

# **Goodman HTS Pipeline User Manual**

**version 0.1**

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# Introduction

This document is the User Manual for the *Goodman Spectroscopic Data Reduction Pipeline*. It provides an overview of the main features of the pipeline, 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 [this link](#). 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
- Do background subtraction
- 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
- There is yet no flux calibration. We are working on a module that will do this.
- The pipeline does not do miracles. If you have saturated flats, or your flats were taken with a different slit than your science frames, or you have no bias frames, the pipeline will fail.

## 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 facilitate things 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] [--cosmic] [--ignore-bias] [--ignore-flats] [--auto-clean]
              [--saturation <Value>] [--raw-path raw_path]
              [--red-path red_path] [--debug] [--log-to-file]
              [--flat-normalize <Normalization Method>]
              [--flat-norm-order <Order>] [--dcr-par-dir <dcr.par directory>]
              [--keep-cosmic-files]
```

Goodman CCD Reduction - CCDreductions for Goodman spectroscopic data

optional arguments:

<code>-h, --help</code>	show this help message and exit
<code>--cosmic</code>	Clean cosmic rays from science data.
<code>--ignore-bias</code>	Ignore bias correction
<code>--ignore-flats</code>	Ignore flat field correction
<code>--auto-clean</code>	Automatically clean reduced data directory
<code>--saturation &lt;Value&gt;</code>	Saturation limit. Default to 55.000 ADU (counts)
<code>--raw-path raw_path</code>	Path to raw data.
<code>--red-path red_path</code>	Path to reduced data.
<code>--debug</code>	Show detailed information of the process.
<code>--log-to-file</code>	Write log to a file.
<code>--flat-normalize &lt;Normalization Method&gt;</code>	Choose a method to normalize the master flat forspectroscopy. Choices are: mean, simple (model) and full (fits model to each line).
<code>--flat-norm-order &lt;Order&gt;</code>	Defines the order of the model to be fitted.

```
--dcr-par-dir <dcr.par directory>
                        Directory of default dcr.par file.
--keep-cosmic-files      After cleaning cosmic rays with dcr, do not remove the
                        input file and the cosmic rays file.
```

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] [--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.Disabled by default.
--debug               Debugging Mode
--log-to-file          Write log to a file
--save-plots           Save all plots in a directory
--plot-results         Show wavelength calibrated spectrum at the end.
```

## 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

For the rest of this tutorial we will assume your host name is `vnc-server` the display 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`.

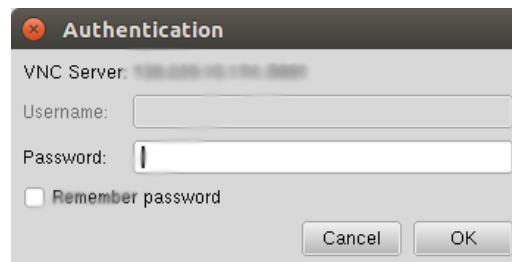
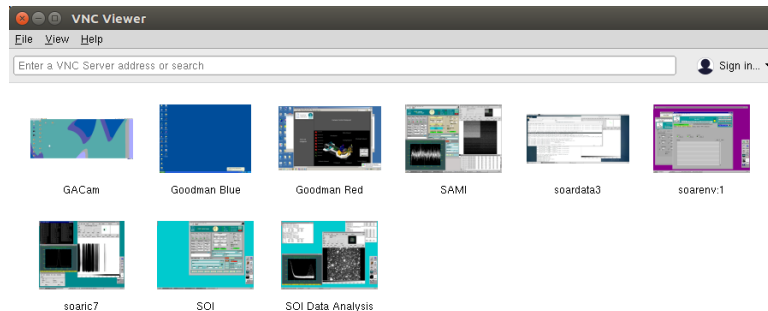
## Running the Pipeline

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

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

## VNC using a Graphical Client

Using a graphical VNC client is quite similar and intuitive

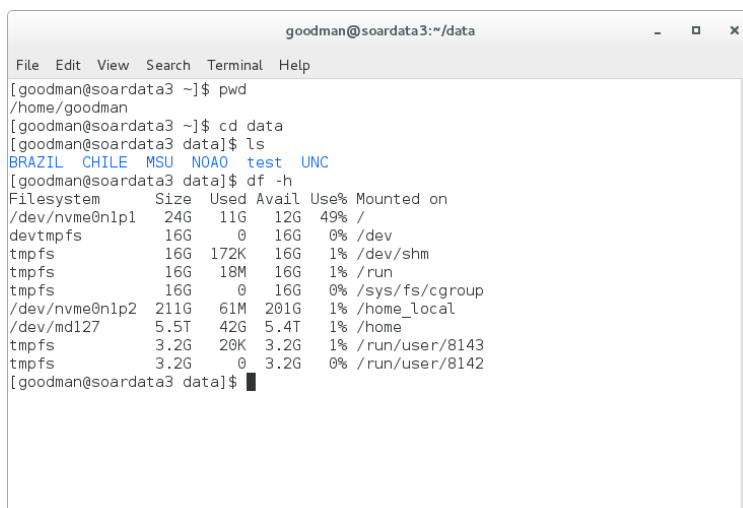


In this case the *IP address* was used, which is equivalent and sometimes better.

## 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, acquisition 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 properly) processed should have the new name (including the reduced data folder):

```
cfzsto_image_file.fits
```

Where *c* stands for *cosmic ray rejected*, *f* for flatfielded, *z* for zero or bias corrected, *s* for slit trimmed, *t* for trimmed and *o* for 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.

## 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.

# Installation Instructions

## Install prerequisites

## Downloading the Goodman HTS Spectroscopic Pipeline

## Installing on Linux Ubuntu 16.04 and CentOS 7

## Installing on MacOSX

## Importing Parts of the Code

You can import almost every function in this pipeline:

```
1 from goodman_ccd.core import spectroscopic_extraction
2 # do some stuff here
3 print('Hello World')
```