Manual for XMM-Newton EPIC data reduction and production of light curves, images and spectra

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Chapter 1

Data reduction

1.1 Setup

The manual explains how to perform pipeline processing to the raw XMM-Newton EPIC data in order to produce cleaned event files. Also, the manual shows how to use these event files to produce spectra, images and light curves. The provided software is a wrapper that uses the software package called XMM-Newton Science Analysis Software , i.e. SAS (see **http://xmm.esac.esa.int/sas/8.0.0**) , maintained by the XMM-Newton team.

In order to run the reduction, you must have FTOOLS, ds9, IDL and XSPEC working. The analysis programs are tested to work with versions FTOOLS 6.0 and XSPEC 11.3 .2 (under HEASOFT 6.0.2), ds9 3.0.3 and IDL 6.1, in University of Helsinki Linux 2.6.9-34.0.1.EL_UHL3 platform.

IDL (http://www.ittvis.com/ProductServices/IDL.aspx) is a fortran- and C- based programming language, commonly used in X-ray astronomy community, which has been used to write a part of the analysis programs needed for this work. It should start just by typing **idl** in the Observatory machines (test this).

FTOOLS (http://heasarc.gsfc.nasa.gov/docs/software/ftools/ftools_menu.html) is a package that enables the processing of FITS format files (http://heasarc.gsfc.nasa.gov/docs/heasarc/fits.html) which is a commonly used format in X-ray observations. FTOOLS should be already installed in the Observatory computers. Test this by typing "**fhelp ftools**" which should give a list of FTOOLS commands and "**xspec11**" which should start a XSPEC session. If this does not work, try executing these lines:
alias heainit "source $HEADAS/headas-init.csh"
heainit
alias xspec xspec11
You may have to type first "**tcsh**" to change into C-shell. If the above lines are needed, write them into .cshrc -file in your home directory (if that works), so that FTOOLS is invoked automatically, when you open a terminal.

ds9 (http://hea-www.harvard.edu/RD/ds9/) is an application that you need to examine the FITS images.It should start by typing **ds9**.

1.2 Scripts

Copy a file **/data/jnevalai/XMM/sas_setup.script** into your home directory. Edit the **sas_setup.script** file by setting the variable **XMM_DATA_PATH** into the directory under which you will keep the data products, e.g. **/wrk/***yourname*/**XMM**. This path is referred as */your_data_path* in this manual. The script will enable the usage of the SAS software in your account. The script is executed by typing "**source sas_setup.script**". You should execute this command every time you start a SAS session (or write it into .cshrc file if that works). If all goes fine, you should get SAS software working by typing "**sas**". You can test this by typing "**sasversion**" , which should produce information about the installed SAS version. Make sure that FTOOLS is activated before running SAS.

Copy a file **/data/jnevalai/XMM/install.script** into your home directory. This script will produce a directory tree and copy relevant programs into your account necessary for the analysis. After running **sas_setup.script** , execute **source install.script**. This should be done only once, the first time you install the software. Under */your_data_path*, you should now have subdirectories "**/pipe**" ,"**/data**" , "**/scripts**" and "**/IDL**". You should have several script files under */your_data_path*/pipe/scripts . The pipeline processing of the raw data will be done with the above scripts under a directory defined as */your_data_path*/**pipe/data** . The further processing of the data will be done under directory */your_data_path*/**data** using the scripts and programs under */your_data_path*/**scripts** and */your_data_path*/**IDL**. Check that the above mentioned directories do exist and that the **IDL** and **scripts** directories do contain files.

1.3 Obtaining data

Go to **http://xmm.esac.esa.int/xsa/index.shtml** and click **"Start the XMM-Newton Science Archive (XSA) Interface"**. In the new window, click **"login/register"**. You have to register to obtain data.

To query data, the default is to use target name. Use A1795 or A3112 and **execute query**. Choose observation ID (**0097820101** or **0105660101**) and click **retrieve** next to the observation box. Select **ODF**. Download the tar file to your computer into directory */your_data_path*/**pipe/data**. Record the object name, observation date and observation ID for later.

1.4 Processing the raw data

Go to directory */your_data_path*/**pipe/data** . Copy there a file */your_data_path*/**pipe/scripts/do_chain** . Edit the parameters of "**do_chain**" file to match the data in hand. Each line corresponds to one data set. Change the "***.tar**" file into the file obtained above. 4. and 5. term are the object name and observation ID, referred as *objname* and *obsid* in the following. A subdirectory */objname/obsid/* will be created under which the data products will be placed. 6. term is the observation date in format "*yyyy-dd-mm*". 7. term is the ID of the EPIC instrument (P, M or PM) depending on whether you want to process data from PN, MOS or both. In the course we will use only the PN instrument.

Executing (after starting SAS and FTOOLS) "**source do_chain**" will run the processing of the raw data with current calibration information. Often a large number of warnings and error messages appears during the run, but usually they can be ignored. If successfully run, the process creates cleaned event files at */your_data_path*/**pipe/data***/objname/obsid/PN*. The cleaned PN event files are "**PN.FITS.gz**" and "**PNOOT.FITS.gz**".