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## CIAO features users liked the least

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- 9 - long parameter inputs
- 14 - hidden parameters
- 18 - Slow, SEGVs happen occasionally, require lots of memory
- 19 - The inability to run multiple instances of the same tool at the same time, even on different machines, without complicated setup (using local parameter files, etc). It is extremely time consuming to, for example, extract spectra for 2000 sources one at a time on a single machine while other available machines sit idle.
- 24 - I don't know. I don't really use the ones I don't like.
- 28 - syntax is nonintuitive and awkward
- 29 - some of the low-level tools (dmlist,dmcopy) are much less intuitive than their ftools counterparts. Also, something like xselect would be nice.
- 33 - Many tools require an unreasonable amount of memory and cpu time.
- 35 - Grating threads are not very straightforward.
- 38 - sherpa - absolutely useless....
- 39 - Very frequent updating of CIAO.  
When is it going to be stable ?
- 43 - sherpa's inscrutable, context-sensitive commands  
chips extreme verbosity for simple tasks.  
slow (any equivalent, e.g., fselect vs dmcopy, is faster).  
hybrid syntax (slang and command line)  
large code size; large parameter sets; frequency of segv's
- 47 - Execution speed. Various tool instabilities. Obscure error messages.
- 60 - Sometimes it is not convenient to download the thread, the website is very slow.
- 62 - chips - there are already plenty of plotting packages in the world - why adding another one.
- 63 - Some of the tools are just too slow. I think you know which ones I'm talking about ;-).
- 64 - I don't use the spectral analysis tools. I prefer XSPEC. Also, it would be helpful if the photometry and/or positions from wavdetect were more reliable.
- 69 - csmooth - its slow and is too much of a 'black box' program. I've started using my own adaptive smoothing programs.

## Software Survey Results – CIAO 3.4

- 71 - parameter files
- 72 - syntax/parameter name changes when changing version of ciao  
(i.e. change from param "ccd" to "chip" in merge\_all, or  
[dm|ps]extract now using aoffs, now asols, now expmaps..)
- 75 - speed (especially sherpa, csmooth), stability
- 82 - that command line inputs change between versions, often breaking dozens of scripts  
that little time/effort is being devoted to PSF library enhancement.
- 83 - I want it to become more faster
- 90 - It is annoying that if one forgets an "=" sign when using pset, that  
other parameters get screwed up.
- 99 - Sherpa manual a disaster to read -finding things difficult,  
written poorly, at times incomprehensible.
- 100 - examples in ahelp are often trivial  
need links to other ahelp tasks that explain how to get the  
files needed by this one
- 105 - Sherpa. I found it difficult to use and I gave up.
- 108 - complicated to do any reprocessing because of many arguments for  
each tool etc. Many can be scripted - like psextract
- 111 - new features, where it is not clear if it is very important to  
use them and to redo the full analysis
- 115 - the way I can waste huge amounts of time puzzling over syntax or  
obscure documentation, without gaining any understanding of how  
anything works
- 121 - sherpa
- 124 - Speed. Speed. Speed.  
Sherpa and many of the tools are excruciatingly slow. One  
reason I fall back to Funtools and Ftools is to get better throughput.  
For example, converting a script over to using funcalc instead of  
dmtcalc provided a big performance improvement. I was using funimage  
instead of dmcoppy for awhile, and I'm thinking of going back to  
funimage. (The main downside is having to fix up the various  
header keywords.)
- I always use funtools if they will do the task (e.g., I always  
use funhead to examine the FITS headers.)
- The ~/cxcds\_param is a royal pain. I often have multiple  
analyses going on. The only way to keep from clobbering myself  
is to work hard to ensure that everyone has their own local uparm.  
A large motivation for wrapping everything in scripts is to allow  
me to have the script set up the (huge) ciao environment, and  
set up a local uparm.
- Periodically I find myself deleting the contents of  
~/cxcds\_param and then write-protecting it.

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URL:  
<http://cxc.harvard.edu/ciao3.4/survey/responses/ciaoworstfeat.html>  
Last modified: 11 August 2006

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