The next task would be to extract individual spectra from the five observations (using the CIAO command *specextract*) and fit them simultaneously in Xspec.

**CIAO/specextract**

You will need to create a region file of radius 1 Mpc centered on the cluster. Use the merged5\_imgALL.fits file for drawing the region (located one folder up from here).

Save the region file in fk5 coordinates in the CIAO format.

You will also want to be sure that the region file excludes point sources. A sample region file is shown (272arcsec\_sample.reg). This means that BELOW the primary region, there will be lines of regions that are listed as excluded (with a minus in front). The list of ellipses is the list that is returned as the point source regions by the wavdetect script.

Once the region (with point sources excluded) is created, you can run specextract on the 5 observations files (evt2.fits) and their corresponding background files.

This will produce 5 spectra (.pi file) and their corresponding calibration files.

**Xspec**

You will then want to get Xspec running and fit the 5 spectra simultaneously.

load all 5 “...grp.pi” spectra into Xspec

cpd /xw (opens a window to show the data)

plot ldata (plots the data on a log-log plot)

setplot energy (makes the x-axis energy rather than channel)

You should restrict the energy range to 0.7-7.0 keV.

ignore \*\*-0.7 7.0-\*\*

Once this is all set up, you can load the model that will be fitted. The model accounts for Galactic (MW) absorption & A1763 ICM Thermal Bremsstrahlung.

Type abund grsa (to set the proper abundance table, for more see below)

<https://heasarc.gsfc.nasa.gov/xanadu/xspec/manual/node117.html>

model phabs\*apec (this loads the model)

You can get the value for nH absorption from the Chandra Colden site. Beware, the value it gives is two orders of magnitude different from the way Xspec expects the value to be entered.

nH = 0.92

The redshift of A1763 is 0.231.

Prior to fitting:

The nH value and redshift should both be frozen

The values for temperature and abundance should be linked between the five observations.

The normalization values for each should be free and unlinked.

Type fit to run the fit.