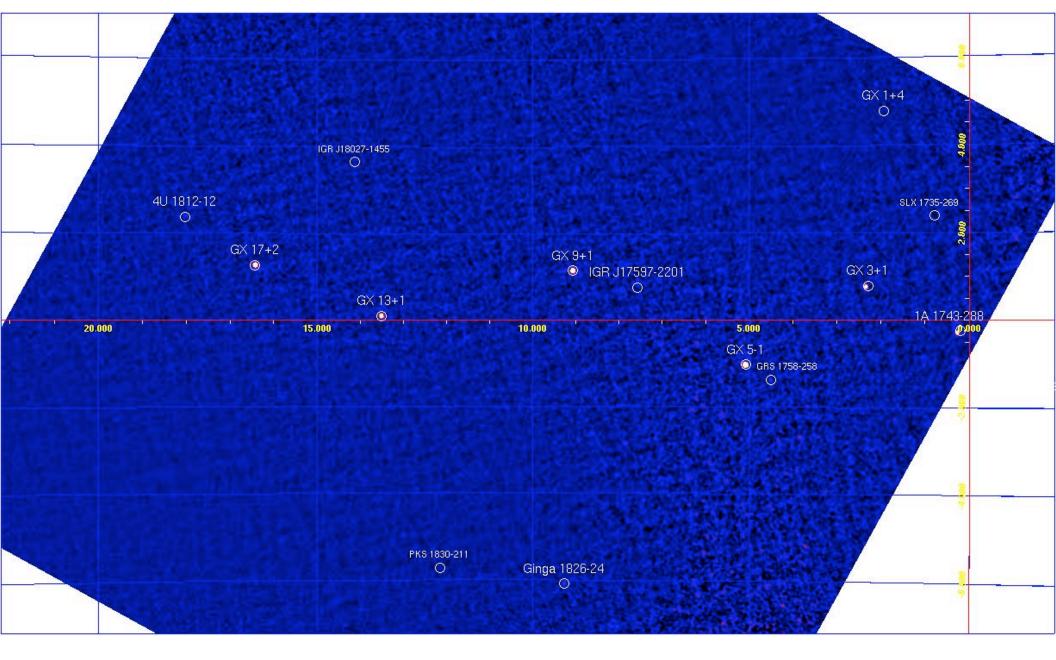
```
tgrosf:/data/darius/Integral/high_level/obs/ESO209-12_JEMX
                                                                                                          2005-11-05T01:17:41 j_ima_mosaic 5.0.4: This is the Exposure time map --STAMP-- OBS_TIME_180.fits[JMX2-MOSA-I
Log_1
MA,1,IMAGE]
       2005-11-05T01:17:41 j_ima_mosaic 5.0.4: -> Plot effective exposure Time map in OBS_TIME_180.fits[3]
Log_1
       2005-11-05T01:17:42 j_ima_mosaic 5.0.4: This is the Effective exposure time map --STAMP-- OBS_TIME_180.fits[J]
Log_1
MX2-MOSA-IMA.2.IMAGE1
Log_2
       2005-11-05T01:17:43 j_ima_mosaic 5.0.4: Work completed: status is 0
Log_1 2005-11-05T01:17:43 j_ima_mosaic 5.0.4: Task j_ima_mosaic terminating with status 0
Log_0 2005-11-05T01:17:43 jemx_obs_analysis 4.5.5: Current working directory is /net/darius/Integral/high_level/obs
/ES0209-12_JEMX
       2005-11-05T01:17:43 jemx_obs_analysis 4.5.5: Running /data/anu/isdc/osa_sw-5.0/bin/src_collect group="og_jmx2|
Log_0
fits[GROUPING,1]" instName="DEFAULT" results=".///jmx2_obs_res.fits(JMX2-OBS.-RES.tpl)" select="" attach="yes" chatt|
er="2" 2>> data_analysis.log
       2005-11-05T01:17:44 src_collect 1.1.1: Task src_collect running in SINGLE mode
Log_1
Log_1
       2005-11-05T01:17:44 src_collect 1.1.1: Beginning parameters
       2005-11-05T01:17:44 src_collect 1.1.1: Parameter group = og_jmx2.fits[GROUPING,1]
Log_1
Log_1
       2005-11-05T01:17:44 src_collect 1.1.1: Parameter instName = DEFAULT
Log_1
       2005-11-05T01:17:44 src_collect 1.1.1: Parameter results = .///jmx2_obs_res.fits(JMX2-OBS.-RES.tpl)
       2005-11-05T01:17:44 src_collect 1.1.1: Parameter select =
Log_1
Log_1
       2005-11-05T01:17:44 src_collect 1.1.1: Parameter attach = yes
       2005-11-05T01:17:44 src_collect 1.1.1: Parameter chatter = 2
Log_1
Log_1
       2005-11-05T01:17:44 src_collect 1.1.1: Ending parameters
Log_1
       2005-11-05T01:17:44 src_collect 1.1.1: Running in scripting mode, no parameter prompting
Log_2
       2005-11-05T01:17:54 src_collect 1.1.1: JMX2 observation group, will collect JEM-X results
       2005-11-05T01:17:58 src_collect 1.1.1: Combined source results --STAMP-- jmx2_obs_res.fits[JMX2-OBS.-RES.1.BI
Log_1
INTABLE 1
Log_0
       2005-11-05T01:17:58 src_collect 1.1.1: Wrote 2 entries to output table
Log_1
       2005-11-05T01:17:58 src_collect 1.1.1: Task src_collect terminating with status 0
       2005-11-05T01:17:58 jemx_obs_analysis 4.5.5: Task jemx_obs_analysis terminating with status 0
Log_1
Log_0
       2005-11-05T01:17:58 jemx_science_analysis 4.5.5: jemx_obs_analysis(): Program was finished successfully !
       2005-11-05T01:17:58 jemx_science_analysis 4.5.5: Task jemx_science_analysis terminating with status 0
Log_1
tgrosf [1331] [beckmann]: ls
OBS_TIME_180.fits scw
J_MOSAIC_O.fits J_MOSAIC_2.fits jmx2_obs_res.fits og_jmx2.fits swg_idx_jmx2.fits
tgrosf [1332] [beckmann]: ls scw/013700980010.001
jmx2_dead_time.fits jmx2_full_cor.fits jmx2_gti.fits jmx2_srcl_cat.fits swg_jmx2.fits
jmx2_evts_shd.fits _jmx2_full_dsp.fits _jmx2_sky_ima.fits _jmx2_srcl_res.fits
tgrosf [1333] [beckmann]: [
```

# iemx science analysis

OBSTIME: observation time, effective exposure time

```
J_MOSAIC_0.fits: intensity, significance image
```

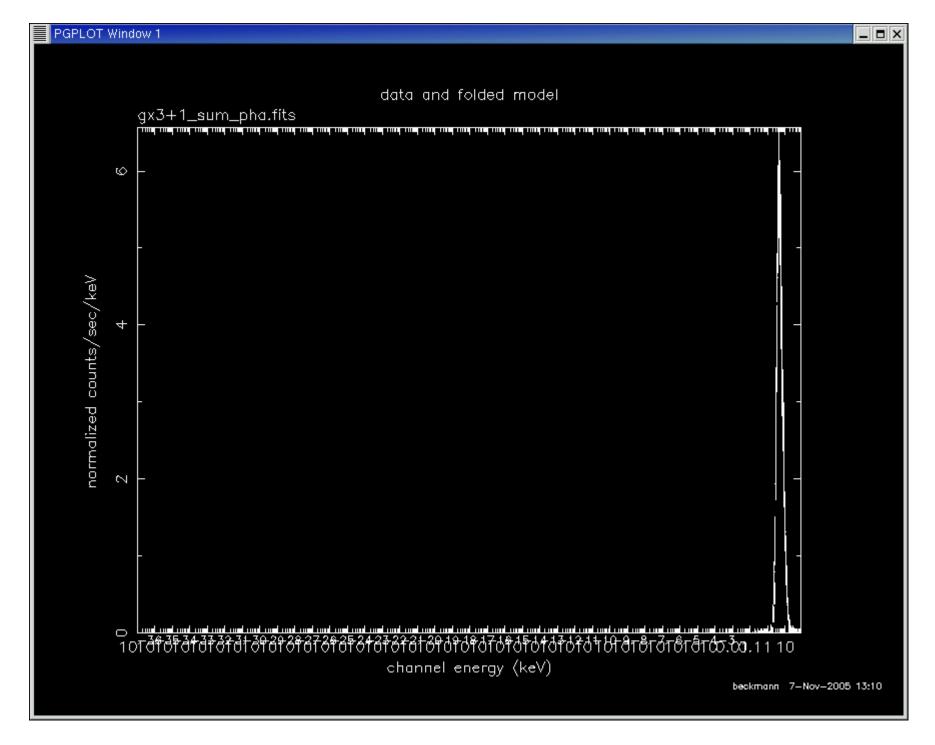
JEM-X and SPI use the IROS method scw/directories: jmx2\_sky\_ima.fits (raw, variance, residual, residual + source)



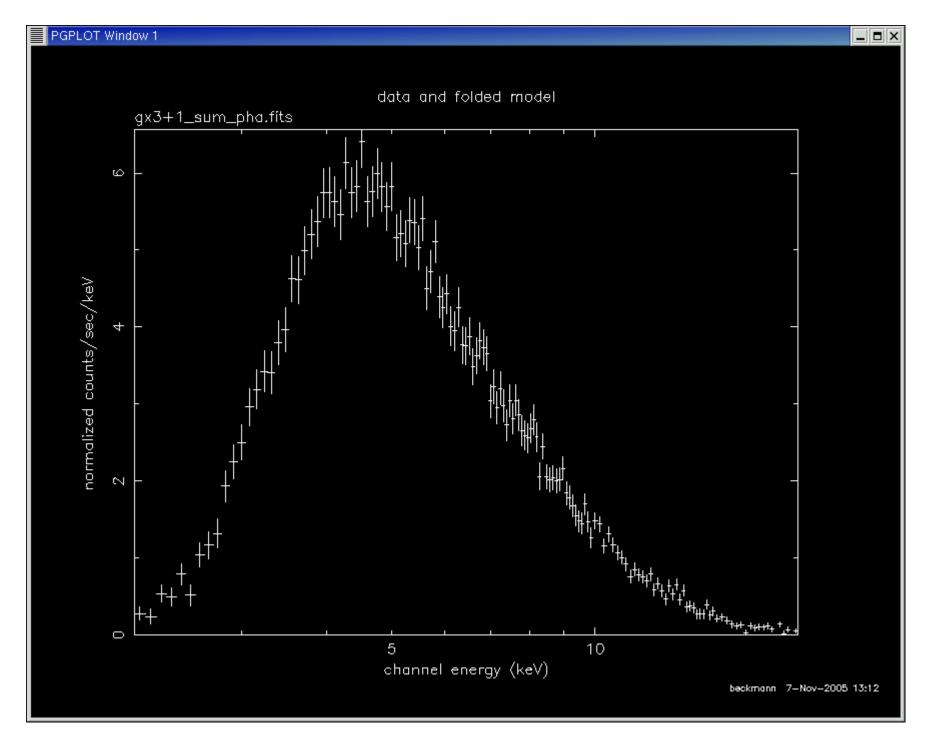
JEM-X mosaic image (1.5 - 12 keV) of the GCDE revolution 175 observation.

- \_ in order to combine spectra:
  \_ spe\_pick group="og\_jmx2.fits[1]"
  instrument="JMX2" source="J....."
  rootname="GX3+1" sum =y

  \_ GX3+1\_single\_pha2.fits
- \_ GX3+1\_single\_arf2.fits
- \_ GX3+1\_sum\_pha.fits
- \_ GX3+1\_sum\_arf.fits
- \_ RMF is already linked



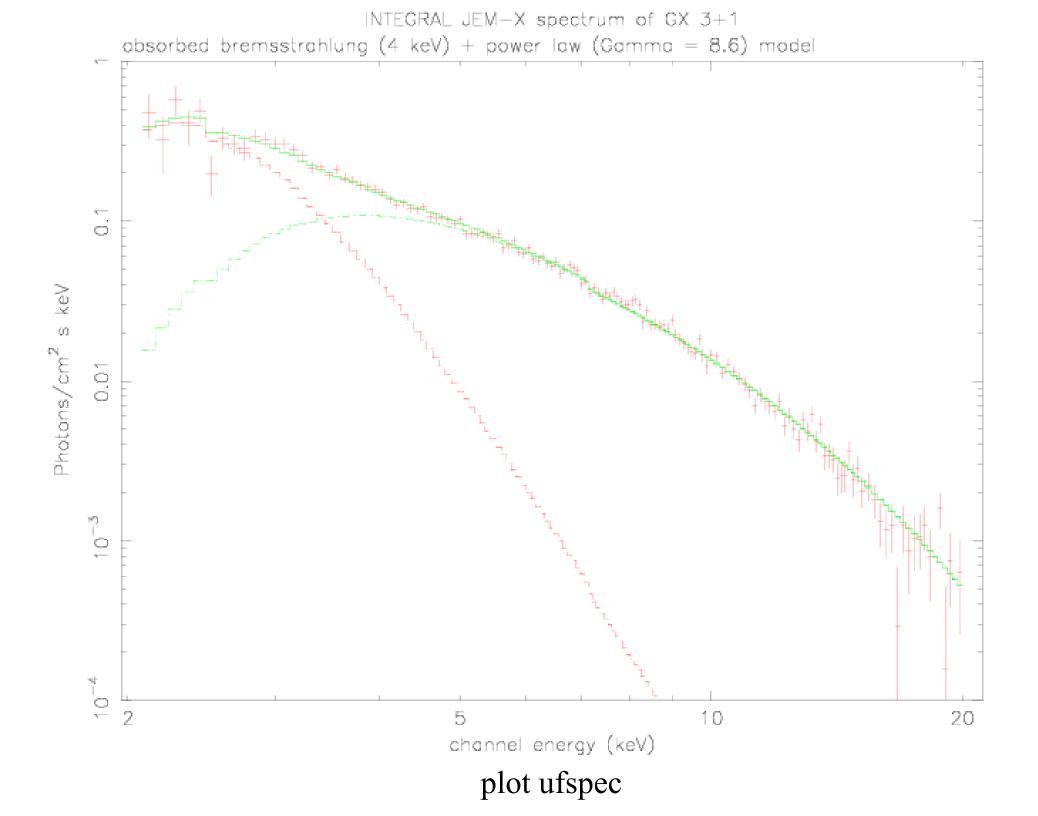
Spectrum loaded into XSPEC 11: cpd/xs setplot energy plot ldata



ignore \*\*-2.0

ignore 20.0-\*\*

plot ldata



- \_ spectrum from a given position (where nothing was detected) :
- \_ create a catalog and include the position
- \_ add this catalog to all the catalogs in the science window tree (see cookbook for instructions)
- \_run jemx\_science\_analysis from SPE to SPE
- \_ fluxes only from spectral extraction

# JEM-X science analysis summary

Use og create with JMX1 or JMX2 go to the directory in the obs/ branch \_ run jemx\_science\_analysis from COR to IMA2 \_ cat2ds9 for creating a region file \_ look at the mosaic significance image with ds9 "J MOSAIC\_0.fits[2]" \_ extract the spectrum with spe\_pick \_ use the extracted spectrum in XSPEC to

determine the flux