

# **Goodman HTS Pipeline User Manual**

**version 0.2**

**Simón Torres, César Briceño and Bruno Quint**

**April 13, 2018**



# Contents

<b>Introduction</b>	<b>1</b>
<b>Overview</b>	<b>1</b>
Features	1
Ways to run the pipeline	1
What the pipeline does not do	2
<b>General Considerations on using the pipeline</b>	<b>3</b>
Command line arguments	3
Lists of Reference Lamps Available	5
Adding new reference lamps	5
On Goodman's Radial Velocity Precision	5
Headers	6
General Purpose Keywords	6
Non-linear wavelength solution	7
Combined Images	7
Detected lines	7
<b>Running the pipeline in the SOAR data reduction computer</b>	<b>8</b>
Establish a VNC connection	8
VNC from the Terminal	8
VNC using a Graphical Client	8
Running the Pipeline	9
Using the Interactive Mode	10
Troubleshooting	17
<b>Installation Instructions</b>	<b>18</b>
Anaconda	18
Install DCR	19
Install binary DCR	19



# Introduction

This is the User Manual for the *Goodman Spectroscopic Data Reduction Pipeline*. It provides an overview of the pipeline's main features, instructions on its use and how to run it on our dedicated *SOAR Data Reduction Server*, and installation instructions for those who wish to run it on their own computers.

## Overview

The Goodman Spectroscopic Data Reduction Pipeline - GOODSPEC - is a Python-based package for producing science-ready, wavelength-calibrated, 1-D spectra. The goal of **goodspec** is to provide SOAR users with an easy to use, very well documented software for reducing spectra obtained with the Goodman spectrograph. Though the current implementation assumes offline data reduction, our aim is to provide the capability to run it in real time, so 1-D wavelength calibrated spectra can be produced shortly after the shutter closes.

The pipeline is primarily intended to be run on a data reduction dedicated computer. Instructions for running the software are provided in the [Using Pipeline](#) section of this guide. The Goodman Spectroscopic Data Reduction Pipeline project is hosted at GitHub at [it's GitHub Repository](#).

Currently the pipeline is separated into two main components. The initial processing is done by `redccd`, which trims the images, and carries out bias and flat corrections. The spectroscopic processing is done by `redspec` and carries out the following steps:

- Identifies multiple targets (spectra of more than one object in the slit)
- Trace the spectra
- Extract the spectra
- Estimate and subtract background
- Saves extracted (1D) spectrum, without wavelength calibration.
- Find the wavelength solution. Defaults to automatic wavelength solution, but can be done interactively
- Linearize data (resample)
- Write wavelength solution to FITS header
- Create a new file for the wavelength calibrated 1D spectrum

## Features

- Self-contained, full data reduction package for the most commonly used spectroscopic setups with Goodman. Given the almost limitless number of possible configurations available with the Goodman instrument, only the most popular configurations will be supported, though we will try to add as many modes as possible.
- Python based, using existing Astropy libraries as much as feasible.
- Extensively documented, using general coding standards: PEP8 – Style Guide, PEP257 – Docstrings Convention (in-code documentation) – Google Style
- Multiplatform compatibility (tested on Linux Ubuntu, CentOS and MacOSX).
- Modular design. Could be used as a library within other Python applications.

## Ways to run the pipeline

There are two ways to use the pipeline.

1. **Run it directly on a SOAR data reduction server** that you can access using VNC.
2. **Download and install the pipeline** (go to the [Install](#) section of this manual). Though we will try our best to provide answers to quick and simple installation issues, we cannot provide general installation support.

## What the pipeline does not do

- In its current version the pipeline does not perform combination of individual spectra. If you obtained several individual exposures of the same object, they will be output as separate 1-D, wavelength-calibrated spectra.
- It does not combine lamps. If there are more than one comparison lamp associated with a spectrum they will be processed and saved separately.
- There is yet no flux calibration. We are working on a module that will do this. But this will be left for a later release.
- This pipeline does not evaluate nor select data by quality. It will simply try to run using all existing files. **Make sure you only have good data in the folder that will be reduced.**

# General Considerations on using the pipeline

The Goodman Spectroscopic Pipeline is meant to work as a single package. However, the full process is split in two separate modules: `redccd` and `redspec`. The first does the basic 2D image reduction, applying bias, flat field corrections, and cosmic ray removal. The second module, `redspec`, takes the corrected 2D images output by `redccd` and produces wavelength-calibrated 1D spectra.

The pipeline is run from the command line in a terminal window. Each module is run separately, first `redccd` followed by `redspec`, however, you could run both sequentially from e.g. a shell script, just make sure you move to the the right directory.

In order to make things easier you should organize your data:

1. Make sure all the data in your folder corresponds to the same binning, readout mode, region of interest (ROI), and grating/wavelength mode combination.
2. You should have bias, flats (quartz or dome flats), and the appropriate comparison lamps. Other files like acquisition images, slit images and focus images should be deleted.
3. Do not mix dome flats with quartz lamp flats. As an example, suppose you took both quartz lamps and dome flats for your targets. You could create two folders, one with the science data and the dome flats, and another with the same science data and the quartz lamps. Then, if you run the pipeline in each folder you can compare the results and decide which type of flat works best for my particular case.

## Command line arguments

For a list of the options and command line arguments type `--help` argument:

For `redccd`

```
usage: redccd [-h] [--auto-clean] [--cosmic <method>] [--combine]
              [--dcr-par-dir <dcr.par_directory>] [--debug]
              [--flat-normalize <normalization_method>]
              [--flat-norm-order <order>] [--ignore-bias] [--ignore-flats]
              [--keep-cosmic-files] [--log-file <log_file>]
              [--raw-path <raw_path>] [--red-path <red_path>]
              [--saturation <value>]

Goodman CCD Reduction - CCD reductions for Goodman spectroscopic data.
Pipeline Version: 1.0b6

optional arguments:
  -h, --help            show this help message and exit
  --auto-clean          Automatically clean reduced data directory
  --cosmic <method>    Clean cosmic rays from all data. Options are: 'dcr',
                       'lacosmic' or 'none'. Default is 'dcr'. See manual for
                       full description of dcr.
  --combine             Combine compatible data
  --dcr-par-dir <dcr.par_directory>
                       Directory of default dcr.par file
  --debug               Show detailed information of the process.
  --flat-normalize <normalization_method>
                       Choose a method to normalize the master flat
                       forspectroscopy. Choices are: mean, simple (model) and
                       full (fits model to each line).
  --flat-norm-order <order>
                       Defines the order of the model to be fitted. Default
                       to 15
  --ignore-bias         Ignore bias correction
  --ignore-flats        Ignore flat field correction
  --keep-cosmic-files   After cleaning cosmic rays with dcr, do not remove the
                       input file and the cosmic rays file.
  --log-file <log_file>
```

## General Considerations on using the pipeline

```
Name for log file. Default name is <goodman_ccd.log>.  
The file is written in <red_path> and will be deleted  
each time you run this program  
  
--raw-path <raw_path>  
          Path to raw data.  
--red-path <red_path>  
          Path to reduced data.  
--saturation <value> Saturation limit. Default to 65.000 ADU (counts)
```

And for redspec

```
usage: redspec [-h] [--data-path <Source Path>]  
                [--proc-path <Destination Path>]  
                [--search-pattern <Search Pattern>]  
                [--output-prefix <Out Prefix>] [--extraction <Extraction Type>]  
                [--reference-files <Reference Dir>] [--interactive] [--debug]  
                [--log-file <log_file>] [--max-targets <max targets>]  
                [--save-plots] [--plot-results]  
  
Extracts goodman spectra and does automatic wavelength calibration. Pipeline  
Version: 1.0b6  
  
optional arguments:  
-h, --help            show this help message and exit  
--data-path <Source Path>  
                      Path for location of raw data. Default <./>  
--proc-path <Destination Path>  
                      Path for destination of processed data. Default <./>  
--search-pattern <Search Pattern>  
                      Pattern for matching the goodman's reduced data.  
--output-prefix <Out Prefix>  
                      Prefix to add to calibrated spectrum.  
--extraction <Extraction Type>  
                      Only fractional pixel extraction is implemented.  
--reference-files <Reference Dir>  
                      Directory of Reference files location  
--interactive         Interactive wavelength solution. Disabled by default.  
--debug              Debugging Mode  
--log-file <log_file>  
                      Name for log file. Default name is <goodman_spec.log>.  
                      The file is written in <red_path> and will be deleted  
                      each time you run this program  
--max-targets <max targets>  
                      Maximum number of targets to be found in a single  
                      image. Default 3  
--save-plots          Save all plots in a directory  
--plot-results        Show wavelength calibrated spectrum at the end.
```

## Lists of Reference Lamps Available

The automatic wavelength calibration relies on having previously calibrated reference lamps obtained in the same configuration or mode. It is also important that the lamp names are correct, for instance HgAr is quite different than HgArNe. For interactive wavelength calibration, reference lamps are used as a visual aid only. It lets you find the matching laboratory lines values that will be used to fit a pixel to wavelength relation that we call *Wavelength Solution*. The list of lamps is the following.

Grating	Mode	Filter	Lamp
400	M1	None	HgAr
400	M1	None	HgArNe
400	M2	GG455	HgAr
400	M2	GG455	HgArNe
600-old	Blue	None	HgAr
600-old	Blue	None	CuHeAr
1200	M2	None	CuHeAr
1200	M3	None	CuHeAr
1200	M5	GG455	CuHeAr

## Adding new reference lamps

It is possible to add new lamps very easily you just need a raw lamp that meets the following specifications with respect to your science project:

- Same instrument configuration or mode
- Same Grating
- Same order blocking filter if present
- Same binning
- Same lamp/combination that you use in your observations
- Smallest slit possible. Equal is OK too.

Then you can use the interactive mode or other software (such as IRAF) to produce a wavelength-calibrated 1D spectrum. Now you have two options, identify the system folder where the lamps that come with the package are saved and simply put it there or put it in another directory and use the argument --reference-files

```
redspec --reference-files /path/to/ref-lamp-location
```

Or contact storres [at] ctio [dot] noao [dot] edu and we will make it available as a package file.

## On Goodman's Radial Velocity Precision

Here we present a summary of the best *radial velocity* precision that can be obtained with a given configuration. The equations used are listed below.

$$R = \frac{\lambda}{\Delta\lambda} = \frac{c}{v}$$

Then,

$$v = \frac{c}{R}$$

We can calculate the central wavelength for a given configuration which will correspond to  $\lambda$ .  $\Delta\lambda$  is the dispersion in units of Angstrom/Pixel obtained from the Goodman Spectrograph Cheat Sheet.

The smallest grating available is the 0.45", then:

$$FWHM = \frac{\text{slit-size}}{\text{pixel-scale}} = \frac{0.45}{0.15} = 3.0$$

Then the limiting factor is not the spectrograph's dispersion but the *FWHM*,

## Headers

$$\Delta\lambda = 3 * dispersion$$

Grating	Mode	Central Wavelength	Dispersion	Resolving Power (R)	RV Limit
400	m1	505.281	1.00	1516	197.773 km / s
400	m2	700.154	1.00	2100	142.727 km / s
600	UV	442.270	0.65	2041	146.867 km / s
600	Blue	492.529	0.65	2273	131.881 km / s
600	Mid	578.827	0.65	2672	112.218 km / s
600	Red	777.885	0.65	3590	83.502 km / s
930	m1	384.521	0.42	2747	109.151 km / s
930	m2	469.125	0.42	3351	89.466 km / s
930	m3	554.787	0.42	3963	75.652 km / s
930	m4	639.418	0.42	4567	65.639 km / s
930	m5	724.936	0.42	5178	57.896 km / s
930	m6	809.084	0.42	5779	51.875 km / s
1200	m0	374.297	0.31	3622	82.765 km / s
1200	m1	424.181	0.31	4105	73.031 km / s
1200	m2	492.678	0.31	4768	62.878 km / s
1200	m3	561.804	0.31	5437	55.141 km / s
1200	m4	629.735	0.31	6094	49.193 km / s
1200	m5	699.087	0.31	6765	44.313 km / s
1200	m6	767.000	0.31	7423	40.389 km / s
1200	m7	835.851	0.31	8089	37.062 km / s

## Headers

The pipeline adds several keywords to keep track of the process and in general for keeping important information available. In the following table is a description of all Goodman Spectroscopic Pipeline keywords added, though not all of them are added to all the images.

### General Purpose Keywords

These keywords are used for record purpose, except for GSP\_FNAM which is used to keep track of the file name.

Keyword	Purpose
GSP_VERS	Pipeline version.
GSP_ONAM	Original file name, first read.
GSP_PNAM	Parent file name.
GSP_FNAM	Current file name.
GSP_PATH	Path from where the file was read.
GSP_TECH	Observing technique. Imaging or Spectroscopy.
GSP_DATE	Date of processing.
GSP_OVER	Overscan region.
GSP_TRIM	Trim section.
GSP_SLIT	Slit trim section. From slit-illuminated area.

## Headers

GSP_BIAS	Master bias file used.
GSP_FLAT	Master flat file used.
GSP_NORM	Master flat normalization method.
GSP_COSM	Cosmic ray rejection method.
GSP_WRMS	Wavelength solution RMS Error.
GSP_WPOI	Number of points used to calculate RMS Error.
GSP_WREJ	Number of points rejected from RMS Error Calculation.
GSP_DCRR	Reference paper for DCR software (cosmic ray rejection).

## Non-linear wavelength solution

Since writing non-linear wavelength solutions to the headers using the FITS standard (reference) is extremely complex and not necessarily well documented. We came up with the solution of simply describing the mathematical model from `astropy.modeling.models`. This allows for maintaining the data *untouched* while keeping a reliable description of the wavelength solution.

The way it is currently implemented will work for writing for any polynomial kind of model. Reading is implemented only for `Chebyshev1D` which is the model by default.

Keyword	Purpose
GSP_FUNC	Name of mathematical model. <code>astropy.modeling.models</code>
GSP_ORDR	Order of the model used.
GSP_NPIX	Number of pixels.
GSP_C000	Value of parameter <code>c0</code> .
GSP_C001	Value of parameter <code>c1</code> .
GSP_C002	Value of parameter <code>c2</code> . This goes on depending the order.

## Combined Images

Every image used in a combination of images is recorded in the header of the resulting one. The order does not have importance but most likely the header of the first one will be used

Keyword	Purpose
GSP_IC01	First image used to create combined.
GSP_IC02	Second image used to create combined.

## Detected lines

The *reference lamp library* maintains the lamps non-linearized and also they get a record of the pixel value and the equivalent in angstrom. In the following table a three-line lamp is shown.

Keyword	Purpose
GSP_P001	Pixel value for the first line detected.
GSP_P002	Pixel value for the second line detected.
GSP_P003	Pixel value for the third line detected.
GSP_A001	Angstrom value for the first line detected.
GSP_A002	Angstrom value for the second line detected.
GSP_A003	Angstrom value for the third line detected.

# Running the pipeline in the SOAR data reduction computer

The Goodman Spectroscopic Data Reduction Pipeline has been installed on a dedicated computer at SOAR. The procedure is to open a VNC session, for which you need to be connected to the SOAR VPN. The credentials for the VPN are the same you used for your observing run, provided by your *Support Scientist*, who will also give you the information for the data reduction computer VNC connection.

## Note

IRAF is available in all three data servers. Running `iraf` will open an `xgterm` and `ds9` windows. `iraf-only` will not open `ds9`

## Establish a VNC connection

Separately, you should receive a server hostname, IP, display number and VNC-password. If you don't you can ask for it. We have decided to use a similar organization of vnc displays as for `soaric7`:

For the rest of this tutorial we will assume your host name is `vnc-server` the port is `1` and your password is `password`. Though we recommend using RealVNC, most other VNC clients will work fine (e.g., Remmina in Linux). For GNU/Linux and Mac OSX machines we suggest the RealVNC Viewer client. For Windows machines, we suggest either the RealVNC Viewer client or the UltraVNC viewer client. We also know that Vinagre and vncviewer on GNU/Linux work fine.

## VNC from the Terminal

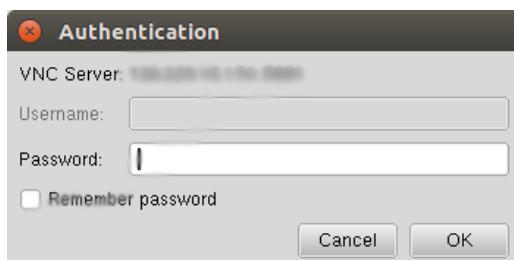
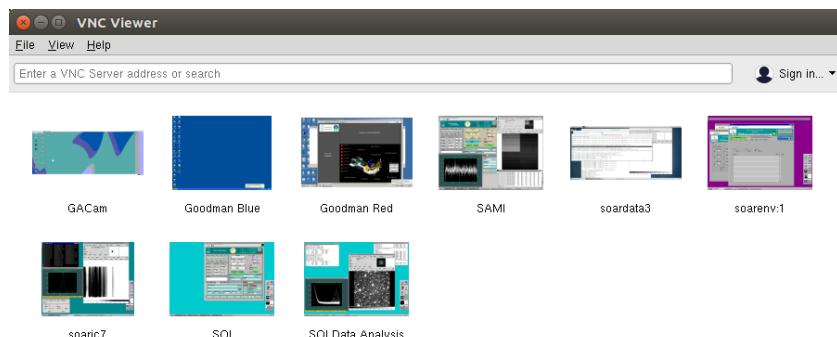
Open a terminal, and assuming you have installed `vncviewer`.

```
vncviewer vnc-server:1
```

You will be asked to type in the *password* provided.

## VNC using a Graphical Client

Using a graphical VNC client is quite similar and intuitive



## Running the Pipeline

In this case the *IP address* was used, which is equivalent and sometimes better.

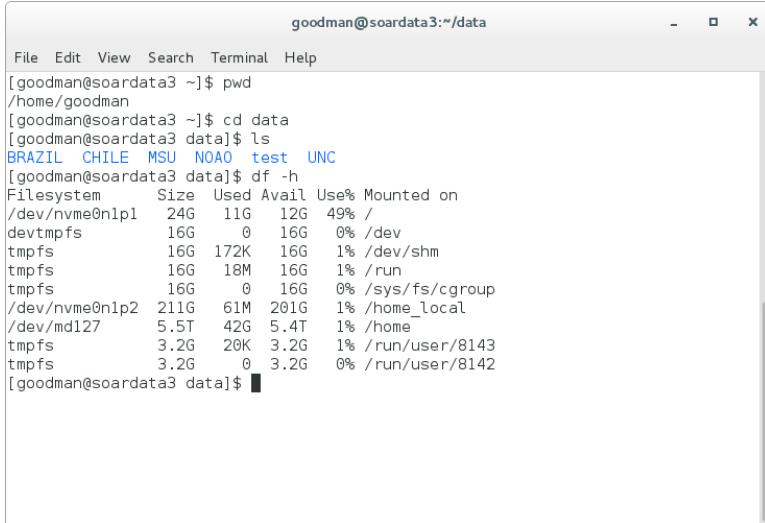
# Running the Pipeline

1. Open a Terminal

2. Go to /home/goodman/data

```
cd /home/goodman/data
```

3. Here you have a workspace to put your data according to your institution.



The screenshot shows a terminal window titled "goodman@soardata3:~/data". The window contains a command-line session:

```
goodman@soardata3 ~]$ pwd
/home/goodman
[goodman@soardata3 ~]$ cd data
[goodman@soardata3 data]$ ls
BRAZIL CHILE MSU NOAO test UNC
[goodman@soardata3 data]$ df -h
Filesystem      Size   Used  Avail Use% Mounted on
/dev/nvme0n1p1    24G   11G   12G  49% /
devtmpfs        16G     0    16G  0% /dev
tmpfs          16G  172K   16G  1% /dev/shm
tmpfs          16G   18M   16G  1% /run
tmpfs          16G     0    16G  0% /sys/fs/cgroup
/dev/nvme0n1p2   211G   61M  201G  1% /home_local
/dev/md127       5.5T   42G  5.4T  1% /home
tmpfs          3.2G   20K   3.2G  1% /run/user/8143
tmpfs          3.2G     0   3.2G  0% /run/user/8142
[goodman@soardata3 data]$
```

4. Create a data folder inside your workspace.

```
cd NOAO
```

```
mkdir 2017-07-05
```

```
cd 2017-07-05
```

5. Copy your data from Goodman Computer

```
scp observer@soaric7:/home3/observer/GODMAN_DATA/NOAO/2017-07-05/ ./
```

6. Make sure you have a full data set. At this point your observing logs will become very useful, eliminate focus sequence, aquisition exposure and any other file present that will not be needed for the processing. The following list summarizes the kind of data that you need to fully process your data.

- BIAS: Bias
- FLAT: Flats
- COMP: Comparison Lamps
- OBJECT: Science Frames

Also make sure your data has the same *readout speed*, *binning*, and *ROI*. If you used different configurations during the same night, we recommend you to set up a separate folder for each.

7. Run redccd:

If you are running `redccd` for the first time you can use `redccd` alone but if it's a second or third time you will need to use `--auto-clean` which is a built-in protection for your data, in case you don't want to delete what has been done. Also you might want to consider `--saturation <new value>` to change the saturation level if you get all your flats rejected due to saturation. Sometimes there is a hot column at the end that produced very high values.

```
redccd --auto-clean
```

In case you want to use `--saturation` here is an example:

```
redccd --auto-clean --saturation 70000
```

## Running the Pipeline

This changes the saturation level to `70000 ADU`` in this context the saturation value works as a threshold for rejecting images and it varies from one instrument configuration to another.

By default, `redccd` puts reduced data in a subdirectory `RED`, you can provide a different one by using `--red-path`.

An image `image_file.fits` that has been fully (and properly) processed should have the new name (including the reduced data folder):

```
cfzsto_image_file.fits
```

### 8. Run `redspec`:

By default `redspec` will search for images with the prefix `cfzsto`, in case you have produced a different prefix you can change it by using `--search-pattern`

You can just run `redspec` in case everything is the default but if this is the first time you run the pipeline we suggest:

```
redspec --plot-results
```

In that way two important plots will be shown full screen, the comparison lamp fitted to a reference comparison lamp and some values for the wavelength solution fit and the extracted spectrum plotted with the wavelength solution.

Before the wavelength solution is calculated, the extracted spectrum (1D already) is saved with an `e` as prefix. The final image has a `w` added to the start of the name, following the above example your final 1D and wavelength calibrated image will be named:

```
wcfzsto_image_file.fits
```

### 9. Finally, review the results. Below is a table with the definition of all letters used in the construction of the prefix.

The meaning of every letter in `wcfzsto` is summarized in the following table:

Letter	Meaning
w	Wavelength calibrated
e	Extracted spectrum, 1D
c	Cosmic ray cleaned or mask created depending on the method.
f	Flat corrected
z	Zero or Bias corrected
s	Slit trimmed, trims off the non-illuminated sections of the detector
t	Initial Image trimming
o	Overscan corrected

## Using the Interactive Mode

If you need to make sure that your solution is the best possible you can use the *Interactive Mode*. Some of the key features are:

- Manually match spectroscopic lines
- Zoom in to get a better reference
- Evaluate the quality of your solution
- Uses a visual reference for matching the lines
- Uses laboratory values for reference lines

Right now it uses matplotlib as the underlying tool to enable interaction.

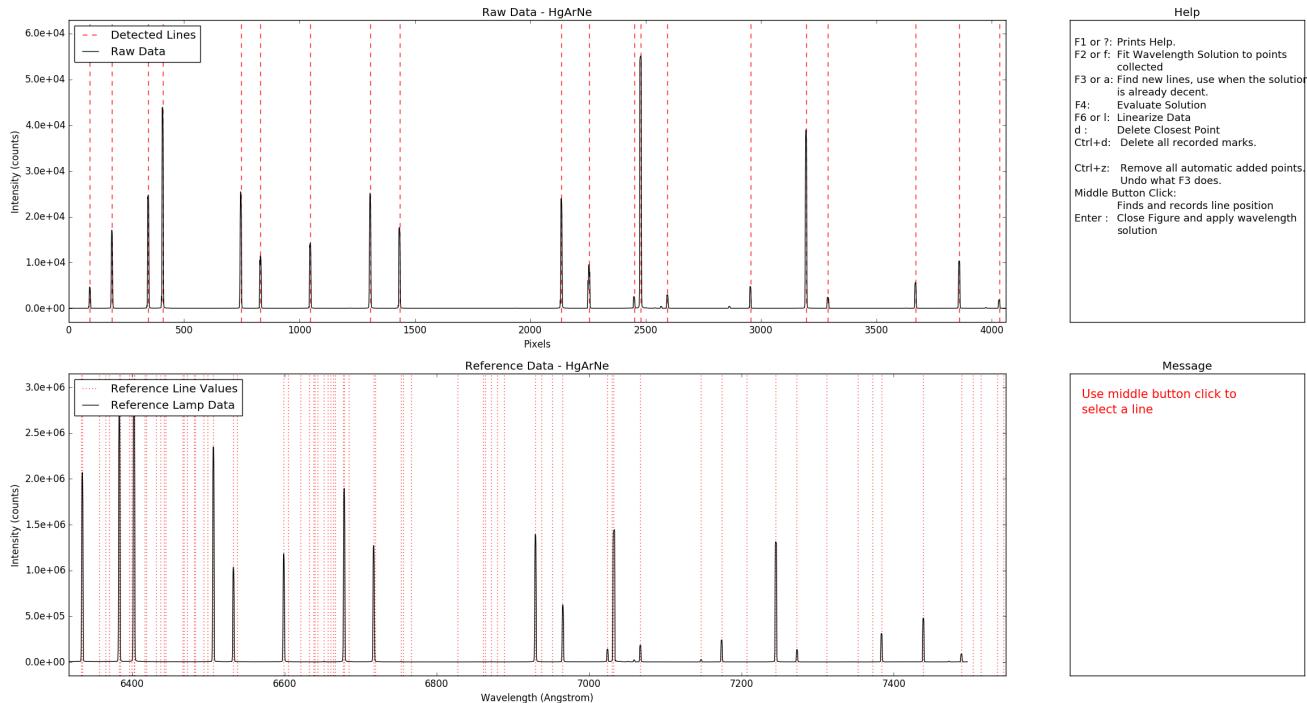
Below you will see a sequence as well as a description of the procedure to use the interactive mode.

1. The interactive screen has four subplots. In the *Upper main panel* you have the raw comparison lamp, i.e. your comparison lamp 1-D-extracted but without wavelength solution, the dashed red lines represent the lines

## Running the Pipeline

found by the pipeline. In the *Lower main panel* you have the reference lamp. This is a previously calibrated lamp that is distributed with the package (also you can use your own). In this case the red lines are the laboratory values obtained from the NIST Atomic Spectra Database site ([https://physics.nist.gov/PhysRefData/ASD/lines\\_form.html](https://physics.nist.gov/PhysRefData/ASD/lines_form.html)). The *Upper right panel* is a static help, intended to give you a quick and easy-to-reach help. Finally, the *Lower right panel* is an information window, in fact it serves three main purposes:

- Display messages and warnings.
- Shows you a zoomed line.
- Displays the wavelength solution quality information.



2. The way you interact is by using your mouse and keyboard. The following table describes all the available keyboard commands with their respective keys and/or buttons, and a summary of their functionality.

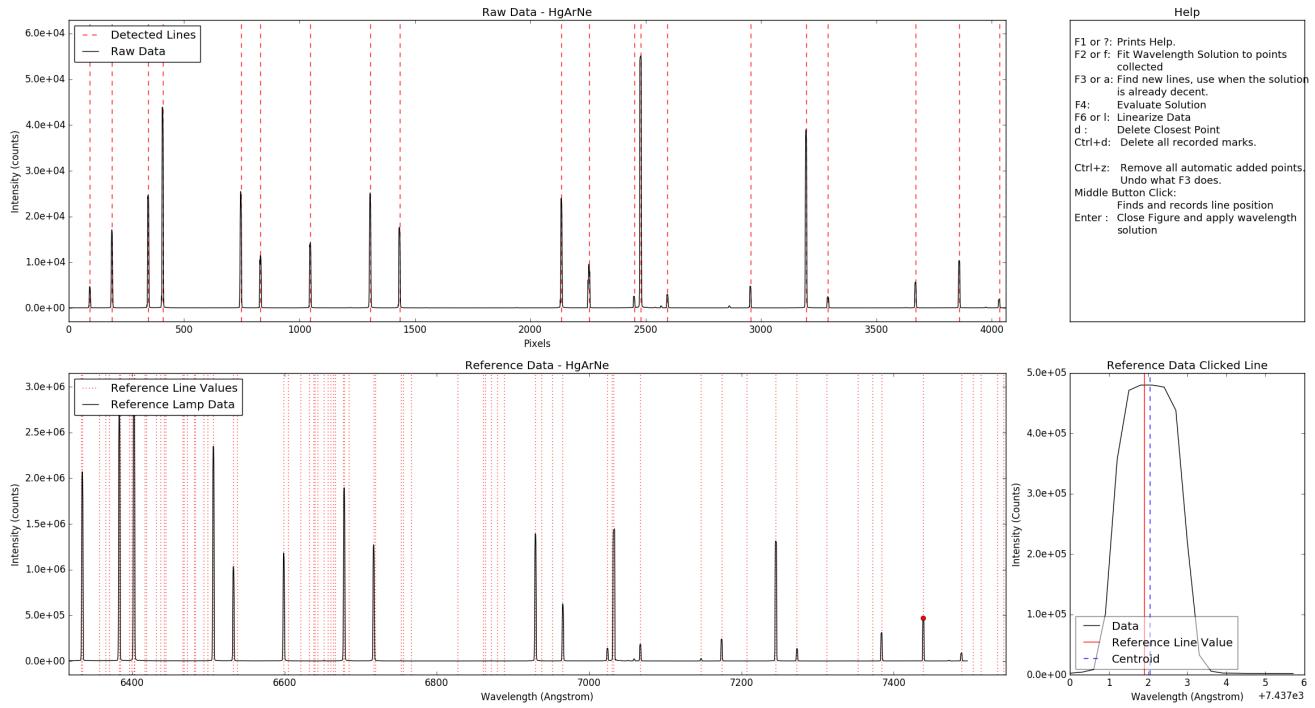
Main Key	Alternative Key	Mouse Equivalent	Description
?	F1	None	Print Help message on the terminal
f	F2	None	Fit a function to collected points
a	F3	None	Find lines automatically
None	F4	None	Evaluate wavelength solution
d	F5	None	Remove point closest to the mouse pointer
l	F6	None	Linearize and smooth spectrum
m	None	Middle Button	Register the line closest to the mouse pointer
ctrl+z	None	None	Deletes ALL automatically added points
ctrl+d	None	None	Deletes all recorded points
ctrl+q	None	None	Ends the program
Enter	None	None	Accepts wavelength solution and closes the figure

It is advisable to practice a little bit to get familiar with this combination of keys and functions. Since we are still in the development stage, if you feel that the use of a key creates problems for you let us know.

In the following image the mouse pointer was placed very close to the center of the line and then with a middle button click the line is marked with a red circle. The software will calculate a centroid (vertical dashed blue line) and then will try to find the closest reference value (vertical red line). Keep in mind that the reference data (red

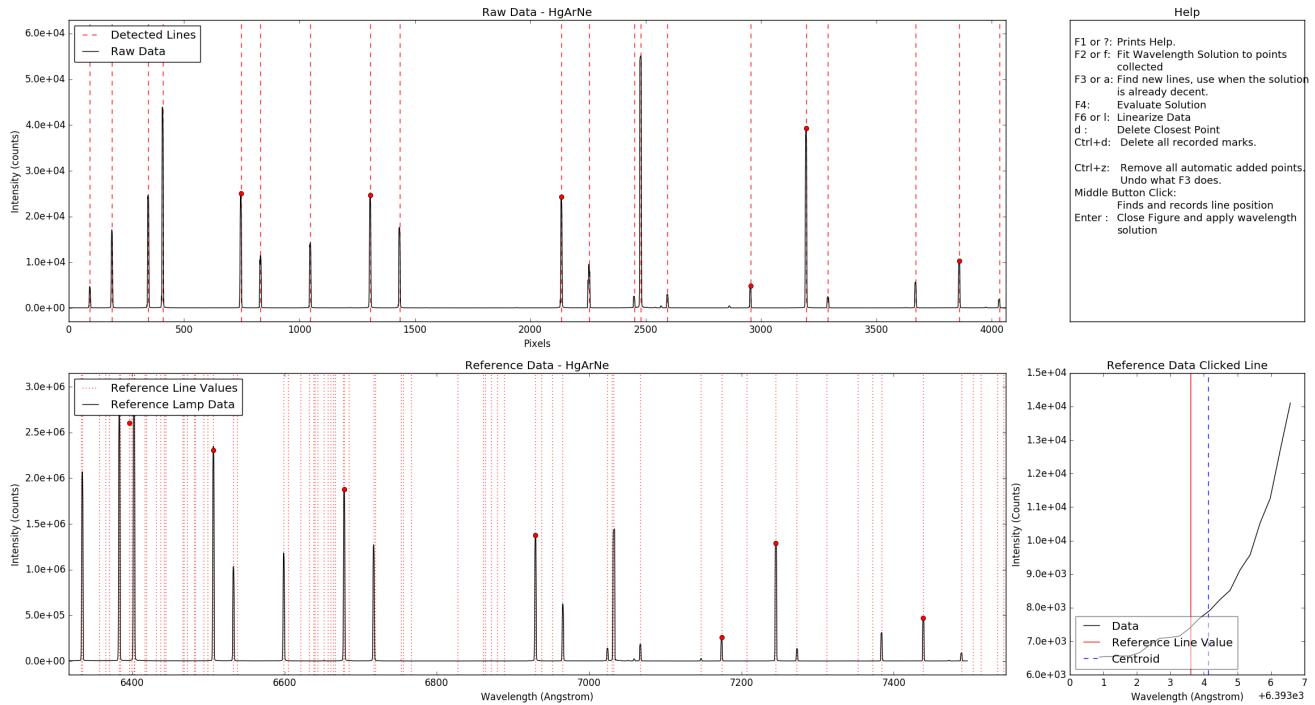
## Running the Pipeline

dotted lines) are not the *reference lamp* lines themselves but values obtained from the NIST site indicated above.



Then you have to find the corresponding line in the opposite plot. There is no preferred plot to start as long as you are consistent with the order in which you mark the lines.

3. In case you miss-identified a line, like in the image below, you can place the mouse pointer above the corresponding red circle and press **d** to delete it. It will search for the closest mark along the horizontal axis and remove it. If there is a counterpart in the opposite plot it will delete it too.

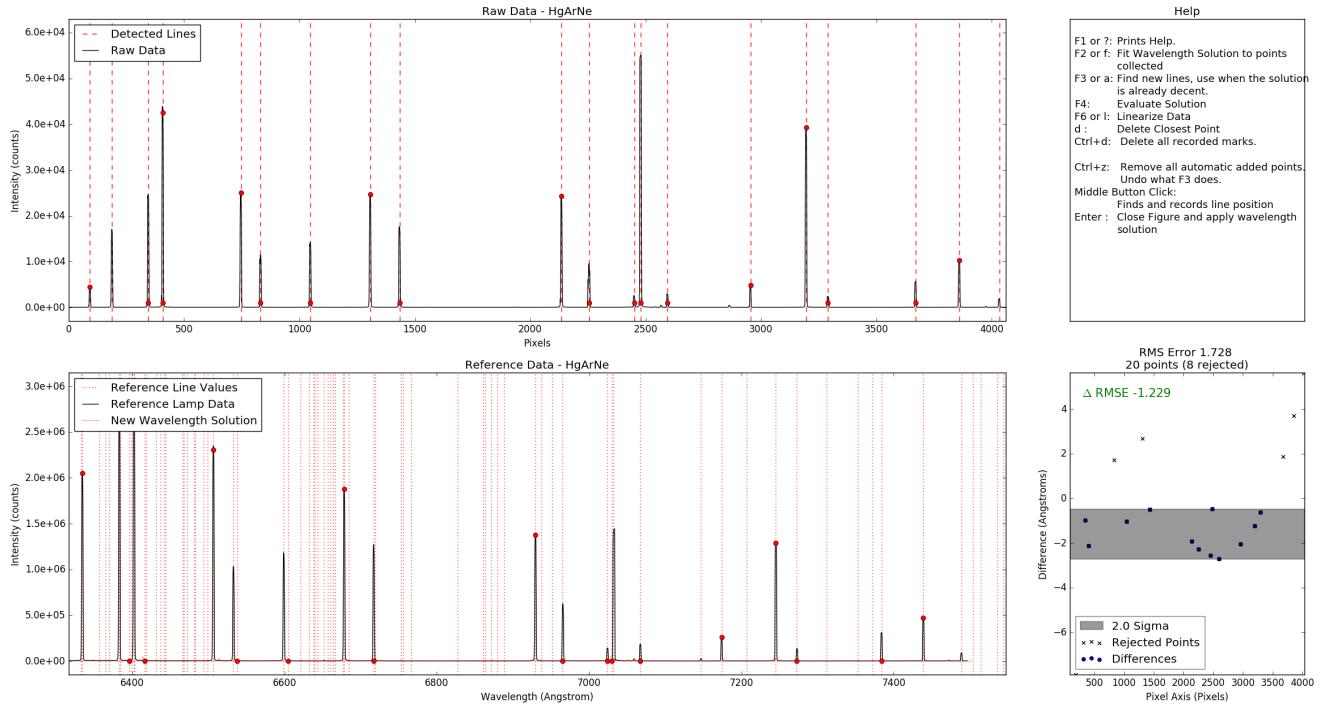


4. Once you matched a good number of lines, the minimum required by the fitting routines are four, you can either press F2 or f to make a fit of the pixels and angstrom values collected. Now the *Lower Right panel* will show the scatter plot of the fit. It is important to note here that the points in this plot do not represent the points you marked but rather each of the lines detected in your extracted 1-D comparison lamp spectrum (red dashed lines in the *Upper main plot*). It does one iteration of a 2-sigma clipping to reject outliers, and then it uses those values to calculate the Root Mean Square Error. In the example we show here the RMS is a bit high, but we will fix that below.

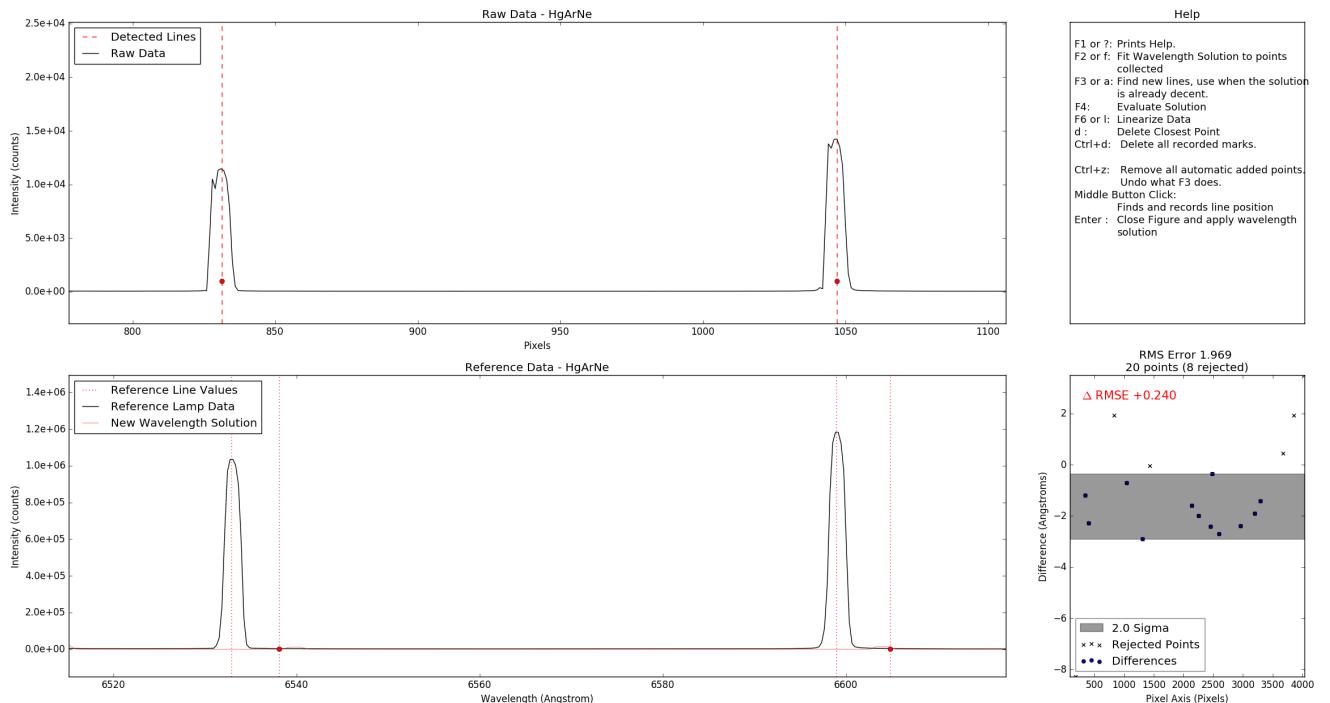
## Running the Pipeline

5. If you see that your current solution is decent you can press F3 or **a** and the pipeline will try to find more points automatically. The new matches found by the software are shown as red dots at the base of each line in the two main *Upper* and *Lower* panels.

The automatic finding routine is not perfect, and indeed it depends on the preliminary wavelength solution. It uses the detected lines in the uncalibrated 1-D lamp, applies the preliminary solution and tries to find a match in the reference line values. In most cases it improves the solution, but not always so keep that in mind. In this case the RMS error is reduced by almost half, which is good, but if you look closely you can see the mismatches; also the *Bottom right* panel will show you this.

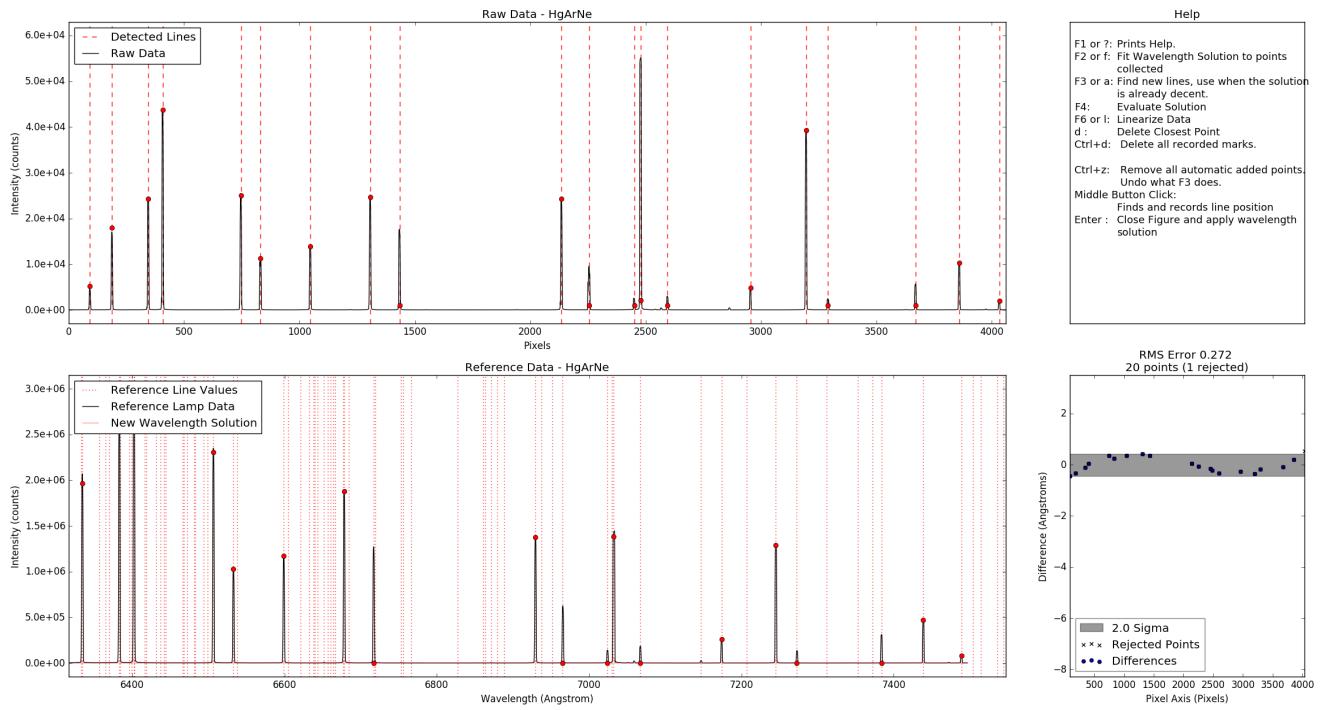


6. Now you we show an example of when the match is apparently good but in fact it's not. Here you need to zoom-in to see that there is an offset between the line centers and the matched laboratory line values, as shown in the figure below. You may have to apply different zoom values to your lamp and the reference lamp to get the plot to look like show it here. The solution in this case is locate the offending line(s), and delete it(them) pressing **d**. Then do a new match by clicking with the middle mouse button on the lines in the laboratory/reference plot, and the respective line in your 1-D uncalibrated lamp.



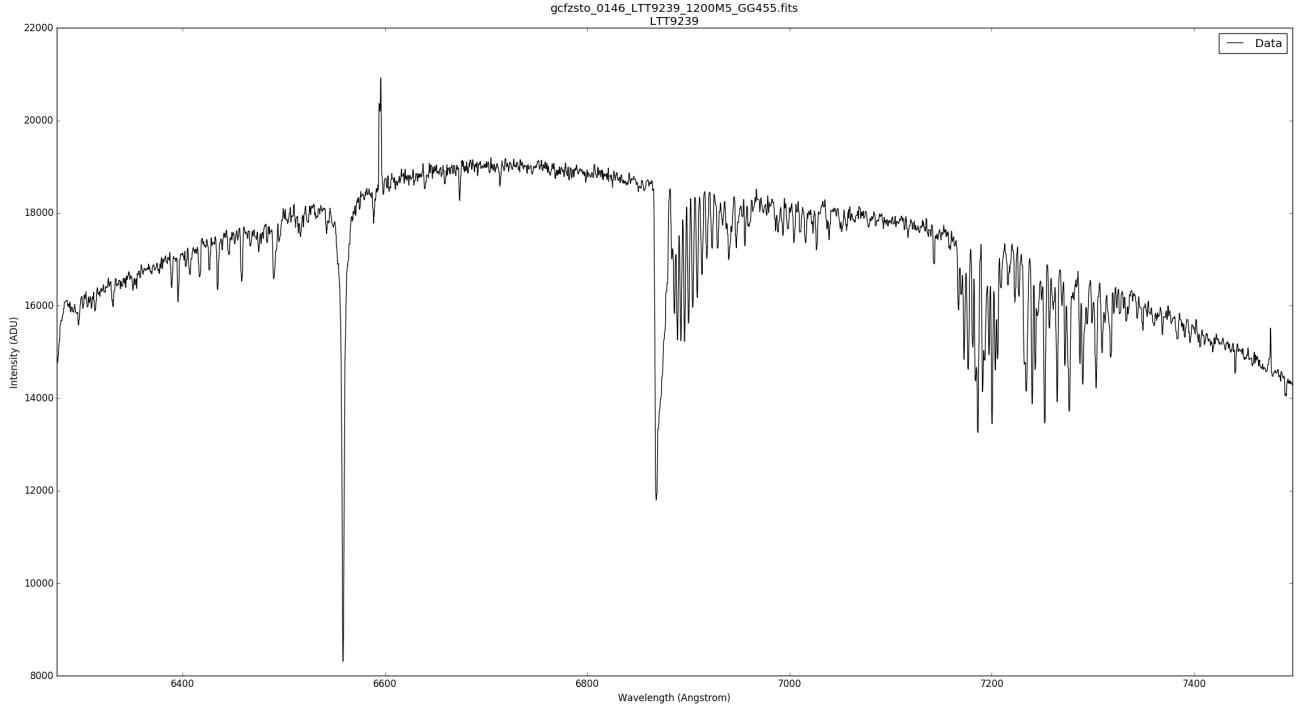
## Running the Pipeline

7. After you checked all the identifications and are happy with it, fit the solution again and you will obtain something like this:

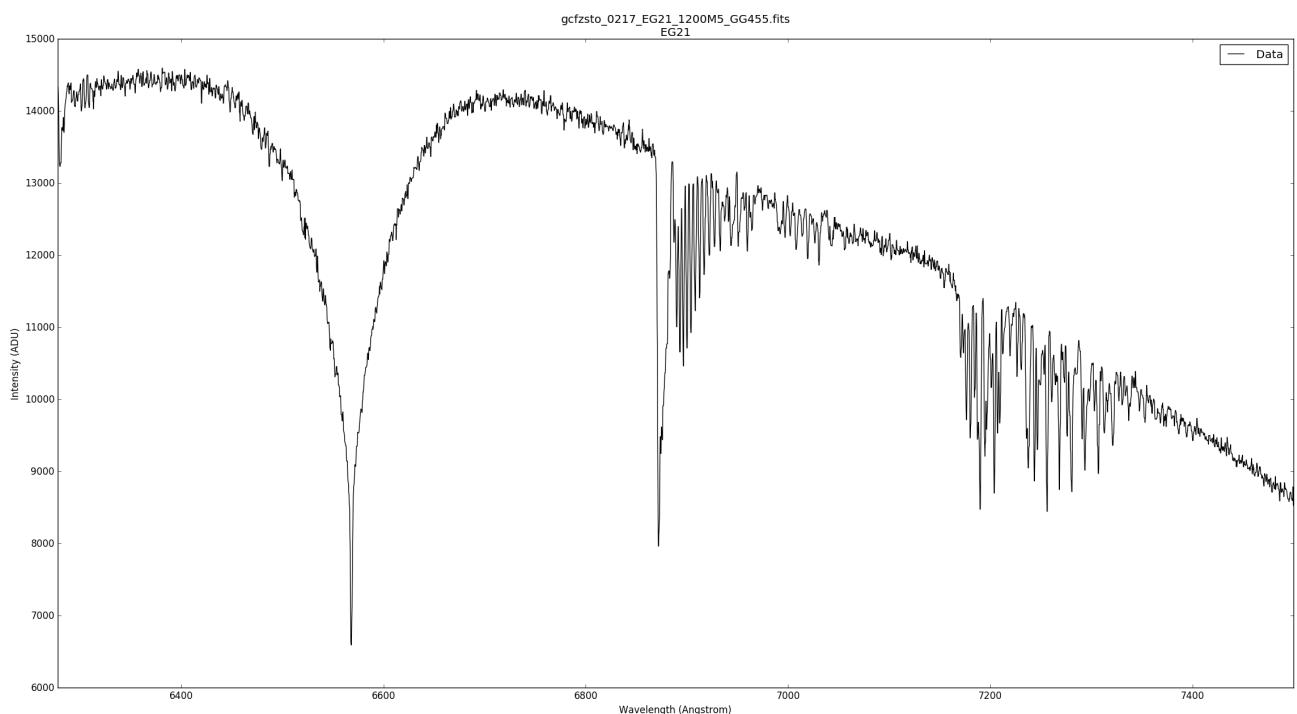
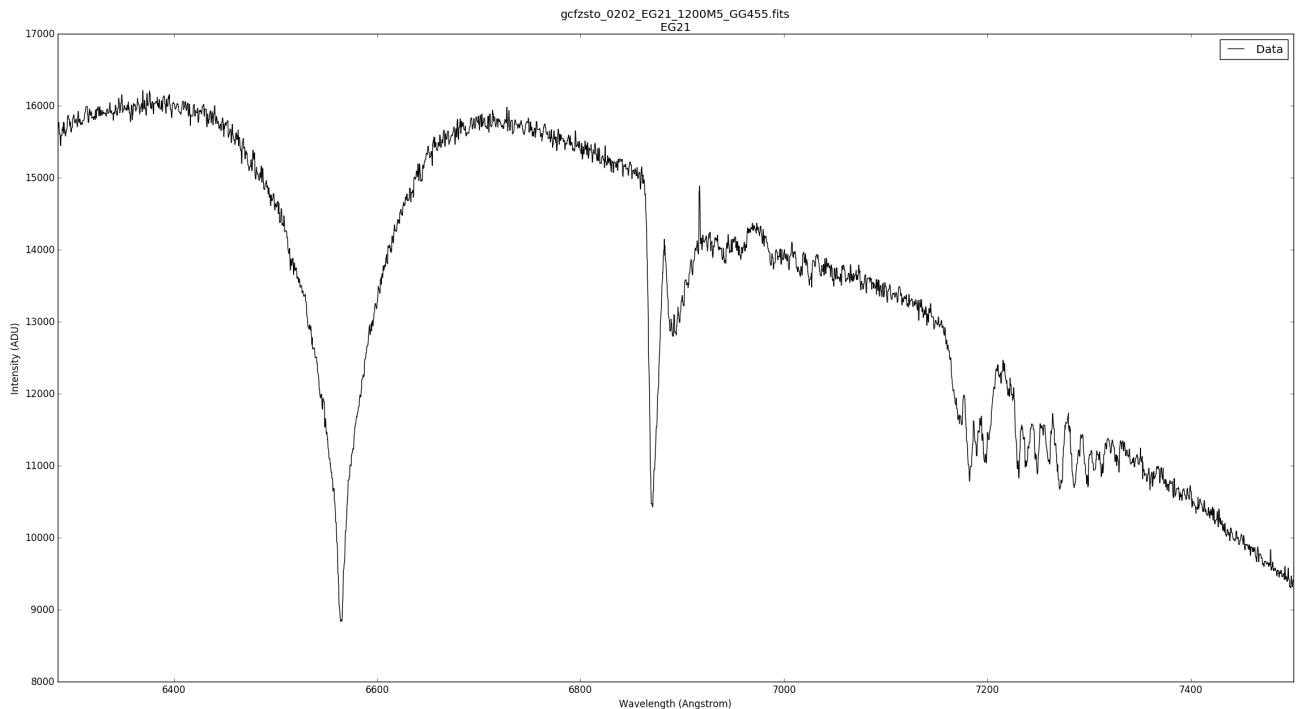


Here you can see that the *Bottom Right* panel shows the differences have a sinusoidal shape, which is also a sign that the solution can be improved. There are ways this can be implemented to refine the fit even further, but this is at present deferred to a later version.

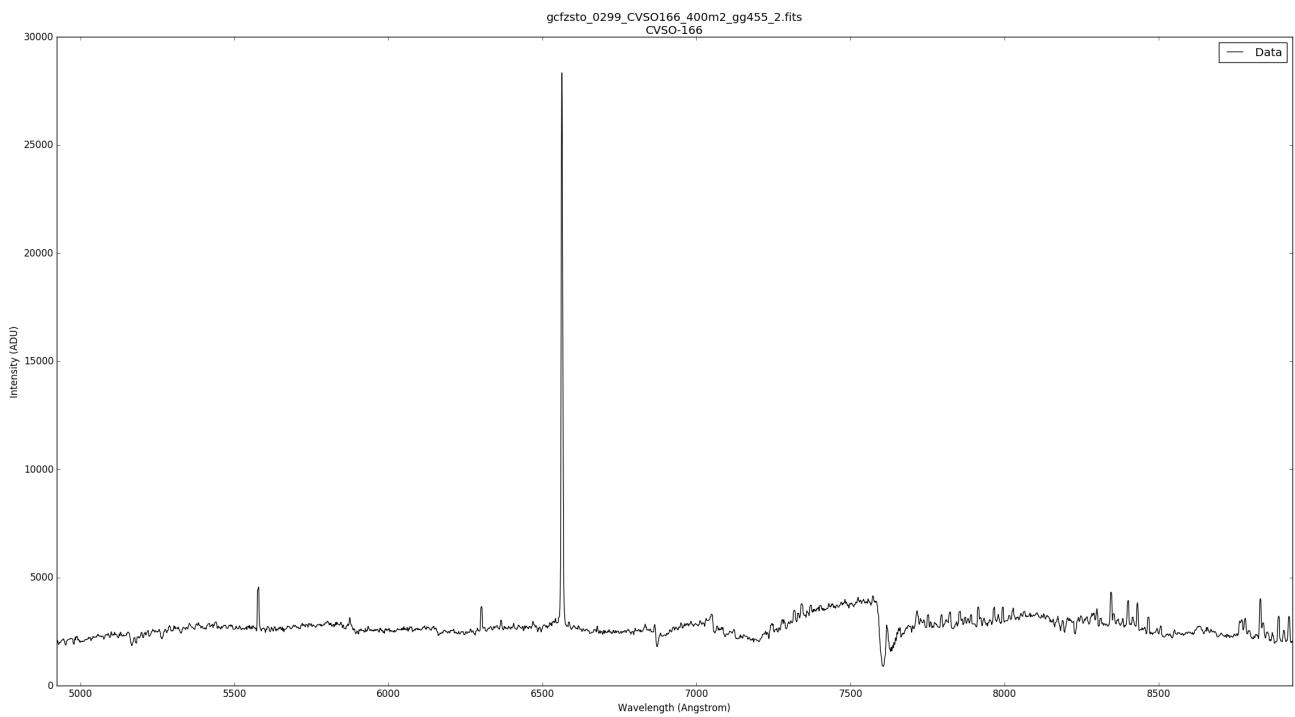
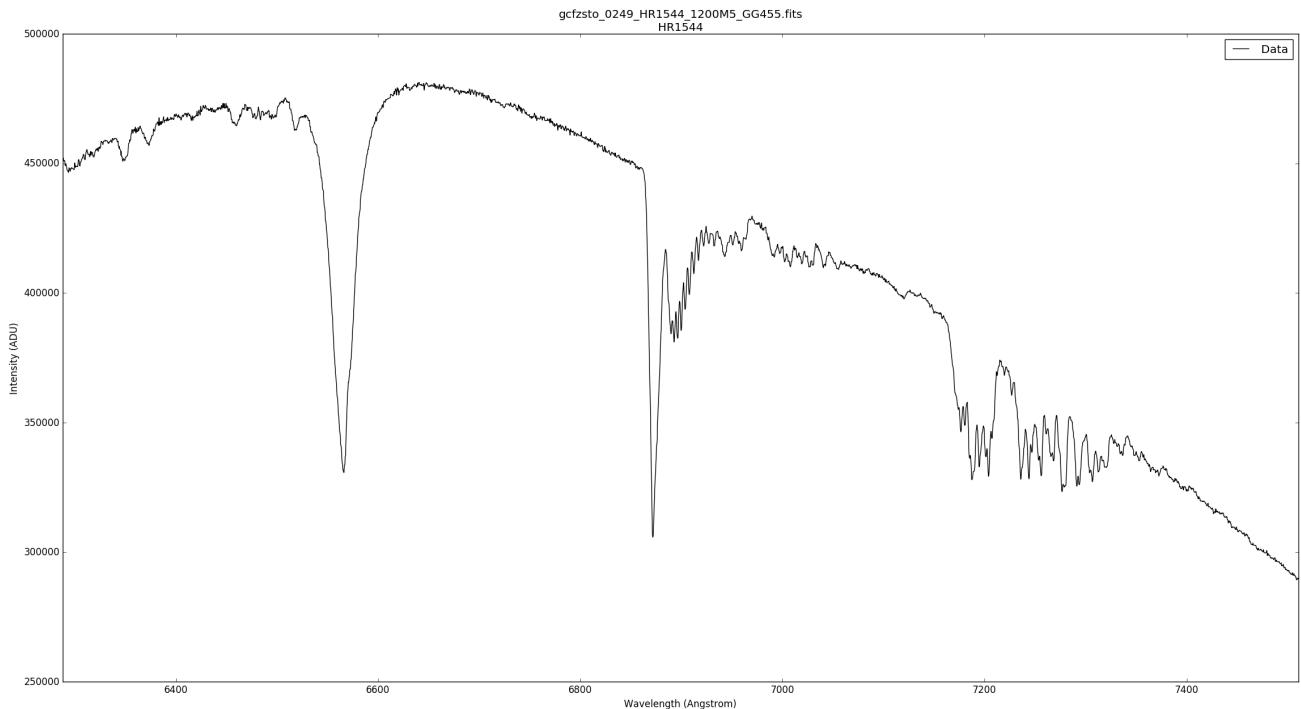
8. Finally, a few samples of the spectra extracted by the pipeline.



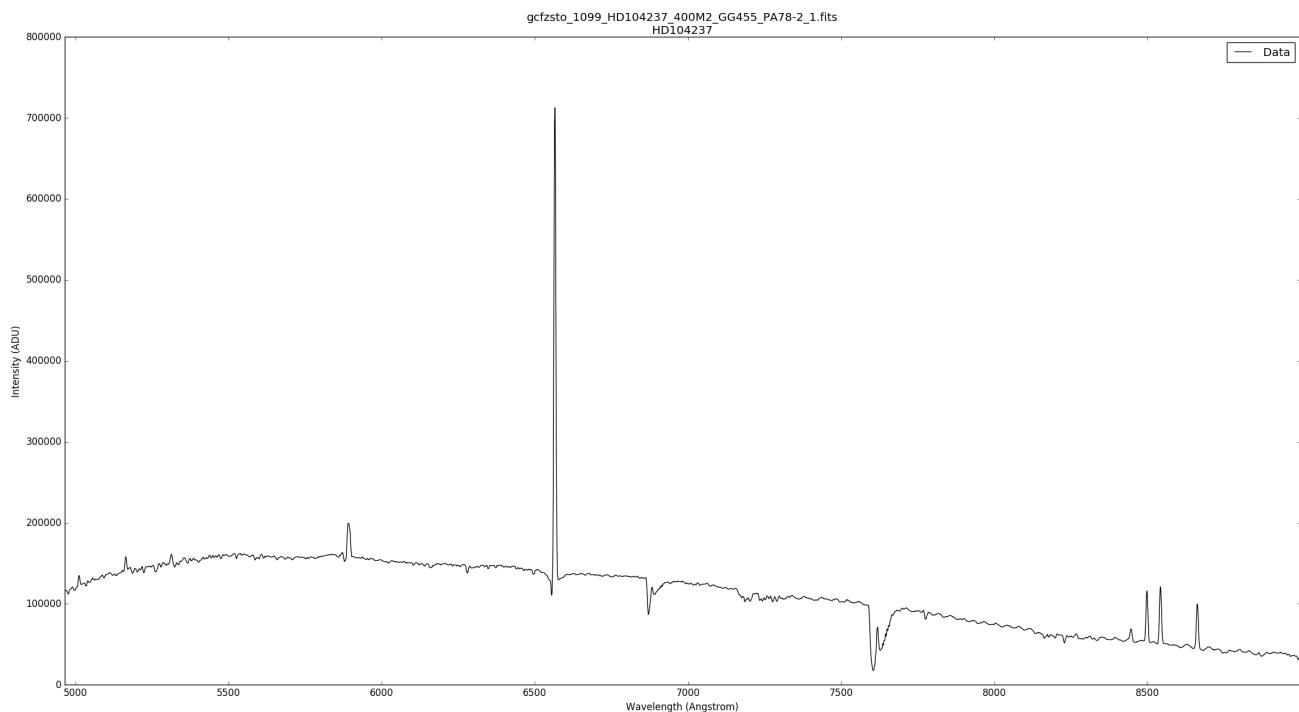
## Running the Pipeline



## Running the Pipeline



## Troubleshooting



## Troubleshooting

- The wavelength Solutions is way off: Check that the lamp was correctly registered in the header. Also check that the corresponding reference lamp exist. for instance is not the same to have HgArNe to HgAr
- Can't detect any objects: Check that the keyword OBSTYPE is correct.
- The reference data plot, in interactive mode, doesn't show anything or only vertical dotted lines: The reference lamp doesn't exist for that configuration, since this is used only for visual reference sometimes it will display the same lamp but in other instrument configuration, this will not affect the quality of the solution.

# Installation Instructions

We strongly recommend installing the pipeline using *virtual environments*. Below you will find a summary of installation steps.

## Warning

Remember that we are not providing any kind of support for installation. This documentation will be the only existing.

- Install anaconda
- Add astroconda channel
- Create virtual environment
- Activate environment
- Install requirements
- Install pipeline

## Anaconda

For anaconda installation we recommend you to check the [astroconda channel's documentation page](#). The instructions will be reproduced here but they might change for newer versions.

## Warning

Anaconda installer requieres BASH. Don't try with other shell.

1. Installing anaconda - Go to <https://www.anaconda.com/downloads> and download the appropriate *anaconda installer* for your platform, most likely it has been automatically selected.
  - Run the installer.

```
cd <download_directory>
bash <install_script>
```
  - Once completed, check the bottom of `~/.bash_profile` or `~/.bashrc` there should be a new PATH definition with anaconda included.
2. Check anaconda installation

```
which conda
```

You should get a response similar to this:

```
~/bin/anaconda3/bin/conda
```

If you don't get this response check the detailed instructions on the astroconda site. Otherwise continue to the next step.
3. Configure Conda to use the *Astroconda Channel*

```
conda config --add channels http://ssb.stsci.edu/astroconda
```
4. Create a virtual environment. We have dropped support for python2.7 so you have to use >3.5.

```
conda create -n astroconda python=3 stsci
```

*astroconda* is the name of your environment, you can use any name you want.
5. Activate your environment.

```
source activate astroconda
```

### 6. Get latest release of the *Goodman Spectroscopic Pipeline*

```
visit https://github.com/soar-telescope/goodman/releases/latest and download the *.zip or *.tar.gz  
cd <download_location>  
tar -xvf <pipeline_file>.tar.gz  
or  
unzip <pipeline_file>.zip
```

### 7. Install requirements from requirements.txt

```
cd <goodman_pipeline_unpacked_location>  
pip install -r requirements.txt
```

### 8. Install the pipeline

```
pip install .
```

### 9. Upgrading the pipeline

```
pip install . --upgrade
```

## Install DCR

### Warning

Don't forget to cite: Pych, W., 2004, PASP, 116, 148

In terms of cosmic ray rejection we shifted to a non-python package because the results were way better compared to LACosmic's implementation in astropy. LACosmic was not designed to work with spectroscopy though.

The latest version of the Goodman Spectroscopic Pipeline uses a modified version of `dcr` to help with the pipeline's workflow.

### Important

The changes includes deletion of all `HISTORY` and `COMMENT` keywords, which we don't use in the pipeline. And addition of a couple of custom keywords, such as: `GSP_FNAM`, which stores the name of the file being created. `GSP_DCRR` which stores the reference to the paper to cite.

You are still encouraged to visit the official [Link](#) own by the author and let me remind you once more that you have to cite the paper mentioned several times in this manual.

## Install binary DCR

### 1. Open a terminal

### 2. In your home directory create a hidden directory `.bin` (Home directory should be the default when you open a new terminal window)

```
mkdir .bin
```

### 3. Move the binary of your choice and rename it `dcr`. If you compiled it most likely it's already called `dcr` so you can ignore this step.

```
mv dcr.Ubuntu16.04 ~/.bin/dcr
```

### 4. Add your `$HOME/.bin` directory to your `$PATH` variable. Open the file `.bashrc` and add the following line.

```
export PATH=$PATH:/home/myusername/.bin
```

## Install DCR

Where `/home/myusername` is of course your home directory.

5. Close and reopen the terminal or load the `.bashrc` file.

```
source ~/ .bashrc
```