CROSS CALIBRATION FOR XMM-NEWTON

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Project: automated cross calibration fitting tool

XMM-SOC has created an automated cross calibration tool to fit the X-ray data from XMM-Newton

In order to "check in" new observations manual steps must be made such as region definition and finding the best fit models

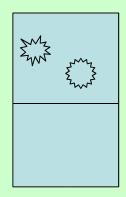
Throughout the presentation we will find out:

- Why pileup appears and how it can ruin our spectra
- How the fit concept appears and why it is helpful
- What mathematical and statistical tools and knowledge we use to do the fitting
- How we use these to know if our fit is a good one

EPIC Pile-up

It's the arrival of more than one photon in a pixel or adjacent pixels before it's read out
 2 photons or 1 with high energy?

- Technology can not detect it
- Affects psf and the spectra

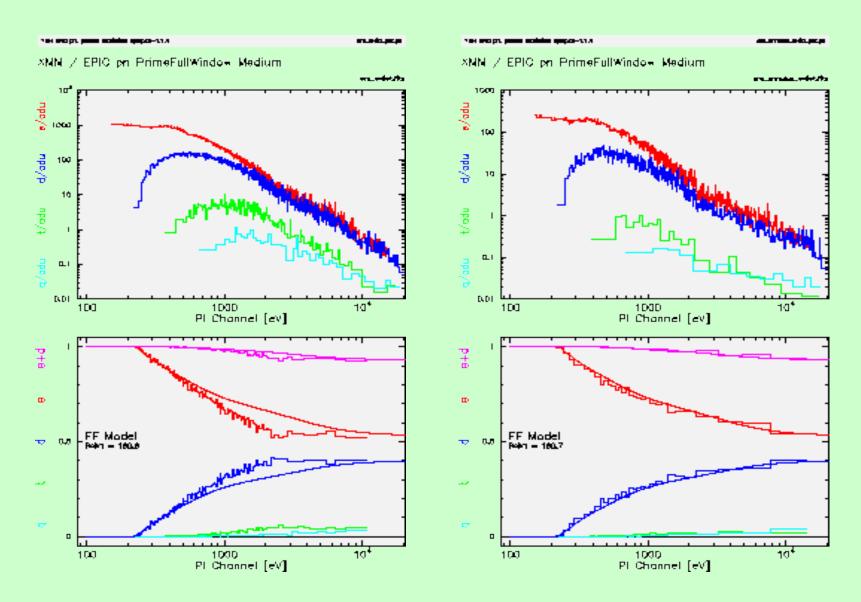


Solving pile-up

- SAS epatplot gives relation of single and double events
- Compare with models
- Exclude regions with heavy pileup

Source with pile up

Clean of pile up



XMM-Newton does not give us the actual spectrum but photon counts from each instrument channel. Both are related as follows:

$$\mathbf{C(I)} = \int_{0}^{\infty} f(E) R(I, E) dE$$

Known data:

C(I): photon counts R(I,E): instrumental response • Variable:

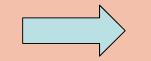
f(E) = the actual spectrum

Our goal is to clear out f(E) as a function of all the rest known variables from the relation: ∞

$$C(I) = \int_{0}^{\infty} f(E) R(I, E) dE$$

The problem

 Very tough restrictions (that usually do not occur) are needed to invert the equations. This makes inversions to be **non-unique** and **unstable** to small changes.



inversion **impossible**!

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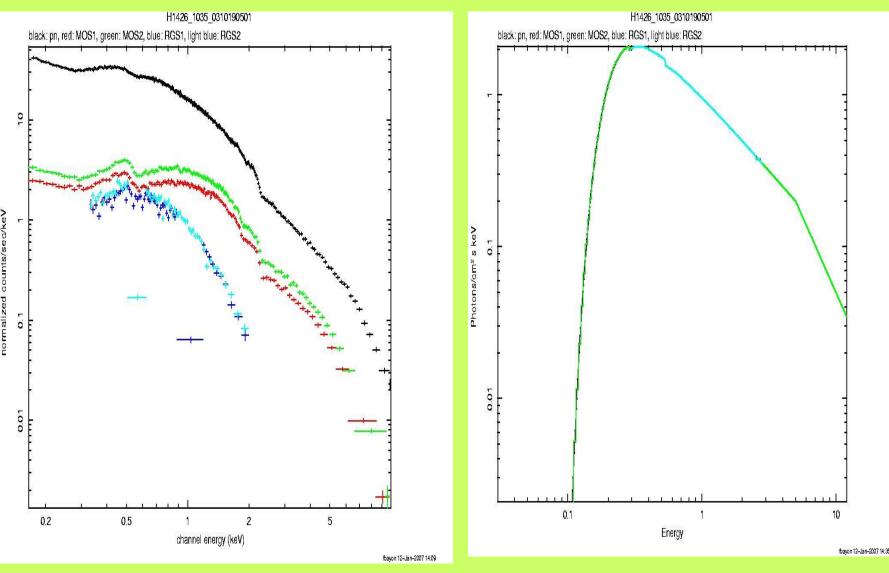
fit concept is needed

The solution: fitting

- The general idea is to find a simple model with few parameters that models well our data.
- **First: w**e choose a model spectrum in terms of few parameters $F(E, p_1, p_2..., p_n)$

Observed spectrum C(I) for obs ID 0310190501

Model Spectrum Phabs*Brokenpowerlaw



Then: calculate the predicted count spectrum for our model in each channel.

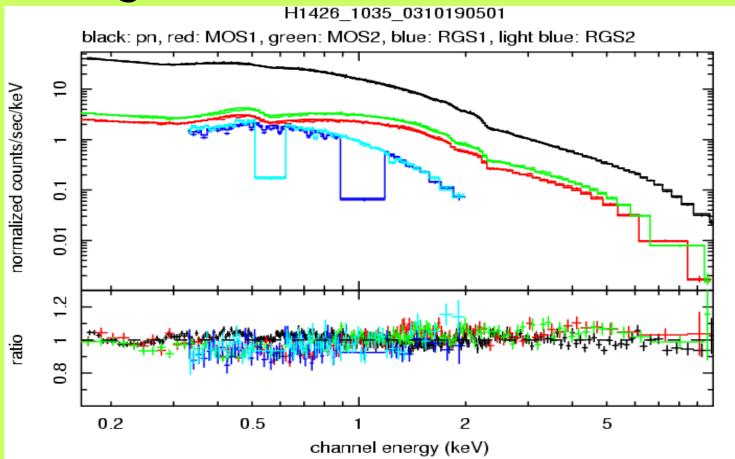
$$\mathbf{C}_{\mathsf{m}}(\mathsf{I}) = \int_{0}^{\infty} f(E, p_1, p_2 \dots p_n) R(I, E) dE$$

And **compare** this value to the observed one with the Chi-Squared stastic to test if we have chosen a good model $\frac{\sum_{N} (C(I) - C_m(I))^2}{\sigma(I)^2}$

Now: vary the parameters p₁,p₂...p_n to find the best fit

To obtain:

• Fitting for 0310190501



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Comparison of model and data

 How do we know if the model we have chosen really 'fits' our source data? To study this we will consider the Chi-Squared statistic.

In general:

$$\int_{N} \frac{(y_i - f(x_i))^2}{\sigma_{i^2}}$$

In general:

- N = the number of data points
- σ_i = error made in iteration i, usually
 estimated by the square root of the number
 of iterations for i
- y_i = model variable
- $f(x_i) = actual value$

In our particular case:

- N = number of channels
- σ_i = error for channel i
- C(i) = number of counts observed
- $C_m(i)$ = folded model spectrum

So for our particular case the chi square is now:

 $\int \frac{(C(i) - C_m(i))^2}{(C(i) - C_m(i))^2}$ $X^{2} =$ $o_{i^{2}}$

 If we have chosen a good model, the difference between the observed counts and the expected model counts in each channel should be about the same as the error expected for this channel.

 $C(i) - C_m(i) = \sigma(i)$ and if this happens it implies

$$\frac{C(i) - C_m(i)}{\sigma(i)} = 1 \qquad \Longrightarrow \qquad \frac{(C(i) - C_m(i))^2}{\sigma(i)^2} = 1$$

We have this equality for all N channels. If we remember how we had defined the chisquared we arrive to:

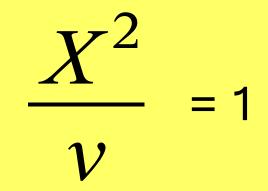
$$X^{2} = \sum_{N} \frac{(c(i) - c_{m}(i))^{2}}{\sigma(i)^{2}} = N$$
spec X² = N \longrightarrow X² = N - p

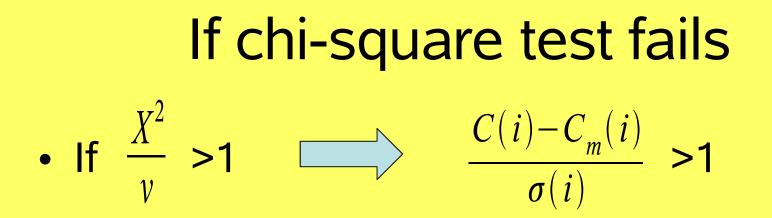
In Xspec $X^2 = N$ $\langle -p \rangle X^2 = N - p = v$ p small compared to N

degrees of freedom

So in general to see how good a model is we will look for:

The reduced Chi Squared

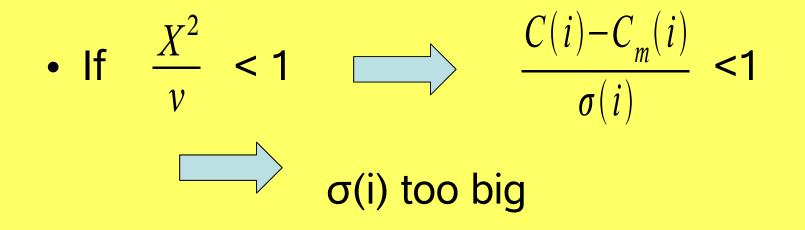


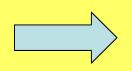


2 cases:

$C(i) - C_m(i)$ too big compared to $\sigma(i)$ wrong model

errors have been underestimated





errors have been overestimated

My part of the project

- Defining pile-up free regions for observations in the archive: aprox 300 regions defined
- Finding the best fit model and parameters for the spectra

Many left in the archive