# Goodman HTS Pipeline User Manual

## version 0.1

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# Contents

# 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
- 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 avaliable 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
- Multiplataform 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
- There is yet no flux calibration. We are working on a module that will do this.
- 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 and 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.

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 I took both quartz lamps and dome flats for my targets. I 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 I run the pipeline in each folder I 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>]
              [--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.

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.
  --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
                        forspectroscoy. 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>
                        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-to-file] [--max-targets <max targets>] [--save-plots]
               [--plot-results]

Extracts goodman spectra and does wavelength calibration.

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>
                        Choose a which extraction to perform. Simple is a sum
                        across the spatial direction after the background has
                        been removed. Optimal is a more advanced method that
                        considers weights and profilefitting.
  --reference-files <Reference Dir>
                        Directory of Reference files location
  --interactive         Interactive wavelength solution.Disbled by default.
  --debug               Debugging Mode
  --log-to-file         Write log to a file
  --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 to 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 send it to me and I will make it available as a package filea.

# 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.

## Establish a VNC connection

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

***VNC ports and working folder assigned to each partner.***

| Port | Partner/Institution | Folder |
|---|---|---|
| :1 | NOAO | `/home/goodman/data/NOAO` |
| :2 | Brazil | `/home/goodman/data/BRAZIL` |
| :3 | UNC | `/home/goodman/data/UNC` |
| :4 | MSU | `/home/goodman/data/MSU` |
| :5 | Chile | `/home/goodman/data/CHILE` |

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*

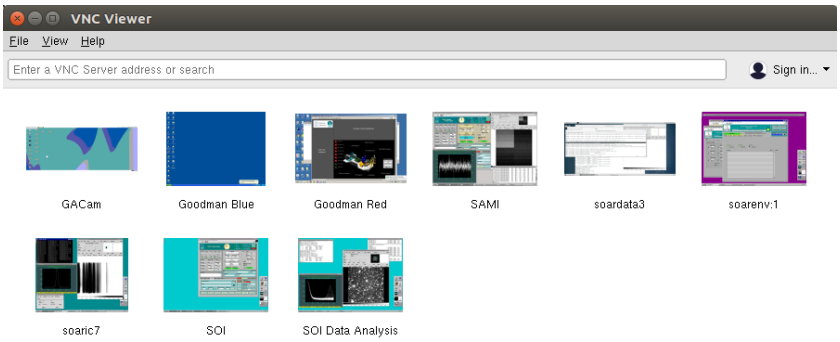
Open a terminal, and assuming you have installed `vncviewer`.

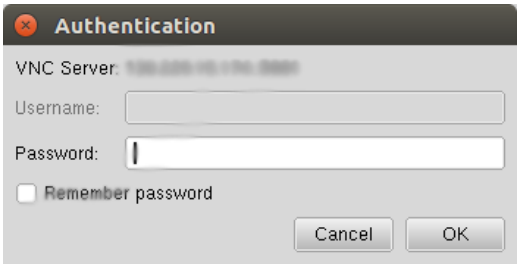
```
vncviewer vnc-server:1
```

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



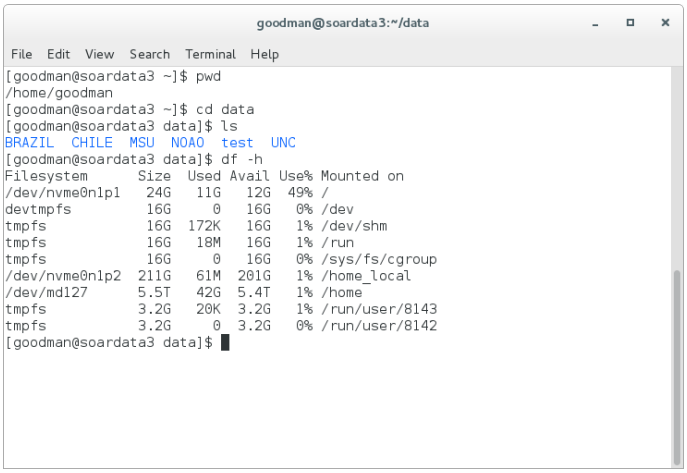

In this case the *IP address* was used, which is equivalent and sometimes better.

# 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.



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/GOODMAN_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`:

   For `redccd` I suggest using `--cosmic` and `auto-clean` 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 --cosmic --auto-clean
```

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

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

   This changes the saturation level to *70000 ADU*` in this context the saturation value works as a threshold for rejecting images.

   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 propperly) processed should have the new name (including the reduced data folder):

```
cfzsto_image_file.fits
```

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

| Letter | Meaning |
|---|---|
| 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 |

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 I 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.

The final image has a g added to the start of the name, following the above example your final 1D and wavelength calibrated image will be named:

```
gcfzsto_image_file.fits
```

## 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:

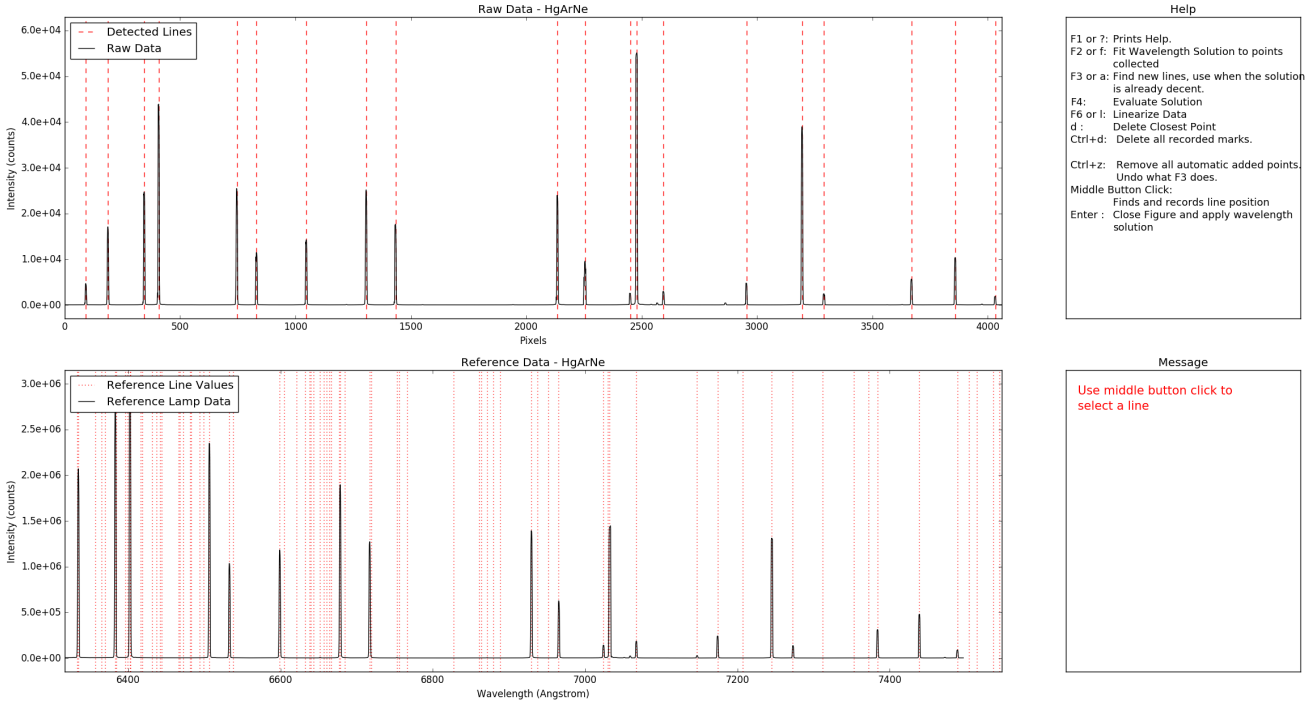
- Manually match spectroscopic lines
- Zoom in to get a better reference
- Evaluate the quality of your solution
- Uses a visual reference for matching the lines
- Uses laboratory values for reference lines

Right now it uses matplotlib as the underlying tool to enable interaction, this has some limitations but

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 Left* you have the raw comparison lamp, i.e. the comparison lamp extracted but without wavelength solution, the dashed red line represents the lines identified by the pipeline. In the *Lower Left* corner you have the reference lamp which is a previously calibrated lamp that is distributed with the package (also you can use your own). In this case the red lines are laboratory lines obtained from a NOAO site. The *Upper Right* plot is a static help, is intended to give you a quick and easy-to-reach help. Finally, the *Lower Right* plot is a dynamic one, in fact it serves three main purposes:

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

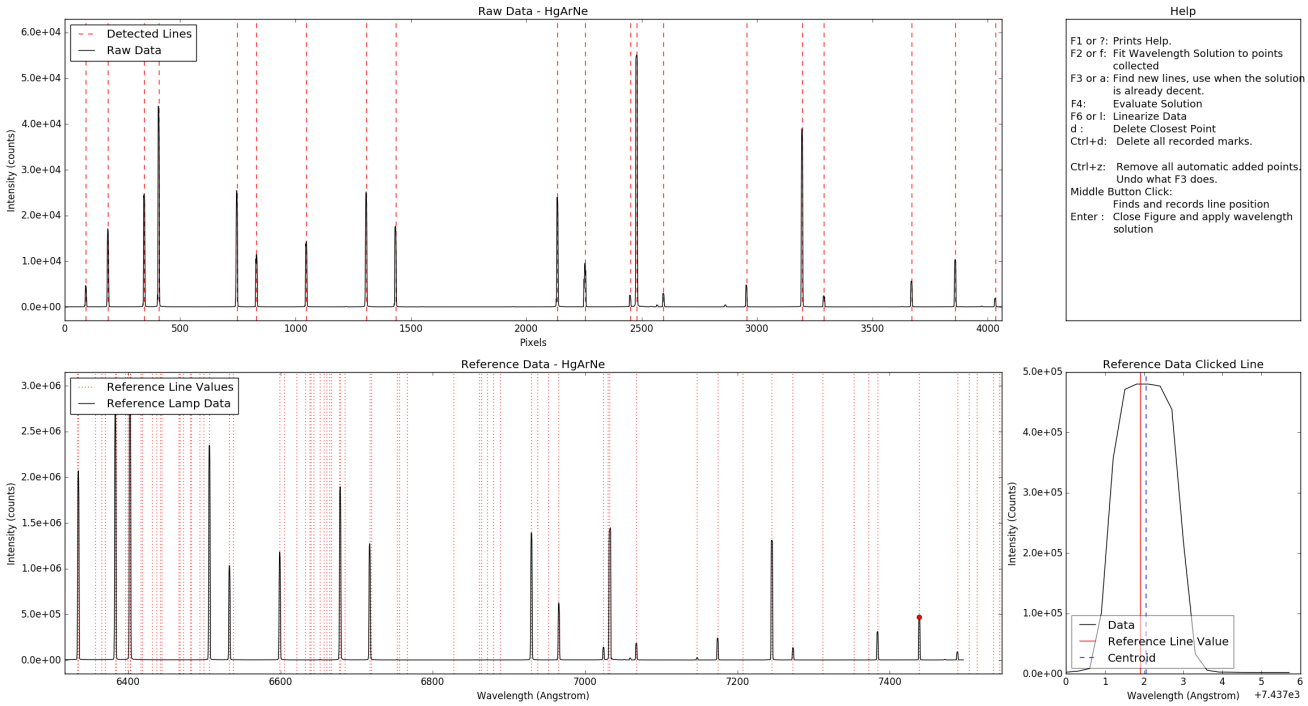



2. The way you interact is by using your mouse and keyboard. The following table describes all the available functions with its keys and/or buttons. It also contains a summary of its function.

| 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 |

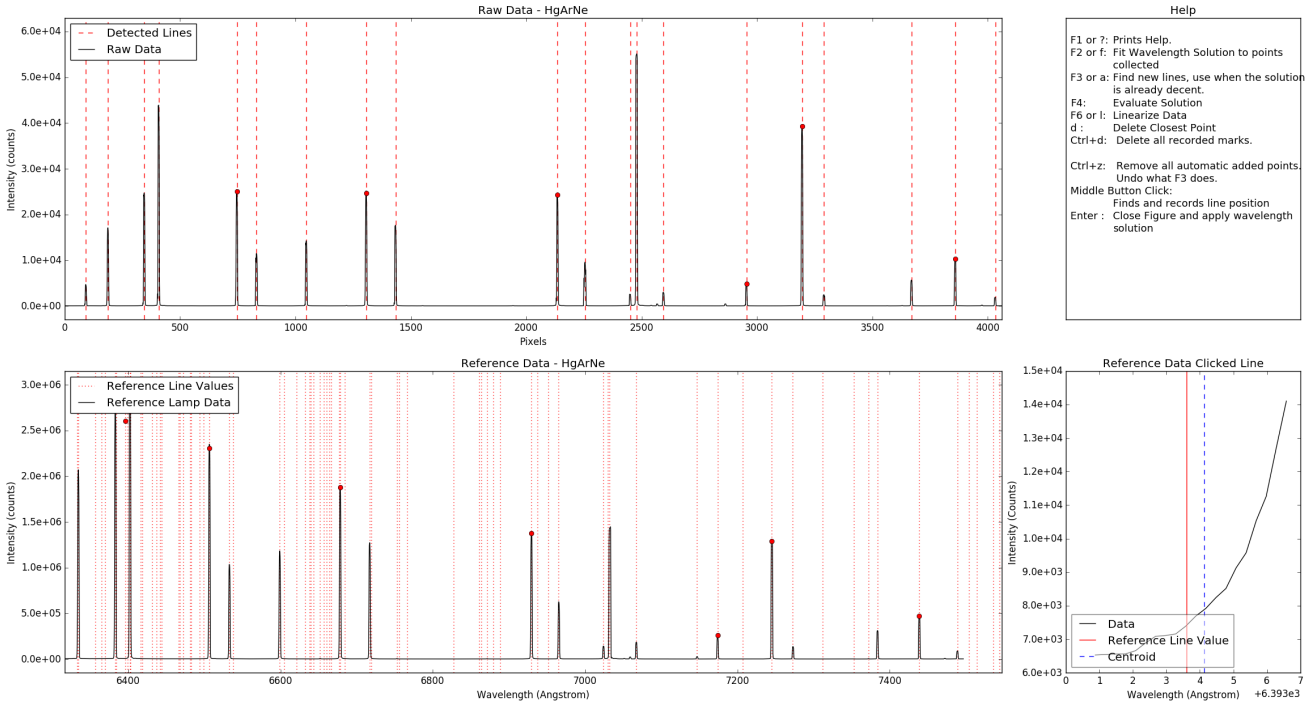
It is advisable to practice a little bit to get familiar with this combination of keys and functions. Since we are still in development stage, if you feel that the use of a key creates problems for you let us know.

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 dotted lines) are not the *reference lamp* lines themselves but values obtained from literature.

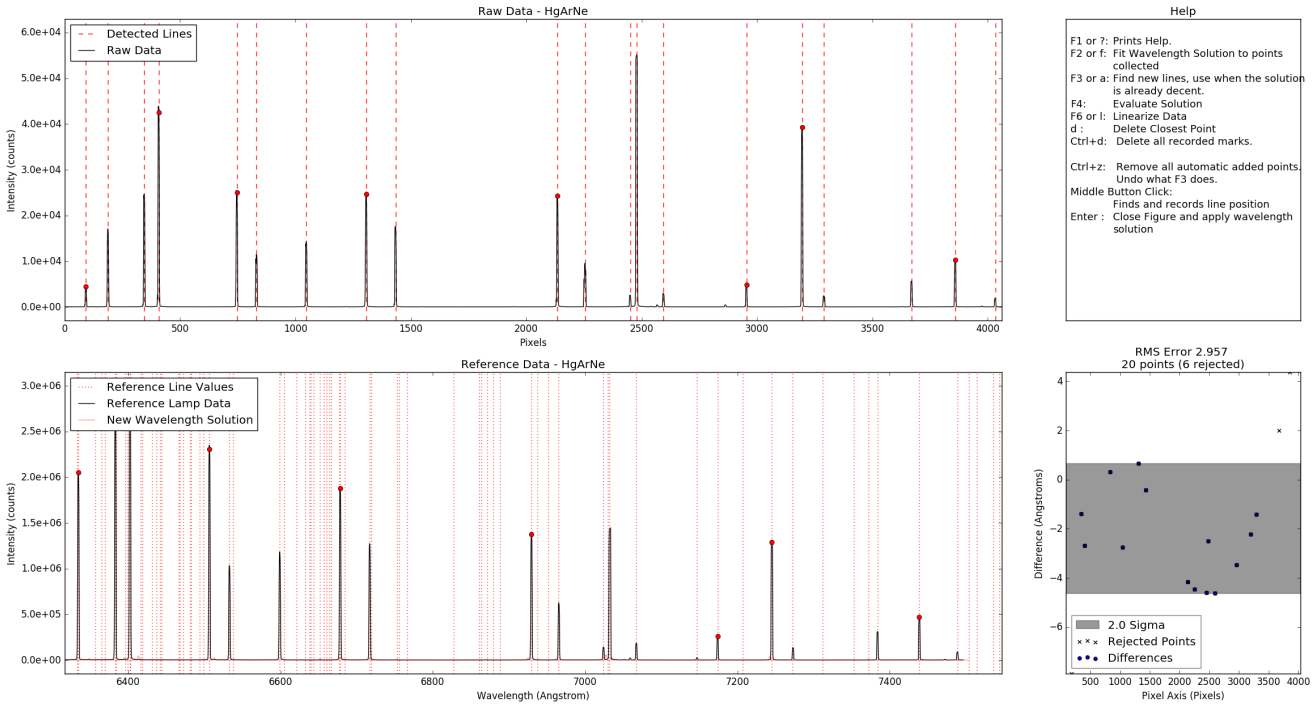



Then you have to find the corresponding line in the opposite plot, there no preferred plot to start as long as you are consistent with your marks.

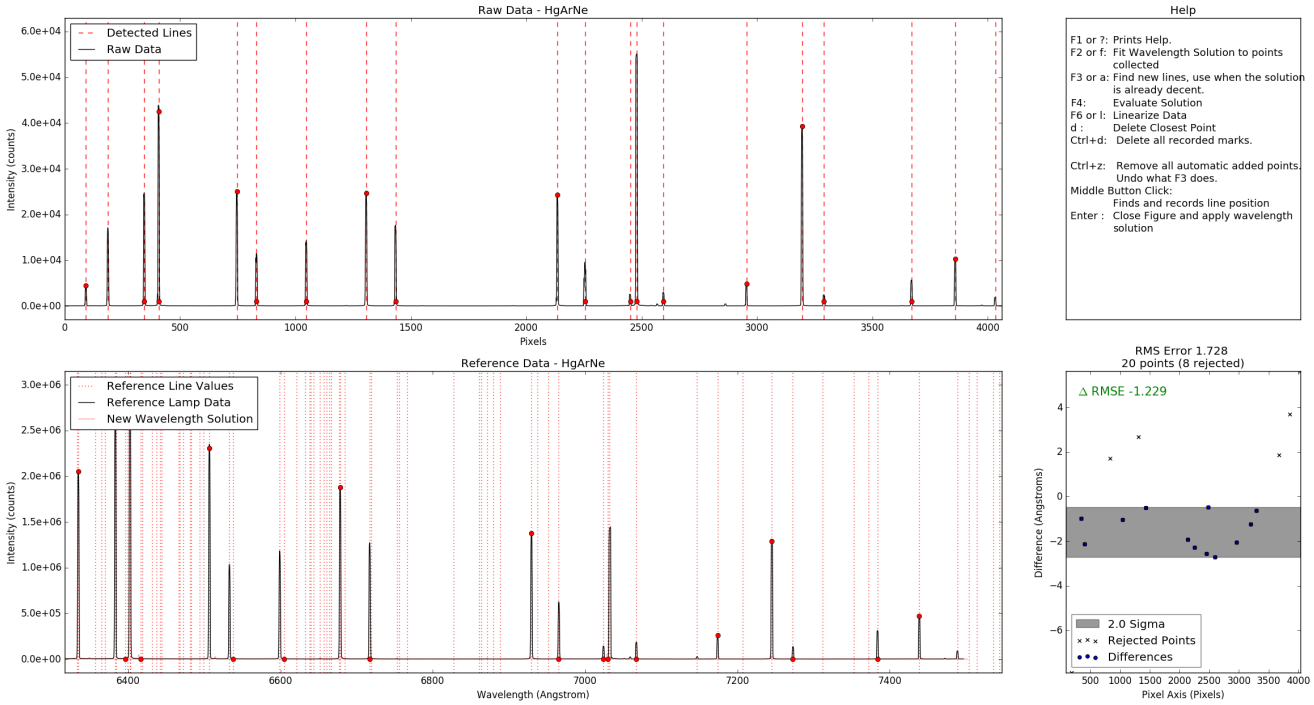
3. In case you miss-identified a line, like in the image below, you can place the mouse pointer above the corresponding red circle and press **d** to delete it. It will search for the closest mark along the horizontal axis and remove it. If there is a counterpart in the opposite plot it will delete it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



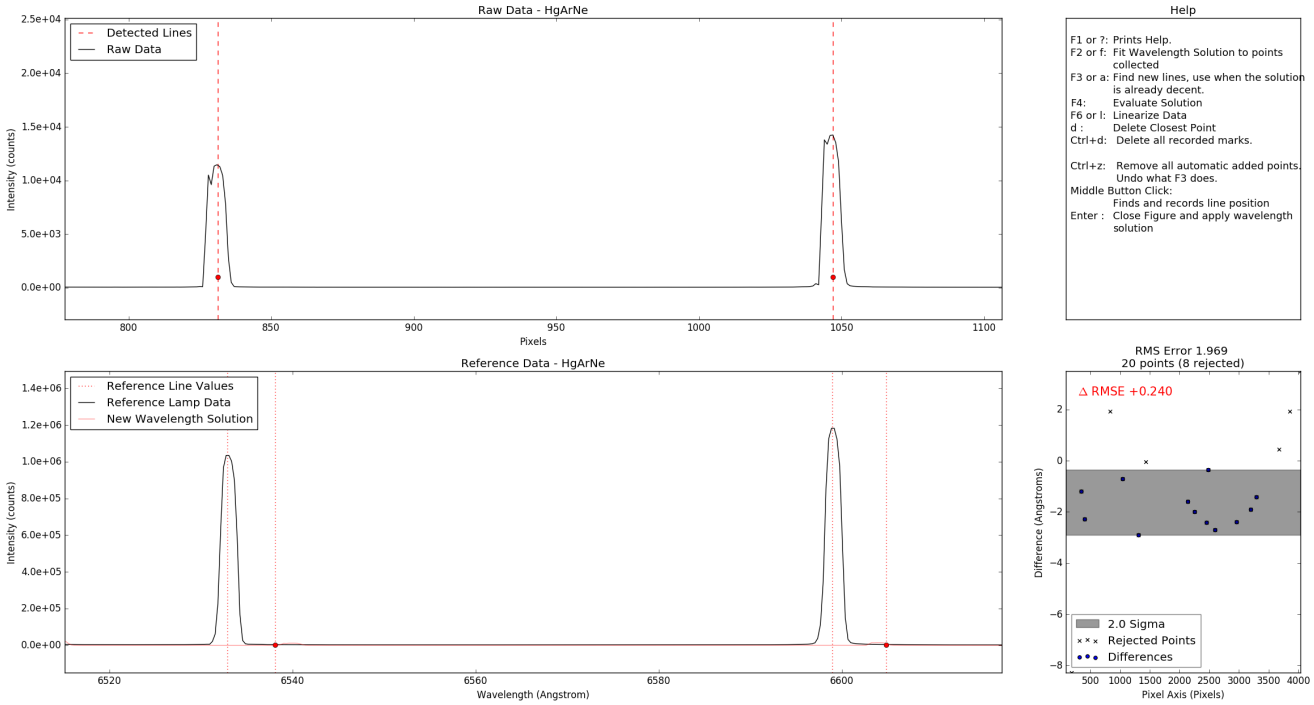

4. Once you matched a good number of lines, the minimum required by the fitting routines are four, you can either press F2 or f to make a fit of the pixels and angstrom values collected. Now the *Bottom Right* plot will show the difference in angstrom for pixel values. It is important to note here that the points in that plot do not represent the points you marked but each line detected (red dashed line in the Raw Data plot, *Upper Left*.) It does a 2 sigma clip once to reject outliers and then it uses the values to calculate the Root Mean Square Error. In this case is a bit high, but we will fix that below.



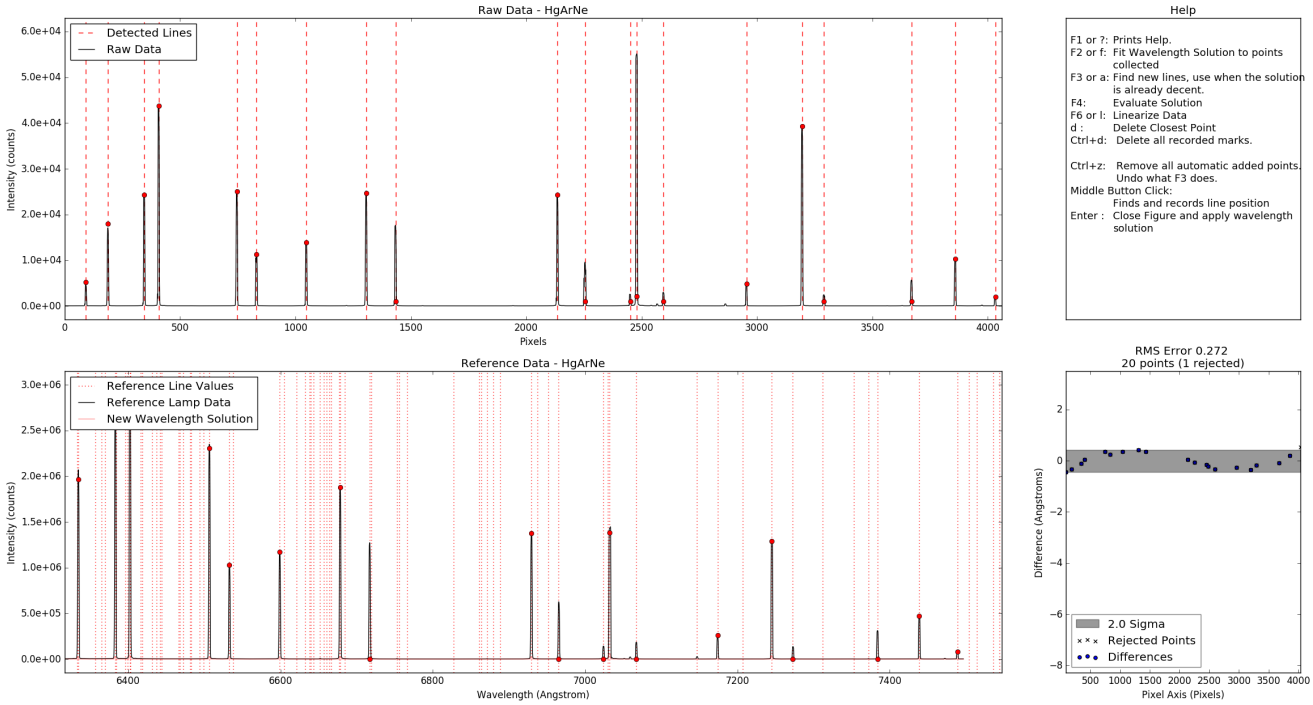

5. If you see that your current solution is decent you can press F3 or a and the pipeline will try to find more points automatically, you will see them in the next plot near the bottom of each plot, at the level of the background. This is not perfect and indeed it depends on the preliminary wavelength solution, it uses the detected lines in the raw data, applies the preliminary solution and tries to find a match in the reference line values, most of the cases it improves the solution but not always so keep that in mind. In this case the RMS error is reduced by almost a half which is good but if you look closely you can see the mismatches, also the *Bottom Right* plot will show you this.




6. Now you will see an example of when the match is apparently good but is not, Here you can zoom in to see the details, unfortunately the raw and reference data are **NOT** synchronized so you have to try a couple of times to get the correct size ratios as in the plot below. So, what you do in this case is: First delete the points using d and then mark them again.

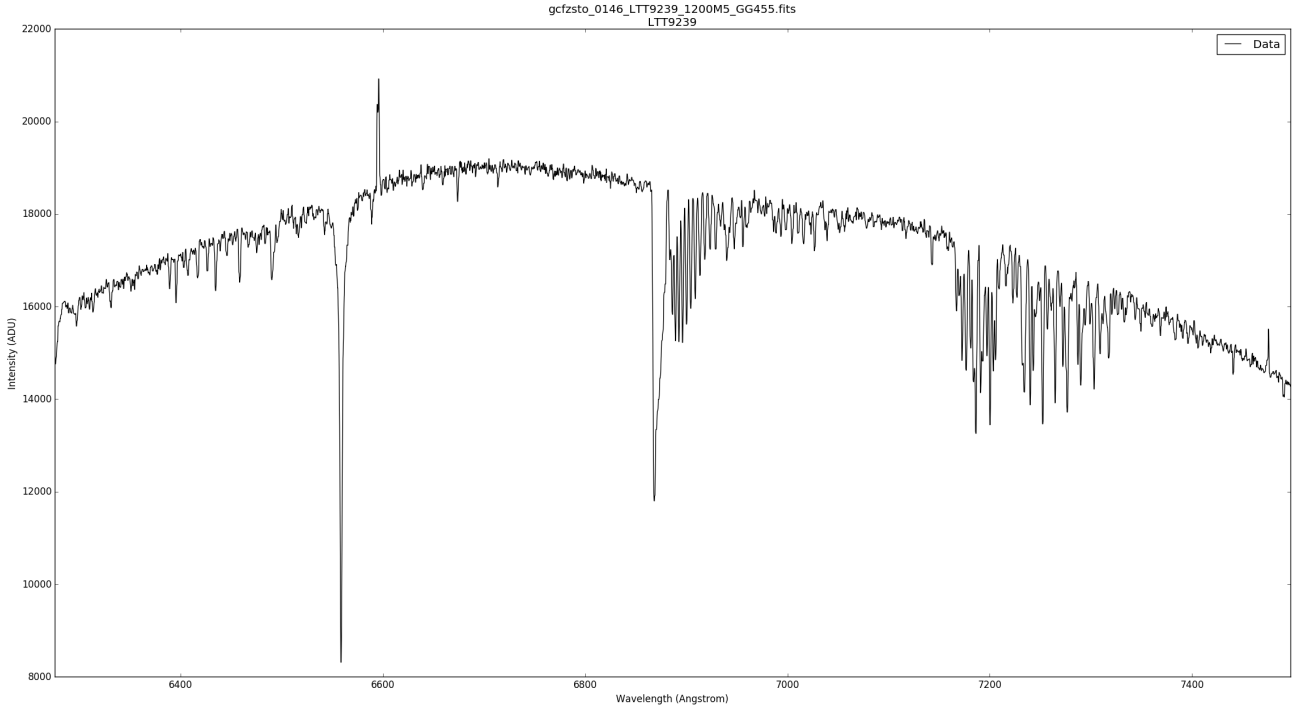


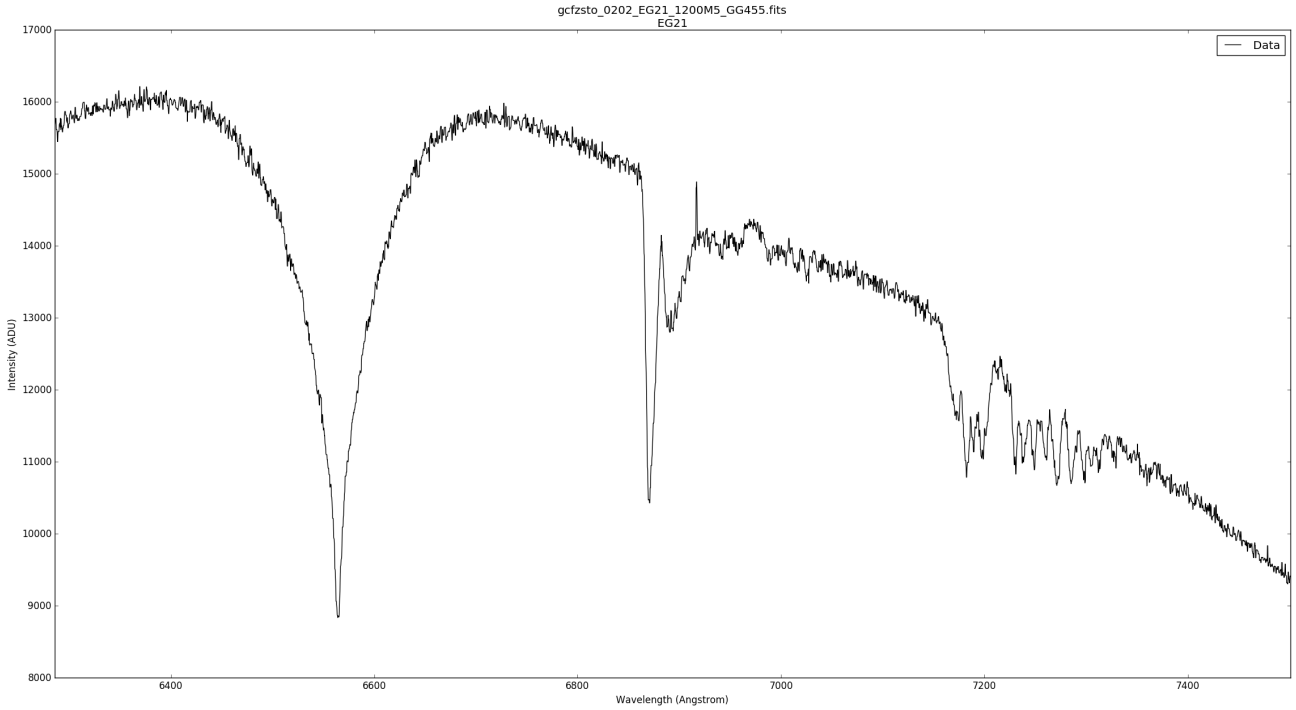

7. I recommend you doing a good check to all the points and then fit the solution again and you will have something like this:

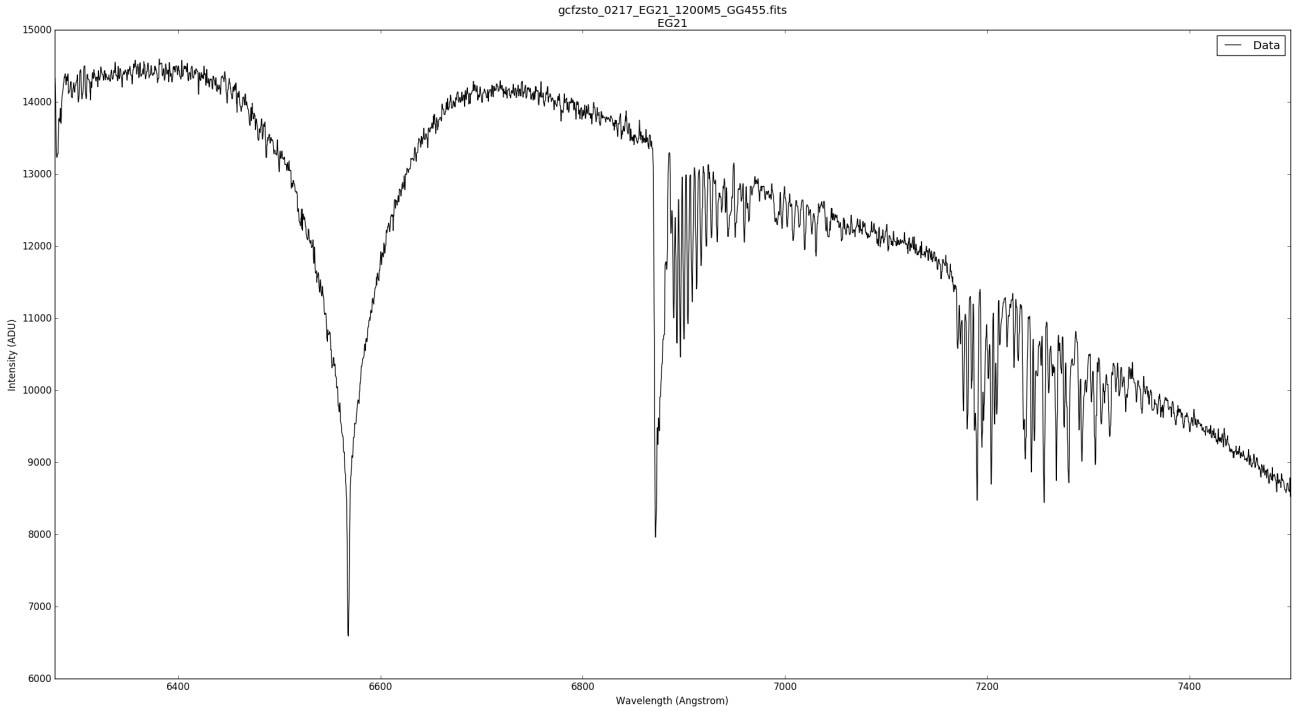


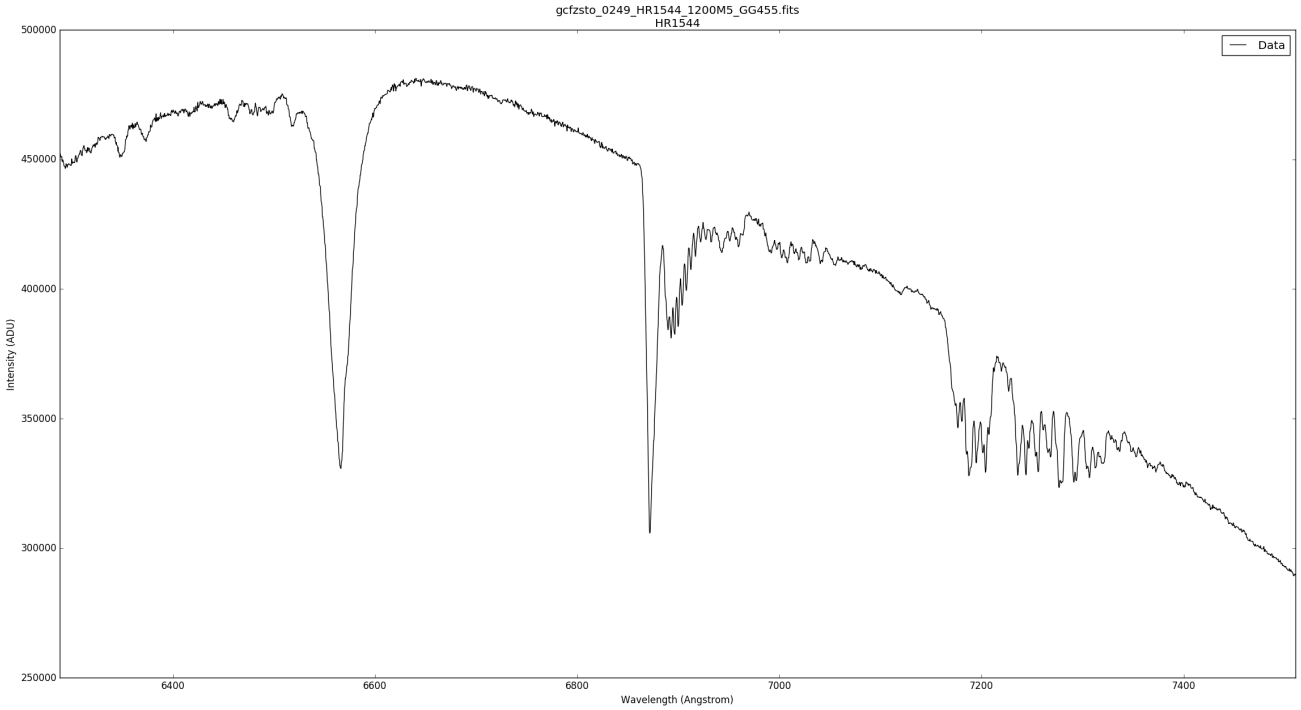

You see that the *Bottom Right* plot shows that the differences have a sinusoidal shape which is also a signal that the solution can be improved. There are ways this could be improved even further but this will be left for a later version.

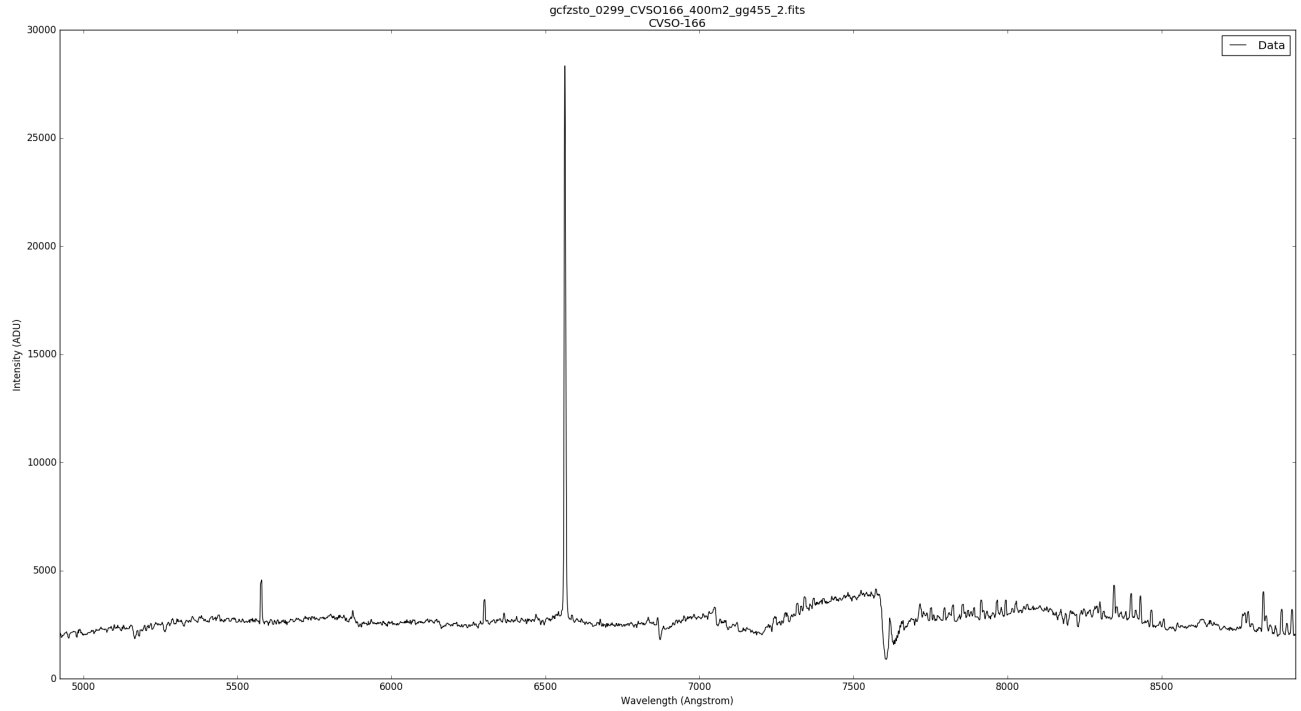
8. Finally, a few samples of the data extracted by the pipeline.

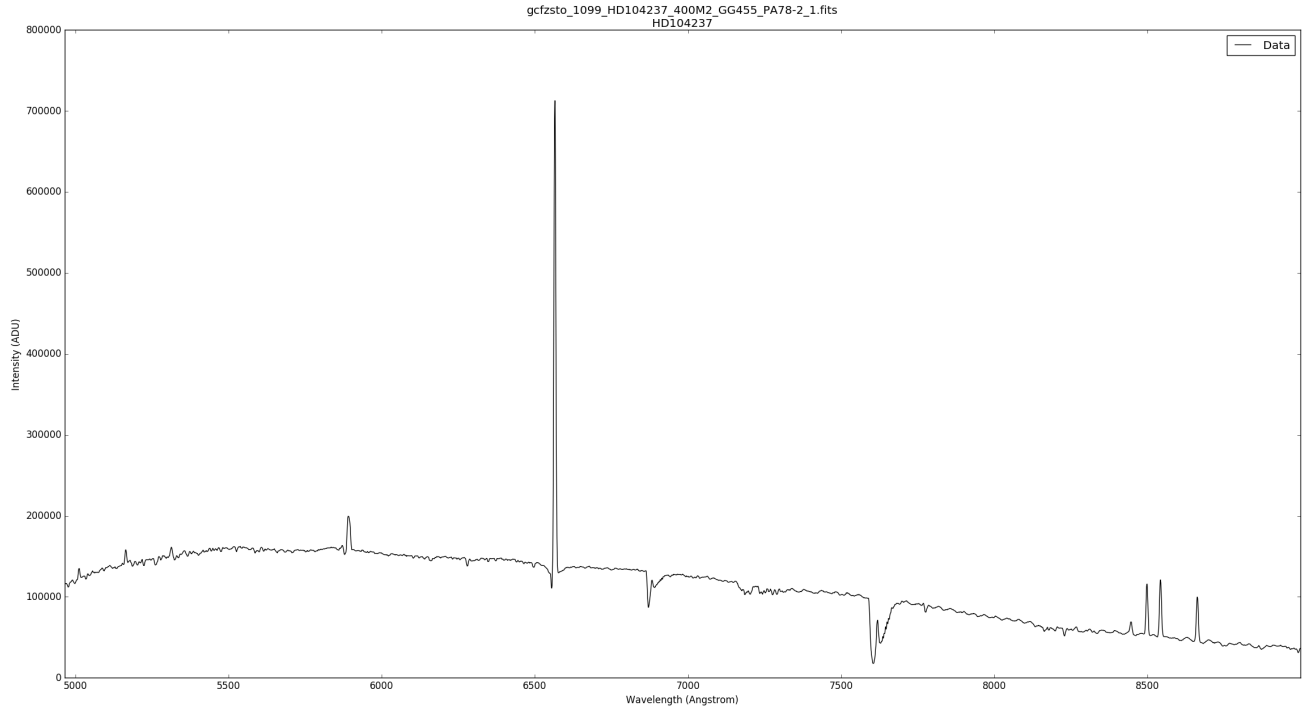



gcfzsto_0202_EG21_1200M5_GG455.fits
EG21
Data
Intensity (ADU)
Wavelength (Angstrom)
17000
16000
15000
14000
13000
12000
11000
10000
9000
8000
6400
6600
6800
7000
7200
7400


gcfzsto_0217_EG21_1200M5_GG455.fits
EG21
Data
Intensity (ADU)
Wavelength (Angstrom)
15000
14000
13000
12000
11000
10000
9000
8000
7000
6000
6400
6600
6800
7000
7200
7400


gcfzsto_0249_HR1544_1200M5_GG455.fits
HR1544
Data
Intensity (ADU)
Wavelength (Angstrom)
500000
450000
400000
350000
300000
250000
6400
6600
6800
7000
7200
7400


gcfzsto_0299_CVSO166_400m2_gg455_2.fits
CVSO-166
Data
Intensity (ADU)
Wavelength (Angstrom)
30000
25000
20000
15000
10000
5000
0
5000
5500
6000
6500
7000
7500
8000
8500




# 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

Installation will slightly depend on the system but in general is simple and can be sumarized in the following steps:

- Download the pipeline code
- Install prerequisites
- Install the pipeline

It is very important to note that this pipeline has been developed using *Python 2.7*, although we have done it in a way that would allow a smooth transition to *Python 3.5* we haven't tested it neither are we planning to do it in the near future.

## Install Dependencies

There are two types of dependencies that have to be met. The system prerequisite installation depends on the platform itself so they will be detailed bellow in their respective subsection.

The python libraries are specified in the file `requirements.txt` and installing them is very easy. But it has to be done later on.

### *Ubuntu 16.04*

Some other python-specific tools, if you already run python code most likely you already have them.

```
sudo apt-get install python-setuptools python-dev build-essential
sudo easy_install pip
```

We have decided to use Qt4Agg backend since Qt seems to be the most multi platform compatible backend.

```
sudo apt-get install python-qt4
```

### *CentOS 7*

Start by installing the `EPEL repository`

```
sudo yum -y install epel-release
```

Update the database with

```
sudo yum -y update
```

This takes a while…

Install pip

```
sudo yum -y install python-pip
```

Upgrade pip

```
sudo pip install --upgrade pip
```

Install python-devel

```
sudo yum install python-devel
```

### *Installing on MacOSX*

Although I have succesfully run the pipeline in two separated MacOS X machines the installation process was a bit tricky and has not been fully tested. I plan to update this section in the next weeks.

### *Install Using Virtual Environments*

Virtual Environment installation has not been fully tested.

# Downloading the Goodman HTS Spectroscopic Pipeline

In order to get the code for the pipeline there a many options, our suggestion is to download the official release `tar.gz` file

https://github.com/soar-telescope/goodman/blob/master/dist/goodman-1.0b1.tar.gz

# Installing the Pipeline

First of all install the python requirements. Your location must be the same as the file `requirements.txt` which should be your recently cloned repository

```
sudo pip install -r requirements.txt
```

Once this has succeeded proceed to install the pipeline using:

```
sudo python setup.py install --record files.txt
```

This will install the pipeline in your system and also will create a file `files.txt` that contains the list of files created at installation time and will be very helpfull if you ever want to fully remove the pipeline.

# Install DCR

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.

Visit this Link to download the code and find the instructions for compiling. I have added a few pre-compiled binaries and if you are lucky they will work right away. The available binaries are located in `goodman/dcr` and the options are:

- dcr.Ubuntu16.04
- dcr.Centos7
- dcr.MacOSSierra
- dcr.Solaris11

Choose whatever version fits your needs and rename it `dcr` and put it in a folder that at the same time is in your `$PATH` variable. If you don't know what that is follow the next section.

## *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 likey 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
   ```

   Where `/home/myusername` is of course your home directory.
5. Close and reopen the terminal or load the `.bashrc` file.

   ```
   source ~/.bashrc
   ```