EUROPEAN SOUTHERN OBSERVATORY

Organisation Européenne pour des Recherches Astronomiques dans l'Hémisphère Austral

Europäische Organisation für astronomische Forschung in der südlichen Hemisphäre

LA SILLA PARANAL OBSERVATORY

Science Operations

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CES Pipeline Manual

Doc. No. 3P6-MAN-ESO-90100-0005

Issue 1.1

Date 11/2005

Keywords: CES, Pipeline, Spectroscopy, High Resolution

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Change Record

Issue/Rev.	Date	Section affected	Reason/Initiation/Documents/Remarks
1.1	16/11/2005	Walkthrough	Simplifications. Minor changes.
1.0	May 2005	All	Creation.

Contents

1 Introduction

1.1 Purpose

This is a manual for the CES pipeline. This manual should make it possible to run the pipeline without problems, and to troubleshoot in case of problems.

1.2 Scope

Intended for CES Support Astronomers, and as a reference for future pipeline development.

1.3 Reference documents

The following documents are referenced in this document:

[1] The CES web pages: `http://www.ls.eso.org/lasilla/sciops/3p6/ces/`

[2] The CES Users Manual; 3P6-MAN-ESO-90100-0004

[3] The CES Cookbook; LSO-MAN-ESO-90100-0007

[4] 'A beginner's guide to IRAF ' J.Barnes (`http://iraf.noao.edu/iraf/web/docs/docmain.html`)

[5] Description of the IRAF *reidentify* task (`http://iraf.noao.edu/scripts/irafhelp?reidentify`)

1.4 Stylistic conventions

Italic is used to highlight words. `Teletype` is used for filenames and for commands to be entered into a shell (usually prepended by `#`). `Teletype` is also used to display screen text output. **Bold** is used for key-stroke commands.

2 Overview

The CES pipeline provides a quick way to check the quality of the data on-line and provides near-science quality reduced data. It is a background task running on the offline data reduction terminal (w3p6off) so the data are automatically reduced and displayed in real time. The program will perform bias subtraction, dark correction, optional flatfielding, and accurate wavelength calibration. It will display the resulting spectrum in units of S/N, providing an immediate measure of the data quality.

2.1 Pipeline structure

The individual tasks of the pipeline have been written as IRAF routines (called scripts), which are called from perl scripts, called by the core MIDAS program. The MIDAS core is retained only for lack of time to make a complete port, but hopefully one day, someone will make away with that relic!

Sect. 5 outlines the individual steps in the reduction process, and lists the scripts involved. Further details can be found in the README file (`/data/e3p6ops/CES/pipeline/README`) and from the comments in the scripts.

3 A walk-through of pipeline operations

All operations regarding the pipeline take place on w3p6off in the directory `/home/astro/CES/pipeWork` as user `astro`. Make sure you are in that directory before proceeding.

3.1 Necessary preparations

The pipeline needs a number of calibration files to run properly. Make sure that the standard calibration set (SCS) has been taken before starting the pipeline. It is not necessary to copy or move files around, since the pipeline takes care of finding the appropriate files. During the execution of the pipeline the evironmental variable `CES_PIPE_HOME` (this will become useful to make the pipeline more portable) is needed. Automatic setting of this variable is still under development, so for the moment it's suggested to execute the command:

```
# CEScheckPipe.pl
```

If the environmental variable `CES_PIPE_HOME` doesn't exist (and it most likely won't), you will be prompted to create it manually by cutting and pasting the displayed text.

3.1.1 The parameter file `runcard1.txt`

This is the file with which you can control the behavior of the pipeline, both before and during execution (see also Sect. 3.3). Here is a simple example:

```
0
390
800
0
5889.0
5894.0
```

Only the first six lines are read, the remaining ones are ignored. The meaning of the lines is the following:

1. printer flag: 0 means do not print, 1 means print the S/N plot displayed in the main graphic window (`MIDAS_77 graph0`).
2. left edge of the spectrum profile. This will be adjusted from within the pipeline, so you should just leave it as it is.
3. right edge of profile. Leave it as it is.
4. flatfielding flag: 0 means don't, 1 means flatfield with the masterflat, if it has been constructed (will be done automatically). if the master flat can not be found, this option will be ignored.
5. starting wavelength of zoom plot displayed in the second (small) graphic window (`MIDAS_77 graph1`). You should adjust this before starting, but it can also be adjusted while the pipeline is running.
6. end wavelength of zoom plot.

3.1.2 Getting the date right

The pipeline can be run for any given date, not necessarily the current one. To prepare to run for the current date, issue the command

```
# setDate.pl <yyyy-mm-dd>
```

where `<yyyy-mm-dd>` is the date at the beginning of the night (this is the same procedure as the off-line execution that you can find in Sect. 3.5). This command tells the pipeline to take the data from the directory `/data/raw/<yyyy-mm-dd>`. A simple inspection of the headers can provide important informations for the execution of the pipeline such as the binning factor (`CDELT1` and `CDELT2`) and the central wavelength (`HIERARCH ESO INS1 GRAT1 WLEN`).

3.1.3 The scheduler

Next you need to start the program that makes sure that all raw files are properly reduced and the products moved to their proper place. Issue the command

```
#  CESqueueIms -bN -wL &
```

where `N` is the binning of the images to be reduced, (i.e. either 1 or 4) and `L` is the central wavelength (in Ångstrøm).

The pipeline will only accept images of a given binning during one reduction session, all other images being silently ignored.

The wavelength `L` must correspond to one of the files in the directory `dispsol_tmpl`, otherwise you will have to identify lines and determine the dispersion solution manually.

Never mind any warning messages you may get. Actually, the only warning message you can get is because you are running the pipeline on a night that is different from the actual one. This doesn't stop the pipeline and can be safely ignored if you know what you are doing.

3.2 Launching the pipeline

Now start the pipeline with

```
#  ./start_pipe.sh
```

From now on, the terminal in which the command has been given, will be referred to as the "main pipeline window".

The pipeline will start to make a standard reduction. You will be prompted whether you prefer to subtract a dark `d` (the default choice) or a back `b`.

You will see some graphics windows opening (`MIDAS_77 graph_0`, `MIDAS_77 graph_1` and xgterm). Place them conveniently. Now you will have to define the image slicer profile and identify lines for the wavelength calibration. Both tasks are done interactively in IRAF [1] . Read the next section for consolation.

3.2.1 Interacting with IRAF

IRAF is not very difficult to use and, in contrast to MIDAS, the syntax is often quite clear. However, the interactive aspects of IRAF may take some time to get used to, since they often involve pressing keys on the keyboard rather than mouse buttons. The following is an ultra-short crash-course in IRAF interaction — enough to survive. For in-depth reference, please see the IRAF documentation [4], which, in contrast to the MIDAS documentation, contains useful and easy to understand information.

[1] IRAF is distributed by the National Optical Astronomy Observatories, which are operated by the Association of Universities for Research in Astronomy, Inc., under cooperative agreement with the National Science Foundation, U.S.A. For an introduction, see [4] or the IRAF webpage http://iraf.noao.edu/

Generally the tasks of the pipeline pop up a white xgterm window (which will be referred to as "IRAF window"), where you should enter some text (cut and paste from the main pipeline window according to the instructions, in case you decide to type things in the xgterm, please be aware that the tabbing doesn't work and to delete, instead of the `backspace`, you should use `delete`, that on some keyboards is also called `canc`). In addition it may also pop up another plotting window in black and green colors: the "irafterm". The irafterm is the window where you will spend most of your time. While it is active, don't try to enlarge it dragging its edges with the mouse (it doesn't work with some machines). Nevertheless the maximization button still works (under Linux, is the small square with a thick line at the top, close to the small cross at the upper right of the window). Always pay attention to where the mouse is — it jumps back and forth as windows open and close, so restrict your clicking! Especially because you're not supposed to click at all!! Please, never close the irafterm by clicking on the cross at the upper right of the window, IRAF likes to close it by itself.

In the irafterm you will in general position the mouse pointer and use a keybord key instead of a mouse click. Sometimes you will just use keyboard keys without regard to where the mouse pointer is. You can get a short help about the different keystrokes by typing "?".

3.2.2 Defining the aperture

You will see a window named "cl". This is the IRAF window, waiting for your input (the whole pipeline can be run almost without typing but just copying and pasting what needed from the main pipeline window) . In the main pipeline window you will see the text:

```
Enter the following command into the xgterm:

    cesapdef

Answer 'yes' to all questions. When you get back the cl> prompt, enter:
    logout
```

Do exactly what you are told, i.e enter the command into the IRAF window. Note that when IRAF asks you something, it also gives you a default answer in brackets. If the default answer is the same you would type, just enter `return`.

Now the IRAF window will prompt you

```
cl> Edit apertures for masterref?  (yes):
```

Just hit return. Now an irafterm will pop up, showing the slicer profile. If some apertures are already defined it is a good idea to delete them: go to the irafterm with the mouse and type **a** followed by **d** and then **r** (select **a**ll apertures, **d**elete them, and **r**edraw the graph). Now position the mouse pointer (the cross) near the highest slice and type **m** (mark). Next, position pointer at the left edge and type **l** (for lower). Do the same for the **u**pper limit... Now **q**uit and hit return in response to the question about writing to the database. Now find the IRAF window and type `logout`.

After that it will make the master bias. Just wait for the newly opened window to disappear again. Then you are ready for wavelength calibration.

3.2.3 Wavelength calibration

You are now asked

```
Do you want to calibrate using the ThAr frames currently available? [y/n]
```

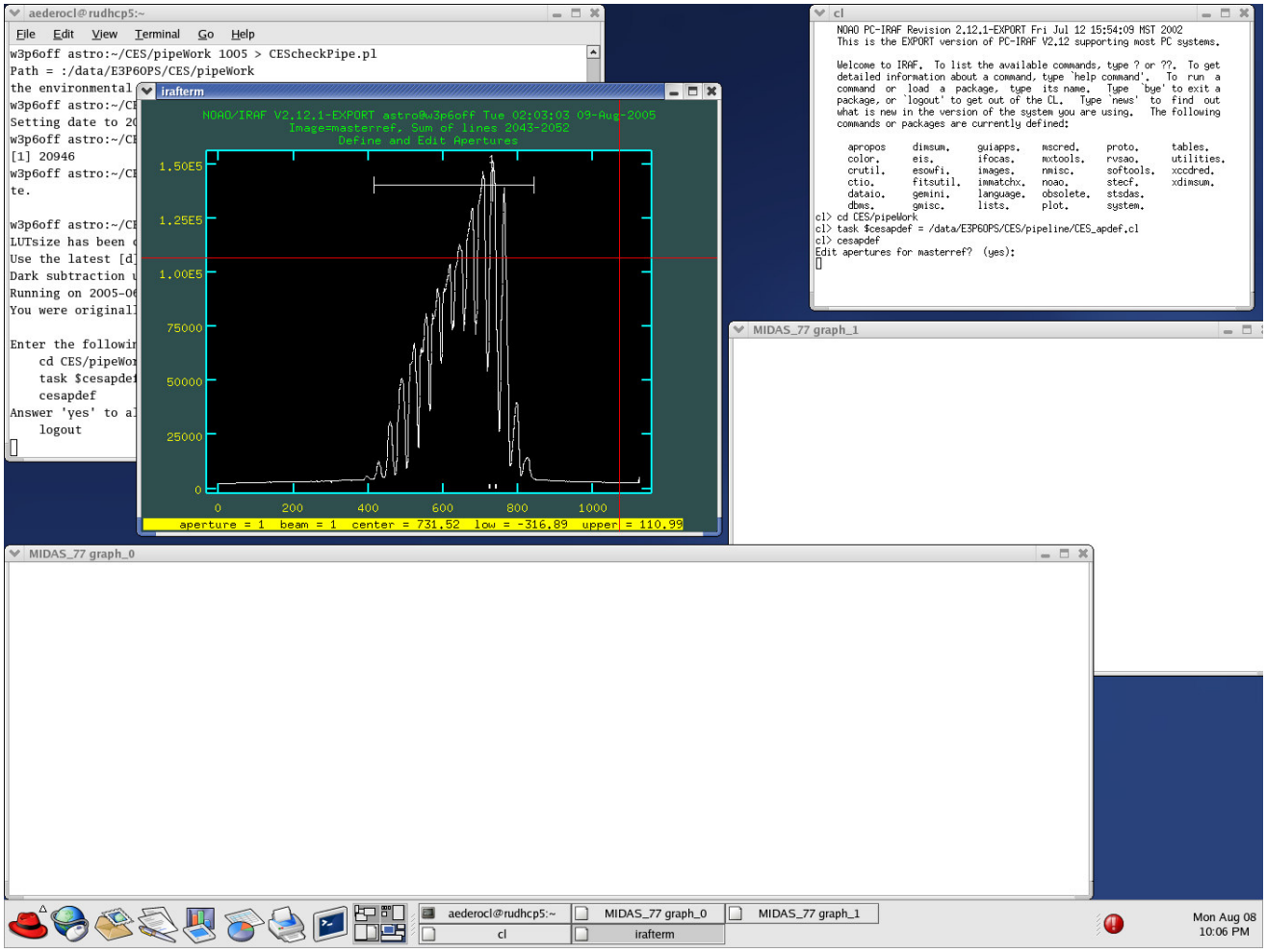

Figure 1: **A screenshot of the pipeline during aperture definition** The green and black window is the "irafterm", on the right the xgterm with IRAF running in it (the IRAF window), behind the irafterm is the main pipeline window, at the bottom the two MIDAS graphic windows. Please note, that each window has three keys at the upper right. They are used to (from left to right): "iconize" the window, make the window full screen (or making the window "normal size" when it's full screen) and closing the window. Don't forget to use the "maximization" key, instead of dragging the edges of the window, to enlarge the irafterm.

and you should obviously type either `y` or `n` followed by return. If you already did the wavelength calibration and, for some reason, are restarting or re-reducing, you can enter **n**. In this case, you can skip the following and go directly to 3.2.5. Otherwise, type `y`. Now you get another IRAF window, and a message in the main window saying:

```
Enter the following command into the xgterm:

    ceswlcal

Answer 'yes' to all questions. When you get back the cl> prompt, enter:
    logout
```

So, do what you're told, and hit return as response to the first question. Now an irafterm will show you the extracted ThAr spectrum.

If you gave the `-w` option to the scheduler (Sect. 3.1.3 and 5.1.1) with a valid central wavelength, you should see small yellow lines over most of the spectral lines and a x-axis showing a reasonable wavelength solution. In this case just hit **f** and check that the RMS is less than 5E-4, then hit **q** twice and you are done.

3.2.4 Manual wavelength calibration

If the plot appears with pixels instead of wavelength, or if it cover a wrong wavelength range and/or there are small yellow vertical lines misaligned with the emission lines, and/or there is only very few small yellow lines, it means that an old and/or wrong solution is being used. If this is the case, you have three choices:

1. Check if you have another solution that may fit better. If that is the case, type **q** and enter "Q" when asked to do so. Then issue the command `stopCESpipe.pl` in another window, and logout of the IRAF session (type `logout`). Now restart the pipeline with the new wavelength solution.
2. If there are some lines that seem to be correctly identified, and the wavelength scale seem to be close to the correct, then you can start with those lines and follow the instructions below from "Fitting a dispersion solution", skipping the **m**arking of features (which is the only really painful task). Even so, you may want to **d**elete some obviously misplaced features.
3. If there is no other solution, and the wavelength scale is wrong or is pixels, then you must proceed manually. First initialize everything by typing **i** in the irafterm. Then follow the instructions below.

Marking features In the IRAF window you will now see a brief help text:

```
m : mark a line
f : fit
q : return from fit
l : automatic find
```

You probably guessed that these are keystrokes, and that to **m**ark a line you have to move the pointer close to it. This can be tricky, so in order to recognize the lines using the CES ThAr atlas, you may have to zoom the plot: position the pointer (the cross, the mouse,...) in the lower left corner of the region you want to zoom on. Then **w**indow the graph. You will see a text message saying `window:` waiting for more input. Now type **e**, and the message changes to `again:`, so move the pointer to the upper right corner of your desired zoom and hit **e** again. To zoom back, simply type **w** followed by **a**.

When you have zoomed on a particular region, place the pointer over a line and type **m**. If you were close enough, a small yellow line will apear over the emission line, indicating that the position of that line has been determined. At the bottom of the window, it gives you the coordinates of the line and now you must enter the

wavelength of the line followed by return. Repeat this for a number of lines across the range, zooming in and out as needed. You will need to identify at least three lines before moving on to the fit. To delete a mark, type **d**.

If you want to verify the position of a line you have already selected, just go close to it and hit `.`. This will give you the position in pixel, the wavelength you provided and the wavelength according to the line list. To move to the next or to the previous line you identified (and read the same output), hit `+` or `-`, respectively. The `spacebar` (that is used for similar purposes in similar IRAF tasks) doesn't work here.

Fitting a dispersion solution When at least three lines have been selected, zoom out, then type **f** for fit. You will now see a plot of wavelength residuals versus wavelength, with RMS written near the top right corner. The fit is initially a third order polynomium. Now type **q** to go back to the ThAr spectrum, now with wavelength coordinates. Check that the coordinates are reasonable — if not, type **i** to initialize and start over, this time including more lines. If everything is OK, type **l** and it will automatically find and identify more lines.

Now type **f** to go back to the fit, which may need adjustment now: To delete a point, place the pointer near it and type **d**, then **f** again to refit. To change the polynomium order type **:order 4** (or 5) followed by return, then **f** to refit. When everything looks OK and RMS is less than 5×10^{-4} then type **q** once to go back to the line-identification window and a second time to quit the task at all. For a detailed manual of this task, see [5].

In the "cl" window you are now asked

```
Write feature data to the database (yes)?
```

Just hit return. Next you are asked

```
Type A to try again [default], type Q to quit...
```

If you do not type "Q" followed by return, you will have to go through it all once more. If there were more than one arc spectrum taken, you will now be presented for solutions for the other ones, based on the solution you just obtained. They should look OK, but you may want to check the RMS (type **f**, then **q**). To accept the solution, type **q**.

Now you get back the prompt, so remember to write `logout` to close the window.

That's it — the pipeline is now running! Reduced spectra and the logfile can be found in `/data/reduced/YYYY-MM-DD`.

3.2.5 Resolution estimate

After a successful wavelength calibration, the resolution is automatically calculated. *Need debugging – pending. Currently disabled. THD*

3.3 On-the-fly adjustments

As mentioned, you can edit the file `runcard1.txt` (see Sect. 3.1.1) at any time, e.g., changing flatfielding and printing options and adjusting the plot range of the small graphics window.

If you want to rereduce some images (e.g., after adjusting flatfielding option) simply add the filename to the file `.CESrereduceIms` e.g., by typing

```
#  ls -1 /data/raw/2005-05-01/CES_hcfa_obs_all_0006.fits >> .CESrereduceIms
```

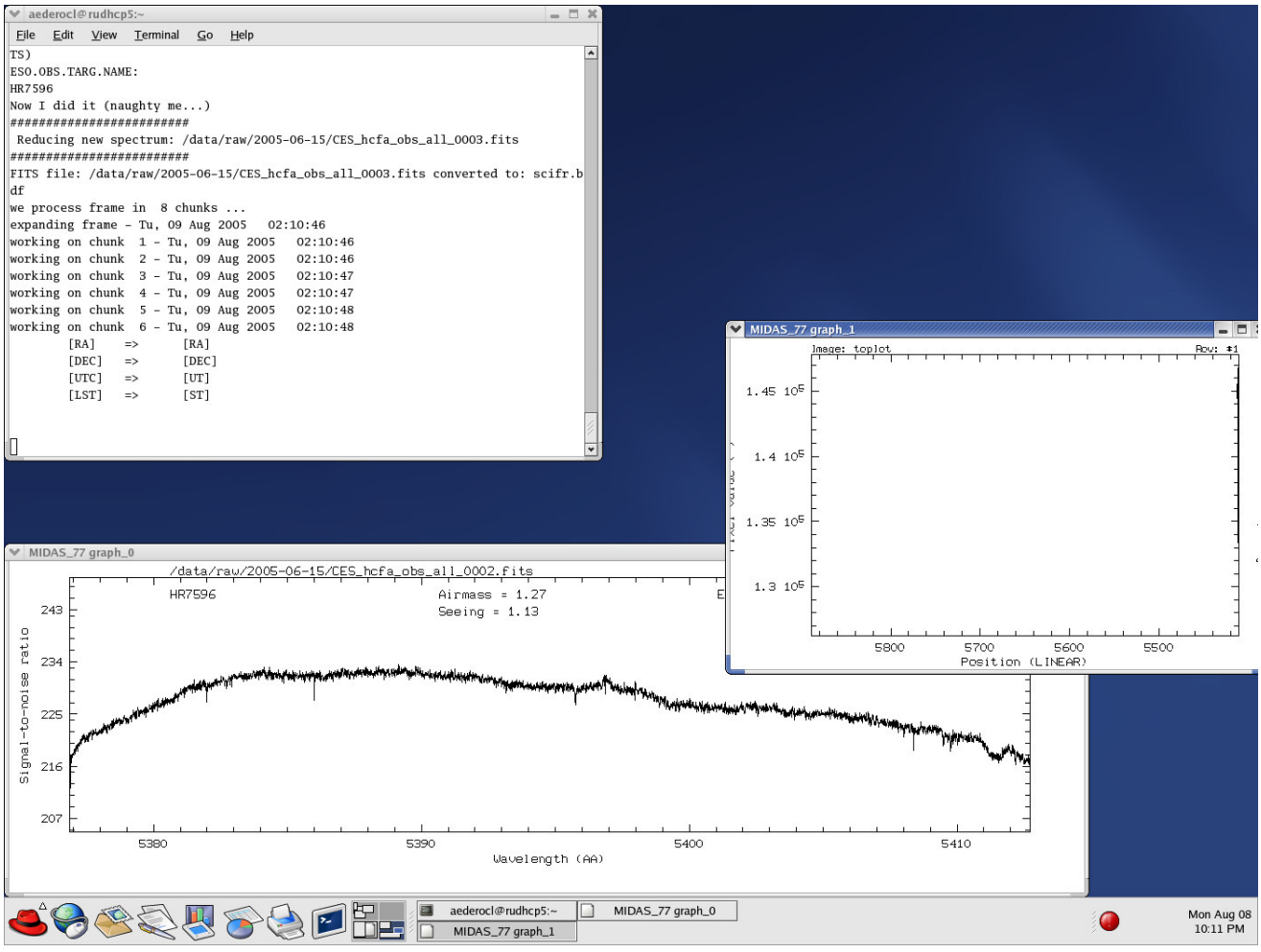

Figure 2: **The pipeline working.** At the upper left the main pipeline window, at the lower left the whole spectrum, and, on the right, the zoom window (empty since the user defined bad limits in the `runcard1.txt` file.

3.4 Stopping the pipeline

Simple! In any other window, give the command

```
# stopCESpipe.pl
```

and wait for all processes to stop and MIDAS to die.

3.5 Running the pipeline off-line

Easy! Follow the same instructions as for the on-line reductions, but with the following changes:

- set the proper date with

  ```
  # setDate.pl YYYY-MM-DD
  ```

- Before starting the scheduler, check which dark/back is the proper one to be used, and if it isn't the latest one, start the scheduler with the `-d` option, e.g.:

  ```
  # CESqueueIms.pl -b1 -d /data/reduced/2005-05-16/Back.fits -w6154 &
  ```

4 Troubleshooting

The pipeline was stopped and now I cannot restart Some of the scheduler files (see Sect. 5) may have been mixed up or maybe deleted. Try killing the scheduler process, then issue the command

```
#  /data/E3P6OPS/CES/pipeline/cleanupPipe.pl -n -a
```

and start all over.

I try to stop the pipeline, but something keeps hanging Probably some files were accidentaly deleted and the program keeps waiting for non-existing processes to finish. Control-C usually cures it. If you want to restart, just check that scheduler files are OK.

5 Structure breakdown and reduction steps

5.1 Background and auxillaries

5.1.1 Scheduler

`CESqueueIms.pl` creates and uses the following three files for queueing images for reduction:

- `.CEStoreduceIms`
- `.CESreducedIms`
- `.CESrereduceIms`

In addition the following housekeeping files, which are not updated during run, are created:

- `.binCES`
- `.pipeDate`
- `.pipePID`

The program accepts the switches `-b`, `-w` and `-d`, which have as argument the allowed binning, the central wavelength and the Dark frame to be used. The `-d` switch is optional, and if set will create a file `.darkToUse` with the name. The `-w` is optional and will result in a file `.wlToUse` with the wavelength.

5.1.2 Other scripts

`CEScheckPipe.pl` checks the presence of the environmental variable `CES_PIPE_HOME`. If this variable doesn't exist, `setDate.pl` fails and the pipeline cannot run.

`setDate.pl` writes the input date to file `date.of.today`. The option `-q` will query for the date. The file `date.of.today` determines the date directory that will be reduced, i.e. `/data/raw/YYYY-MM-DD`.

`stopCESpipe.pl` stops the pipeline using the PID of the scheduler, which it kills. It then edits the file `.stopsign` that the MIDAS core script will read and exit upon, calling the `cleanupPipe.pl` script. It then waits for the completion of that script and then kills any leftover MIDAS processes.

`cleanupPipe.pl` removes all the junk. Takes options `-n` and `-a` for not copying logfiles to `/data/reduced`, and for removing also scheduler files. Must be called with full path — you will be told if you need to do so!

5.2 Pre-reduction (calibrations)

This section presents an outline of the steps taken to prepare the necessary calibrations for the reduction of spectra.

5.2.1 Master dark

The pipeline will prompt for the use of either latest Dark or Back frame, unless the `-d` option was given to `CESqueueIms.pl`. See script `pipe0.pl`. Darks and Backs are generated on a regular basis using the script `makeMasterDark.pl` (not part of the pipeline).

5.2.2 Master bias

There must be at least five bias frames available on the current night before the pipeline will run. If missing, the user will be prompted for an alternative master bias, a retry, or for aborting. See script `check4bias.pl`.

5.2.3 Master flat

If at least five flats are available on the current night, then a master flatfield is created. If not, then the flatfield option in `runcard1.txt` will be set to 0.

The master flat is currently constructed by simple averaging of the available frames and subsequent extraction. This can and should be improved. See script `check4flat.pl` for details.

5.2.4 Profile definition

One of the flatfields will be used to define the upper and lower limits to the image slicer profile. See `pipe0.pl` and Sect. 3.2.2 for details.

5.2.5 Wavelength solution

See `ask.pl` and Sect. 3.2.3 for details. Obviously, there need to be some ThAr frames available, otherwise the pipeline will stop. The dispersion solution will be stored in the directory `database`. Previous solutions are stored in `dispsol_tmpl` from where they are used to generate the IRAF `idsCES_hcfa_cal_thAr` file in the `database` directory. If the solution for the setup is not available the SA will have to do a manual dispersion solution following the procedure in Sect. 3.2.4.

5.3 Reduction (science frames)

When all the preparations outlined in the previoius section have completed, the pipeline enters the main loop in the core MIDAS program (called `pipe.prg`). The program calls the script `pipe.pl` which checks the queue files (Sect. 3.1.3) every 30 sec and exits when a new spectrum is ready to be procesed after updating the queue files. The name of the spectrum to be reduced is copied to the file `runcard3.txt`. Then the following steps are performed:

1. Cosmic removal with a syntactically simple MIDAS command...
2. bias correction after scaling of the overscan (see CES Users Manual)
3. dark correction after scaling of exposure time
4. extraction of spectrum with the relevant profile limits
5. divide by flatfield if that option is turned on
6. correct headers and do dispersion correction (see script `CES_dispcor.pl` for details).

5.4 Post-processing

1. calculate and display the S/N ratio
2. move the reduced spectrum to `/data/reduced/YYYY-MM-DD` (see file `movered.pl` for details).

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