Reducing Flamingos 2 Data

with the *Red Flamingos* pipeline

Available at https://github.com/jgagneastro/red_flamingos

1. Introduction

The *Red Flamingos* pipeline is intended to reduce near-infrared astronomical spectra obtained with the Flamingos-2 (see Eikenberry et al. 2004) spectrograph currently installed at the Gemini-South telescope in Chile. It was not initially written for public distribution, hence the code is far from an optimal state, however it should be functional with some limitations described in the next section.

1.1 Current Limitations of the Pipeline

The *Red Flamingos* pipeline has only been tested with a limited set of observations; it is very likely that the current version of the pipeline will crash if used on a different data set. Any user is welcome to modify it for their own needs, and push back their own modified on GitHub.

Here is a description of the instrumental settings for which the pipeline has been tested on; these settings were chosen in order to obtain low-resolution (resolving power $R \sim 500$) spectra in the $0.9 - 2.4$ μm range for nearby brown dwarfs (typical 2MASS *J*-band magnitudes in the range $13 - 16$).

- Camera: HAWAII-II array, 0.18 arcsec/pix (f/16)
- Filter: *JH* or *HK*
- Disperser: *JH* or *HK*
- Focal Plane Mask: 4-pixels wide slit
- Read Noise : Any (Bright, Medium or Faint)

The data have to be obtained in ABBA patterns along the slit, such that the contribution of the sky can be eliminated by reducing A-B exposures.

1.2 Calibrations

The *Red Flamingos* pipeline requires three types of calibrations: Flat fields for pixel response variations, dark exposures to correct dark current, and argon (Ar) lamp exposures for wavelength calibration. Typically, one ~15 seconds Ar exposure and one ~4 seconds flat field exposure are obtained once after the science and telluric sequences of one target.

These calibrations need to be obtained with both the *JH* and *HK* grism and filter if both types of data are also obtained. Dark exposures are typically obtained once a semester (or more)

and consist of a large set of exposures with varying exposure times with filters that block all light to the detector. Ideally, all combinations of exposure times that are seen in the calibration or science data should have at least one corresponding dark exposure, but the pipeline can work even if it is not the case, by trying to guess a monotonic relation between exposure time and dark current.

2. Download and Install the Reduction Package

The *Red Flamingos* pipeline is intended for IDL v7.0 or later and may not function properly on earlier versions of IDL. Here is a step-by-step description of how to install Red Flamingos for the general users that do not plan on contributing to the development of the code:

- Download the pipeline on GitHub using the "Clone or download"/"Download ZIP" green button on the right side of the Red Flamingos home page (the complete URL is also located in the header of this document).
- Unpack the ZIP directory in a location of your choice, and make sure that this directory is included (recursively) in your IDL path environment variable (for those who don't know what this is, simply follow the next steps that describe how to use IDLDE).
- If you already have your own version of the astrolib IDL library in your path environment, you could remove the "/red_flamingos/pro/astrolib/" directory. The same goes with the spextool package; if you already have it, remove the "/red_flamingos/pro/spextool/" directory. Note that I have not tested the pipeline with all versions of spextool and astrolib, and thus it may be preferable to create an isolated IDL workspace that contains only the routines provided with this package.
- I find it easier to use the IDLDE developer environment when reducing Flamingos-2 data. In order to do so, you can use the following CMD command (OS X or unix):
  /Applications/exelis/idl85/bin/idlde -outofprocess
- Once you have the IDLDE window open, you can go in the "Project Explorer" window, right-click in the blank space and choose "Import". Under the "General" section, choose "Existing Projects into Workspace". Then click "Browse" to the right of the "Select Root Directory" field, and select your local path to the main "red_flamingos" directory. A project called "Red Flamingos" should appear in your list of Projects. You can then click "Finish" and all of the necessary routines should now be included in your IDLDE path environment.
- You can bring up the main program by entering the following command in the "IDL Console" window of IDLDE:
  ```
  IDL> .e red_flamingos
  ```
- You can bring up the main program by entering the following command in the "IDL Console" wind
- Make sure that the "read_noise" variable is set to the value corresponding to your observations (Bright mode = 11.7 e/read; Medium mode = 6.0 e/read; Faint mode < 5.0 e/read, refer to your fits file header in this case)
- Now you will need to set up the IDL path variables and build your target list. Follow the instructions provided in sections 3 and 4 to do this.

3. Setting up the Path Variables

There are three options for setting up the path variables that are needed by *Red Flamingos*. I am listing them in the order that you should prefer if your system allows it:

3.1 Using your Bash profile

If you are using an OS X or unix system, the simplest way to set up your IDL path variables is by adding some shell variables in your bash profile. Here is an example of what you will need to include in your profile :

```
export PIDL_REDFLAMINGOS_BASEDIR="/Users/gagne/Documents/IDL/IDL_library/Public/red_flamingos/"
export PIDL_REDFLAMINGOS_IDL_RESOURCES="${PIDL_REDFLAMINGOS_BASEDIR}idl_resources/"
```

You can find the complete list of commands that are needed in "/red_flamingos/example_bash_profile.txt". Once this is done, completely quit and re-open IDL, and verify if it worked with the following command:

```
IDL> print,gpath('redflamingos_basedir')
```

If the output is blank, it did not work. The output should be the path that you have set up under the PIDL_BASE environment variable. Note that the gpath routine is provided in the *Red Flamingos* pipeline.

3.2 Using *path_library.pro*

If the bash profile option did not work or you are using a system that does not have bash profiles, the next available option is to set up your paths in the path_library.pro routine that is provided in the *Red Flamingos* pipeline. Access it by entering the following command in the IDL console:

```
IDL> .e path_library
```

Figure out your host name by entering "hostname" in a command prompt. If this does not work (it should work under Windows, unix and OS X), then you will need to use the last option described in section 3.3.

In path_library.pro, you will need to add the necessary markers in the "case" statement of the code. In each of the markers begin-end block, you will need to add your hostname and the path that corresponds to the marker, with the following example syntax for the idl_csv marker. In this example, your hostname is assumed to be "Antares" :

```
'redflamingos_basedir': $
        begin
        case hostname of
          strlowcase('antares') : p = ['/your/path/red_flamingos/']
          else : goto, badhost
        endcase
      end
```

IMPORTANT NOTE: You may have noticed that the hostname was entered in lower case "antares" although I mentioned that the true host name was "Antares" with a capital A. **You must enter your host name in lower cases only in the *path_library.pro* code.** Also notice that '/your/path/' must be modified to your actual path.

Here are all the markers that must be defined for *Red Flamingos* to work:

- redflamingos_basedir: This directory contains the path to your main *Red Flamingos* directory.
- redflamingos_idl_resources: This directory contains resources (mostly IDL save files) that are needed by the pipeline.
- redflamingos_raw_logdir: This is the directory where log files (CSV format) should be placed.
- redflamingos_raw_data: This directory contains all of your raw Flamingos-2 data.
- redflamingos_reduced_data: This directory will contain your reduced data.
- redflamingos_screenshots: This directory will contain screenshots of the data reduction process if you require them.
- redflamingos_darks: This directory will contain aggregated dark exposures that you may want to use to correct for dark current.

3.3 Manually setting up the paths

If none of the options above worked, you can use this last resort option;

(1) Open path_library.pro
(2) Remove of comment out these lines at the beginning of the code:

```
;Check on which machine this code is running
  if ~keyword_set(hostname) then $
     spawn, 'hostname', hostname
  hostname = strlowcase(hostname)
```

(3) Choose any hostname for your system. If you are choosing the default "antares", then enter the following line of code where you just deleted the previous lines (use only lower caps !):

```
hostname = 'antares'
```

(4) Set up the markers in path_library.pro, as described in section 3.2.

4. Building your Target List

In order to properly set up *Red Flamingos*, you need to create a comma-separated .csv file that describes your science targets, telluric standards and abba patterns. You can use any software to do this (Excel/Numbers/Google Sheets, etc.) and then export the table as a .csv file. Example .numbers and .csv files are provided in /red_flamingos/flamingos_logfiles/.

Each line in the log file corresponds to a single observing sequence. For each line, the following quantities must be defined:

- **Obj. Name:** An object name describing your target. Make it SIMBAD-resolvable (using spaces when needed) for your A-type telluric standards.
- **Date:** An observing date in the format "yymmdd" (year, month and day).
- **FITS#:** The fits file numbers of the corresponding observing sequence. Ranges or semicolon-separated lists can be used to achieve this. For example, "1-3" means "1 to 3", "1;8" means "1 and 8", and "1-3;9;11" means "1, 2, 3, 9 and 11".
- **Program ID:** Your Gemini program ID.
- **Filter:** Either JH or HK, corresponding to the filter and grism that were used.
- **Type:** Three data types are available :
  - Telluric: For your A-type telluric standard sequence
  - Calibrations: For your flats, Ar lamps and dark exposures.
  - Science: For your regular science sequences.
- **Flat#:** Enter here the fits number(s) of the flat file(s) sequence that should be used for this sequence. This exact string must correspond to one flat sequence in the "FITS#" column that was observed on the same date. It must also have been obtained with the same settings (*JH* or *HK*). For Calibration-type sequences, enter "…" in this column.
- **Telluric#**: Enter here the fits number(s) of the telluric sequence that should be used for this science sequence. This exact string must exactly match one of your telluric seqqence in the "FITS#" column that was observed on the same date. For Calibration-type sequences, enter "…" in this column. For Telluric-type sequences, enter the spectral type (e.g., A0) of the telluric target that you have observed.
- **Lamps#:** Enter here the fits number(s) of the lamp sequence that should be used for this sequence. For Calibration-type sequences, enter "…" in this column.
- **Darks Program ID:** Enter here the program ID in which the dark exposures that you want to use were observed. This string must exactly match the "Program ID" column of one line in your log that contains dark exposures. This must be done for all types of sequences, with the exception of dark exposure sequences. In the latter case, enter "…" in this column.
- **Darks Date:** Enter here the date on which the dark exposures that you want to use were observed. This string must exactly match the "Date" column of one line in your log that contains dark exposures. This must be done for all types of sequences, with the exception of dark exposure sequences. In the latter case, enter "…" in this column.
- **Darks# :** Enter here the fits number(s) of the dark exposure(s) that you want to use. This string must exactly match the "FITS#" column of one line in your log that contains dark exposures. This must be done for all types of sequences, with the exception of dark exposure sequences. In the latter case, enter "…" in this column.
- **abba patterns**: This is the description of the abba patterns along the slit that were observed. If you have 4 exposures that were obtained in a normal "a-b-b-a" pattern, simply enter the string "abba". If for some reason you obtained two "a" exposures, two "b" exposures and then a last "a" exposure, enter "aabba". The length of this string must correspond to the number of exposures in the sequence.
- **Reduce ?**: This cell can be used to track the progress of your data reduction. If you write "1" here, the code will reduce the data. If you write anything from "done" to "avoid" to

"bad data", or really any other string that you like, the code will avoid it. This cell is only used for Telluric-type and Science-type sequences.

- **Binary ?**: The pipeline will eventually be able to extract binary objects that were both placed in the slit. However, for the moment the code will avoid reducing any sequence with a value of "1" in this cell, because the option has not yet been fully implemented.
- **Comments:** This is for your own use; the pipeline does not read this cell.

Keep in mind that telluric standard exposures must always be reduced before the science exposures that will require them. Since the code reduces the data in the order in which your observing log is built, you must always list the telluric sequences before the science sequences.

You also have to place all your dark exposures in a single directory — this is done to make it easier to use darks exposures across several nights. The default directory where to put them is "/red_flamingos/sample_data/raw/DARKS/", but this can be changed (see previous section on how to change paths).

Also note that your data should be placed in the raw_data directory (default is "/red_flamingos/sample_data/raw/") with the following subdirectories : "/Program ID/Date [YYMMDD]/". An example a valid directory would be "/red_flamingos/sample_data/raw/GS-2013B-Q-79/131021/". The program ID and date must match the entires in your log file.

IMPORTANT NOTE: When you build your observing log in a program such as Numbers, Excel or Google Sheets, make sure that there are no comma symbols anywhere in the file before exporting it to a .csv format ! The .csv format uses commas as column separators, and hence the code will not be able to read your log file if you have used commas anywhere.

5. Extracting the Data

You are now ready to launch the data extraction process. You can do so by entering "red_flamingos" in the IDL console, or press the "Run" button at the top of the IDLDE environment. This section will eventually describe exactly what the pipeline does.

In the final step of extraction, the pipeline will save a fits file to your disk that contains one extracted science spectrum per exposure. At this point, the data are not telluric-corrected or combined. The data is saved in a specific format to make it compatible with the Spextool routines that are described in the next three sections.

6. Combining Exposures

The *xcombspec.pro* routine must be used to combine your individual exposures into a single higher signal-to-noise spectrum. You can launch it by simply typing "xcombspec" in the IDL console.

Please refer to the Spextool helpfile located at "/red_flamingos/pro/spextool/helpfiles/xcombspec_helpfile.txt" to obtain more information on how to use this tool.

Note that red_flamingos will ask you to enter ".continue" in the IDL console after you are done using *xcombspec.pro*.

7. Correcting for Telluric Absorption

The *xtellcor_general.pro* routine must be used to apply a telluric correction to your spectra. You can launch it by typing "xtellcor_general" in the IDL console.

Please refer to the Spextool helpfile located at "/red_flamingos/pro/spextool/helpfiles/xtellcor_general_helpfile.txt" to obtain more information on how to use this tool.

Note that red_flamingos will ask you to enter ".continue" in the IDL console after you are done using *xtellcor_general.pro*.

8. Merging *JH* and *HK* observations

The *xmergeorders.pro* routine must be used to combine *JH* and *HK* spectra together into a single *JHK* spectrum. You will notice that the red end of the *JH* spectrum and the blue end of the *HK* spectrum are significantly affected by systematics - Red Flamingos does some post-processing to correct these systematic slopes, but the systematics affecting the very end of the both orders is too unstable to be corrected, and you will need to clip it out while using *xmergeorders.pro*. These bad parts should be very easy to identify by eye, and the rest of the overlapping region should match very well.

Please refer to the Spextool helpfile located at "/red_flamingos/pro/spextool/helpfiles/xmergeorders_helpfile.txt" to obtain more information on how to use this tool.

Note that red_flamingos will ask you to enter ".continue" in the IDL console after you are done using *xmergeorders.pro*.

I have included a PDF version of the complete SpeXTool manual at "/red_flamingos/pro/spextool/spextool_manual.pdf" for reference - note that only the parts regarding *xcombspec.pro*, *xtellcor_general.pro* and *xmergeorders.pro* are relevant here, and it is possible that some features described in the manual not available in Red Flamingos, since SpeXTool has remained in active development since I adapted some of its subroutines for Red Flamingos.

9. Reducing Sample Data

The Red Flamingos package includes a set of sample data for the young brown dwarf 2MASS J23225299-6151275 (this spectrum was published in Gagné et al. (2015, ApJS 219, 33). You can find the data in "/red_flamingos/sample_data/raw/". I have performed each step of

the data reduction using v1.0 of Red Flamingos, and placed all intermediary reduction products in "/red_flamingos/sample_data/sample_reduced/". I have singled out the final spectrum in "/red_flamingos/sample_data/sample_reduced_final/", by copying it from the "sample_reduced" directory. The file name nomenclature will allow you to easily identify your final products; they are named "[Object_Name]_ALLCOMB_merge.fits".

If you would like to make sure that your installation works properly, and at the same time learn how to use the pipeline correctly, you are encouraged to do so - your results will be automatically stored in the directory "/red_flamingos/sample_data/reduced/". Please remember to delete anything from the "reduced" directory before pushing any new branch of version updates of Red Flamingos on GitHub.

It is normal that the code is relatively slow, especially if you are using an older computer. Combining dark exposures takes several minutes depending on how many you are using, and performing wavelength calibration also takes a few minutes per exposure.

10. Acknowledgements

If you use this code to reduce your data, please cite the following references :

- **Gagné et al. (2015) ApJS, 219, 33**
  BANYAN. VII. A New Population of Young Substellar Candidate Members of Nearby Moving Groups from the BASS Survey
- **Cushing et al. (2004) PASP, 116, 362**
  Spextool: A Spectral Extraction Package for SpeX, a 0.8-5.5 Micron Cross-Dispersed Spectrograph
- **Vacca et al. (2002) PASP, 115, 389**
  A Method of Correcting Near-Infrared Spectra for Telluric Absorption
- **GitHub repo**

The part where you mention the data reduction of your Flamingos 2 data should look something like this :

"The data were reduced using the Interactive Data Language (IDL) Red Flamingos pipeline (\citealt{2015ApJS..219…33G,[GITHUB#]}\footnote{Available at \url{https://github.com/jgagneastro/red_flamingos}}) which uses parts of the Spextool package \citep{2004PASP..116..362C,2003PASP..115..389V}."

Do not forget to cite the proper references for using the Flamingos 2 spectrograph too :

- **Eikenberry et al. (2004) SPIE, 5492, 1196**
  FLAMINGOS-2: the facility near-infrared wide-field imager and multi-object spectrograph for Gemini

with the usual acknowledgement paragraph :

Based on observations obtained at the Gemini Observatory through program(s) number GN-[YEAR]A-Q-[NUMBER] (, …). The Gemini Observatory is operated by the Association of Universities for Research in Astronomy, Inc., under a cooperative agreement with the National Science Foundation (NSF) on behalf of the Gemini partnership: the NSF (United States), the National Research Council (Canada), CONICYT (Chile), the Australian Research Council (Australia), Ministério da Ciência, Tecnologia e Inovação (Brazil), and Ministerio de Ciencia, Tecnología e Innovación Productiva (Argentina).

If you are using AAStexV6.0 or more recent, you should also add these commands after the acknowledgement section:

```
\facility{Gemini-South (Flamingos-2)}
\software{IDL by Harris Geospatial}
```

Finally, you are encouraged to improve this code and push it on GitHub. I am not actively developing it for the moment, and I would love to see other people using it and improving it.