X-ray astronomy tutorial

Jean Ballet, AIM/Sap, CEA Saclay

First part: Introduction

- Archives
- XMM SAS
- Data exploration
- Spectral extraction

Second part: Spectroscopy

- Counts vs photons
- XSPEC
- Load a data set
- Choose a model
- Poisson statistics
- Adding components
- Confidence intervals
- XSPEC scripts
- Plasma diagnostics

Data for the tutorial is available in file NGC253.zip

Introduction: archives

Starting point: data set coming from an archive

XMM-Newton, Chandra, GSFC (Goddard) all have their archive

Call XMM-Newton archive from a browser

Look for NGC 253

Click on one observation, look at main image (sum of 3 EPIC instruments)

Need to sign in as a user (right of window) to retrieve data

Introduction: XMM SAS

XMM-Newton SAS easily found in Google

Doc contains useful data analysis threads which can be used as examples:

- Spectrum extraction
- Spectral analysis with XSPEC

Introduction: data exploration

Look into EP directory

Call SUMMAR file in a browser. It describes all available products

Have a look at FBKTSR file (for flare screening)

Go to M1 directory

Call the MIEVLI file (main events list) into xmmselect table=infile

Define two columns (DETX/DETY for detector coordinates)

Create an image: it appears in ds9

Define a source region and call from xmmselect (2D region)

May create a light curve (change the bin from 1 s to 100 s at least)

Introduction: spectral extraction

Continue from previous xmmselect session

Create OGIP spectrum (appears in grace)

The full spectral extraction process involves

- Getting the energy response (rmfgen)
- Getting the effective area (arfgen)
- Getting the background (for point source, can be obtained from annulus around the source

Spectroscopy: counts vs photons

Most X-ray data today is low-resolution spectroscopy

Redistribution is large and complex (see redistribution matrix below)

Effective area has edges (see effective area below)

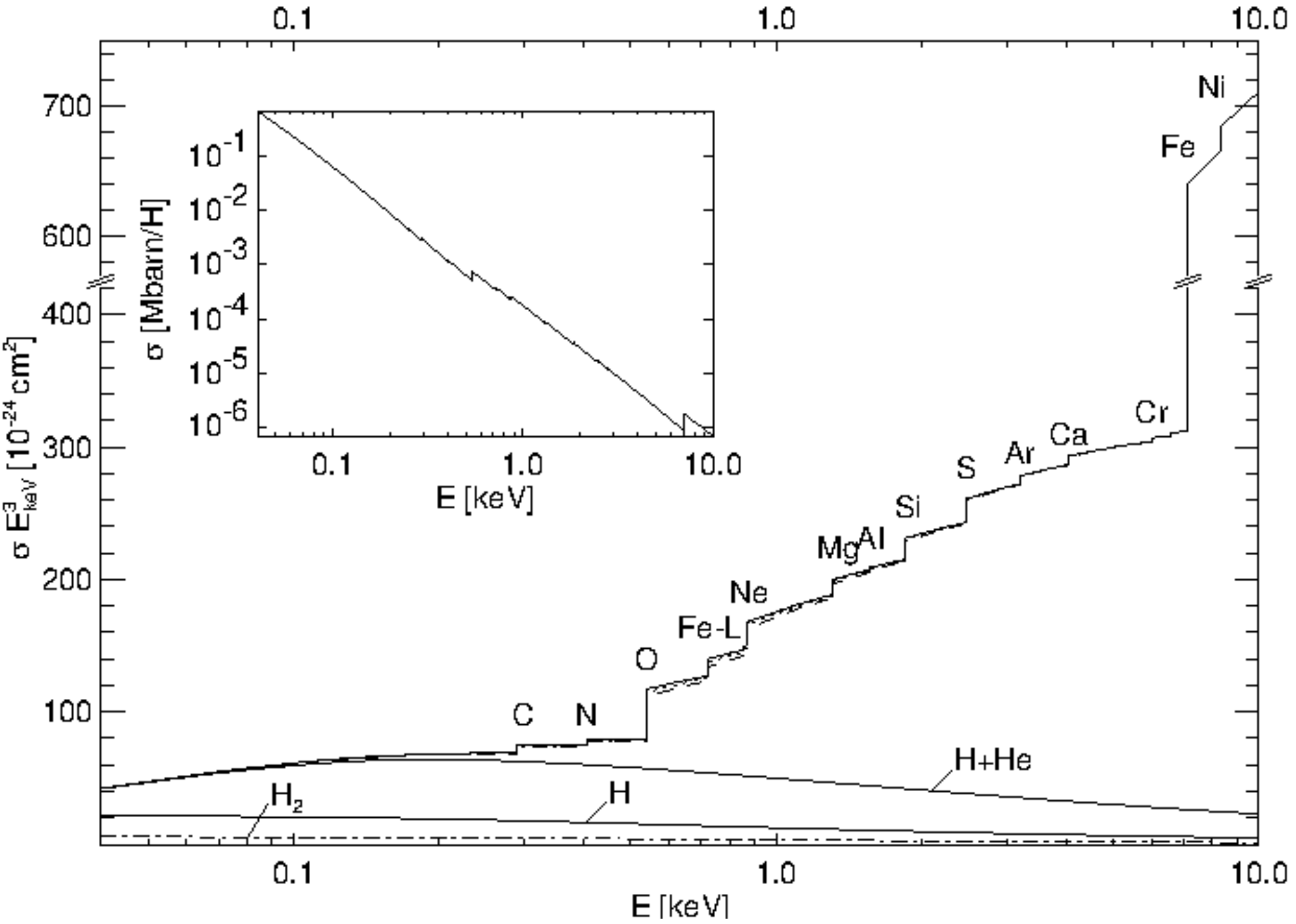
This is because of elemental photo-electric absorption

The same occurs in the interstellar medium (see interstellar absorption below, in which the cross section was multiplied by E^3 to take out the main trend)

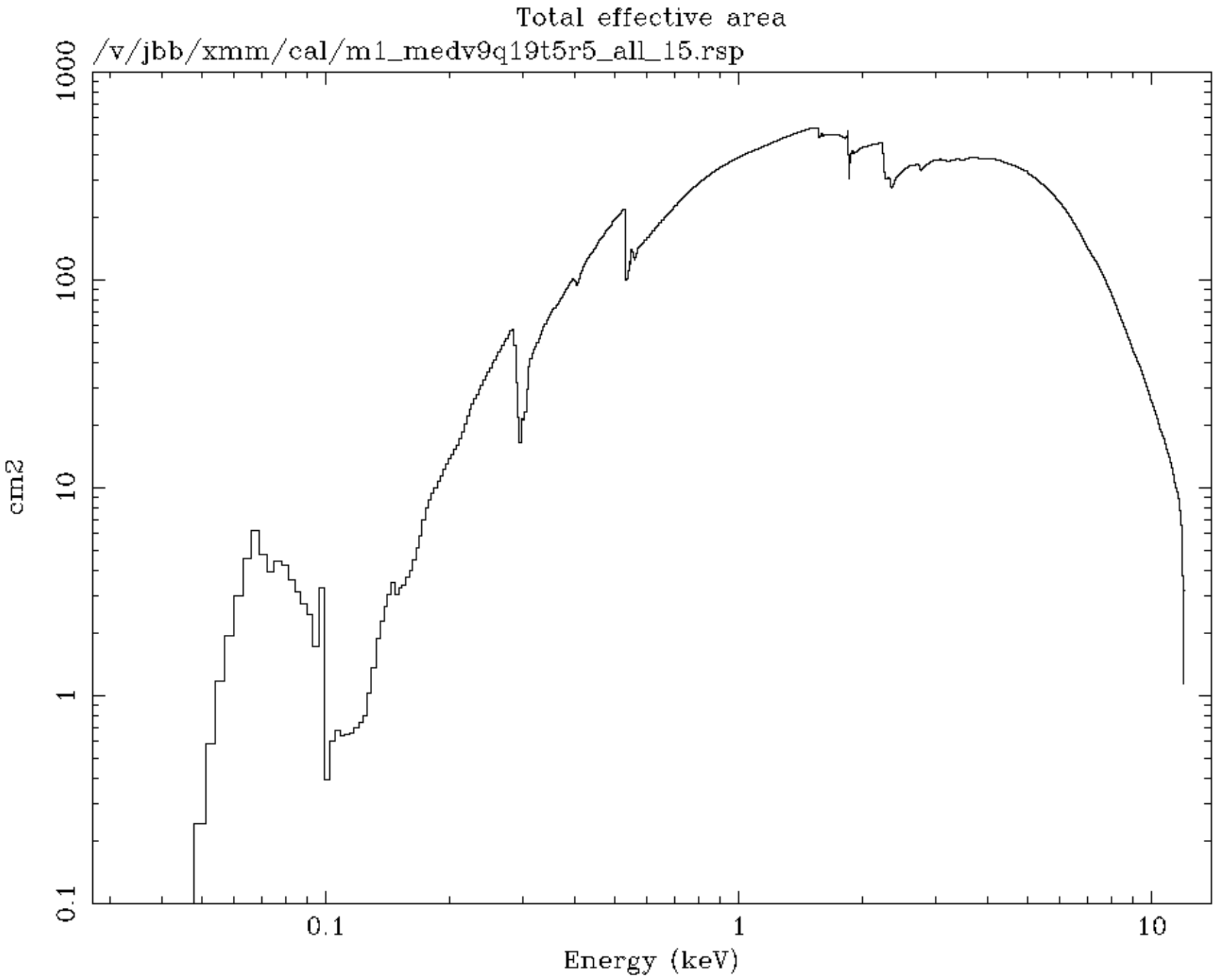
Data always has to be analysed using a redistribution equation between energy (E) and channel (C). In many cases channels are expressed in eV just like energies but are denoted by PI.

$$\frac{dN}{dC} = t \int_E R(E,C) A(E) \frac{dN}{dE} dE + B(C)$$

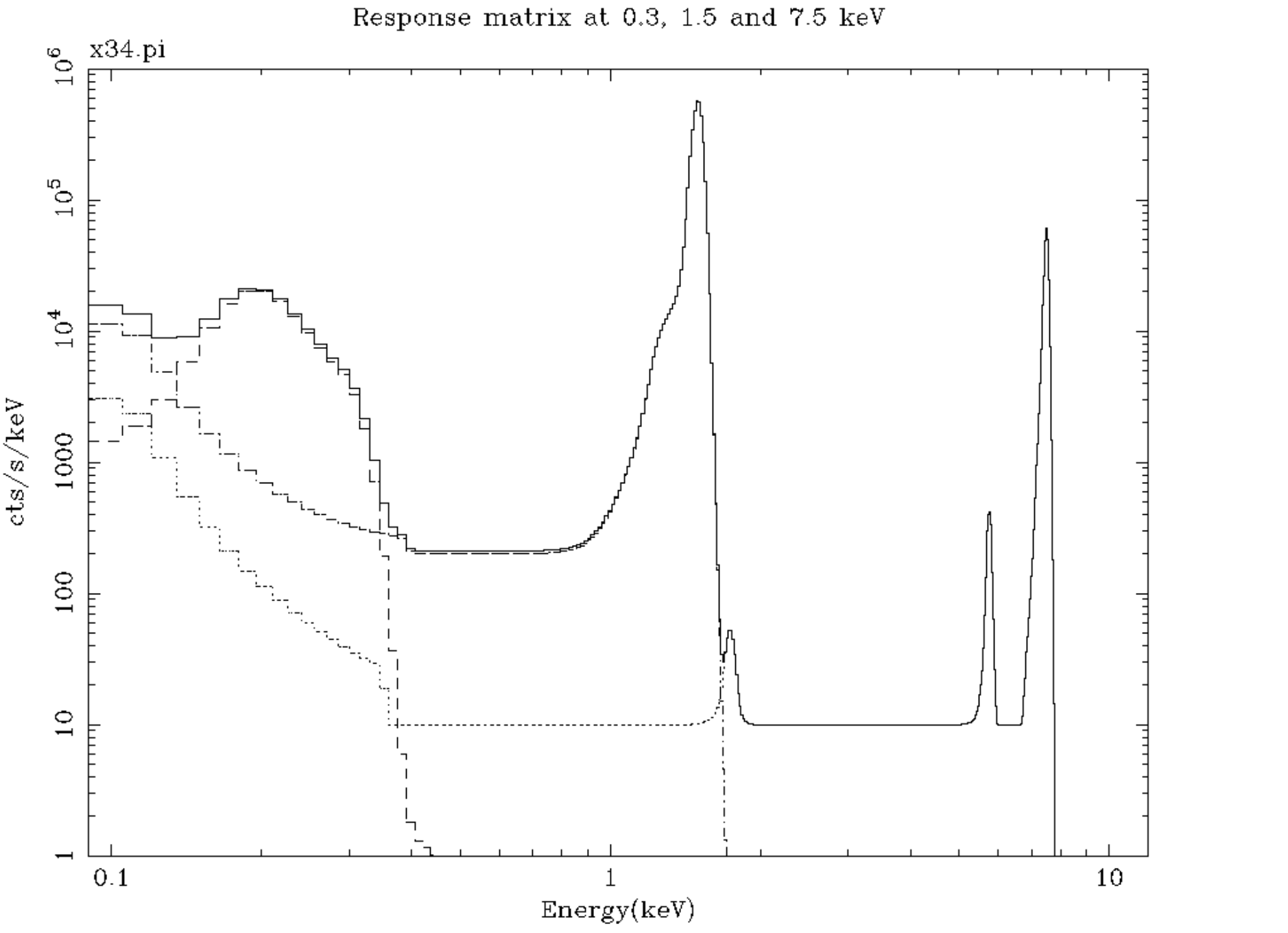
Interstellar absorption



Effective area (.arf)



Redistribution matrix (.rmf)



Spectroscopy: XSPEC

XSPEC is an old fitting tool but still widely used because of its rich library of models

Call XSPEC manual into your browser

Look at the introductory chapters

- Walks through XSPEC
- Overview
- Spectral fitting

Go to Spectro directory and launch *xspec*

Create a plotting window via *cpd /xw*

Spectroscopy: load a data set

Load the data set (nucleus of NGC 253): *data x34.pi*

plot to have a first look

setplot energy and *plot* again

ignore 0.-0.3 and *plot* again (opposite is *notice*)

plot ldata for logarithmic view in Y

setplot background (and *plot* again) to compare background level

setplot rebin 3 50. to rebin channels (for viewing purposes only)

Spectroscopy: choose a model

XSPEC has multiplicative and additive models

Look at doc for list of available models

Enter absorbed thermal model: *model phabs (mekal)*

Default parameter values are fine for a start

renorm to get normalisation similar to data and *plot* to see the overlay

Release the abundance (parameter 4, fixed by default): *thaw 4* (opposite is *freeze*)

Launch your first *fit* and *plot* again

Spectroscopy: Poisson statistics

There are always only few counts per channel at high energy. Most of the time there are only a few counts per resolution element.

The χ^2 statistic is not adequate (amounts to ignoring high energy)

One can rebin data (grppha ➔ group min 25) but at the cost of energy information. Less aggressive rebinning is not enough (x34.grp.pi has 10 counts per bin, but it still underestimates high energy)

Best solution is to use Poisson likelihood: *statistic cstat*

Refit (*fit*) and *plot* to see the difference. High energy is now considered adequately

Implementation of cstat in XSPEC does not handle background spectrum correctly. Best solution is to fit the background and use a model. Alternate is to make it appear that the background is infinitely good (make it RATE and increase EXPOSURE keyword).

Spectroscopy: adding components

The current model is obviously not adequate(clearly bad fit).

Add another similar component: *addcomp mekal*; *addcomp phabs*

Check what is in the model (*show model*)

Force the norm of the new mekal component to be similar to the previous one (10^{-3}) in order to start from a reasonable model: *newpar 7 1e-3*

We will now force the two abundances to be the same: *newpar 4=11* (*untie* is the way to break the link)

fit and *plot* again; Look at individual components: *setplot add*

Check the improvement by looking by how much cstat improved. If the new model is not required, the difference is expected to follow a χ^2 distribution with 3 dof (number of additional free parameters). That would be 11.35 at 99%.

The improvement is large but the fit is not good yet. Add a third identical component in the same way and *fit*. The result is now reasonable.

Spectroscopy: confidence intervals

The *fit* command provides by default quadratic errors (from the covariance matrix around the best fit). This is often not good enough when the errors are not very small with respect to the parameter values.

One can get a more robust error estimate from the true likelihood profile. This is done by calling *error i* where *i* is the parameter number. By default the errors are provided at 90% confidence.

Sometimes this does not work and one needs to look at the profile manually. This is done via *steppar best i x1 x2 n* where *x1* and *x2* are the bounds and *n* the number of points (best means that the other parameters are refit).

To visualise the result, *plot contour* (this is not a contour, I know)

The main application of steppar is for two parameters (real contours): *steppar best i x1 x2 ni j y1 y2 nj* and *plot contour*. In 2D *steppar* can be quite long.

Spectroscopy: utilities

XSPEC provides several useful commands:

- *log outfile* to kep track of what you did during the session in outfile.log
- *save model outfile* to store the current model in outfile.xcm. The resulting file is editable (a simple ASCII file) and can be reingested via *@outfile*.
- One can also *save files* to remember which data files were entered or *save all* to keep both model and data.
- *script outfile* stores all the commands that were passed to XSPEC. This can be replayed via *source outfile*.
- XSPEC can be scripted using the Tcl language.

Spectroscopy: plasma diagnostics

When a source is observed at high spectral resolution (such as the gratings on XMM or Chandra) individual lines can be measured (this is not possible with CCDs, the lines are blended) and specific plasma diagnostics can be achieved.

See the jbb_spectroX.pdf file for a more detailed discussion.