

protonscale

April 16, 2023

Abstract

This task extracts the **BACKSCAL** keyword and average soft proton intensity from the detector map for a specified region. These values are necessary in the spectral fitting process of multiple regions which are linked. This task was originally a subtask of the SAS *esas* task named *proton_scale* prior to SAS-21 and retains all of its functionality.

1 Instruments/Modes

Instrument	Mode
EPIC	Imaging

2 Use

pipeline processing	no
interactive analysis	yes

3 Description

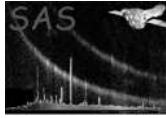
protonscale extracts the **BACKSCAL** keyword and average soft proton intensity from the detector map for a specified region. These values are necessary in the spectral fitting process of multiple regions which are linked.

Warning and requirements: *protonscale* was part of the *esas* package integrated into SAS, but now it is standalone, but is ostensibly limited to work within the *esas* data reduction scheme. In particular, *protonscale* assumes that another task from the package, *mosspectra*, has been successfully run for the exposure to be used, but in principle it can be used on any region mask and spectrum.

4 Parameters

This section documents the parameters recognized by this task (if any).

Parameter	Mand	Type	Default	Constraints
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mode	no	int	1	1 or 2
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mode – 1: do a single region, 2: do multiple regions with the required input provided in a text file (parameter spfile).

maskfile	no	string	mask.fits	
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FOR MODE=1 - File name for the mask file. This is typically the `mosprefix-fovimpdet.fits` file produced for the region by `mosspectra`.

specfile	no	string	spec.pi	
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FOR MODE=1 - File name for the spectral file for the region. This is typically `mosprefix-fovts.pi` file produced region by `mosspectra`.

spfile	no	string	spfile.txt	
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FOR MODE=2 - ASCII text file with the input for multiple regions. The file should contain, on separate lines, the detector number (det), mask file name (mask), and spectral file name (spec) for each region. Number of rows in this file is limited to 100 (100 pairs of masks/spec filenames).

5 Errors

This section documents warnings and errors generated by this task (if any). Note that warnings and errors can also be generated in the SAS infrastructure libraries, in which case they would not be documented here. Refer to the index of all errors and warnings available in the HTML version of the SAS documentation.

badTextFile (*error*)

Input region text file does not exist or is unreadable

maxMask100 (*warning*)

Maximum masks/specs = 100

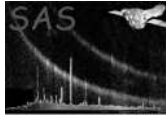
corrective action: do only first 100

6 Input Files

The detector map, product from running `mosspectra`, following the particular nomenclature used in the `esas` package.

7 Output Files

Screen output only – *mode=1*: `BACKSCAL` keyword value converted to units of arcmin^{-2} and the average soft proton flux. *mode=2*: Ordered pairs of the `BACKSCAL` keyword value converted to units of arcmin^{-2} and the relative soft proton value normalized to that of the first region.



8 Algorithm

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For Mode 1:
  Read in maskfile and specfile
  Call spscale in gofutils in goflib
  call CAL_setState
  call CAL_spdetmap to retrieve spdetmap_RP from CCF
  n = 0
  spsum = 0.
  do i=0,XsizeM-1
    do ii=0,YsizeM-1
      if (mask_IP(i,ii) .gt. 0) then
        n = n + 1
        spsum = spsum + spdetmap_RP(i,ii)
      endif
    enddo
  enddo
  spsum = spsum / real(n)
  Return
  Print backscal, avg SP flare flux, scaled avg SP flare flux
For Mode 2:
  Open and read text file list of masks/spectra
  Loop through list as in Mode 1
```

9 Comments

The original code for this task appeared in the *esas* task 2009-2021 as the subtask *proton_scale*. It was removed from the task *esas*, and modularized as a single task for SAS-21. The *esas* task was removed in SAS-21.

References