GEMINI OBSERVATORY
Exploring the Universe, Sharing its Wonders

Gemini IRAF Imaging Tutorial

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General Guidelines

- Check any observing logs that come with the data
  - Gemini includes observing logs with the data
- Visually inspect **all** the data
  - Raw data
  - Data after each processing step
  - Final processed frames
- Write a processing script to record what happened to the data and what OS / software was used (Ureka 1.0!)
  - Reproducibility!

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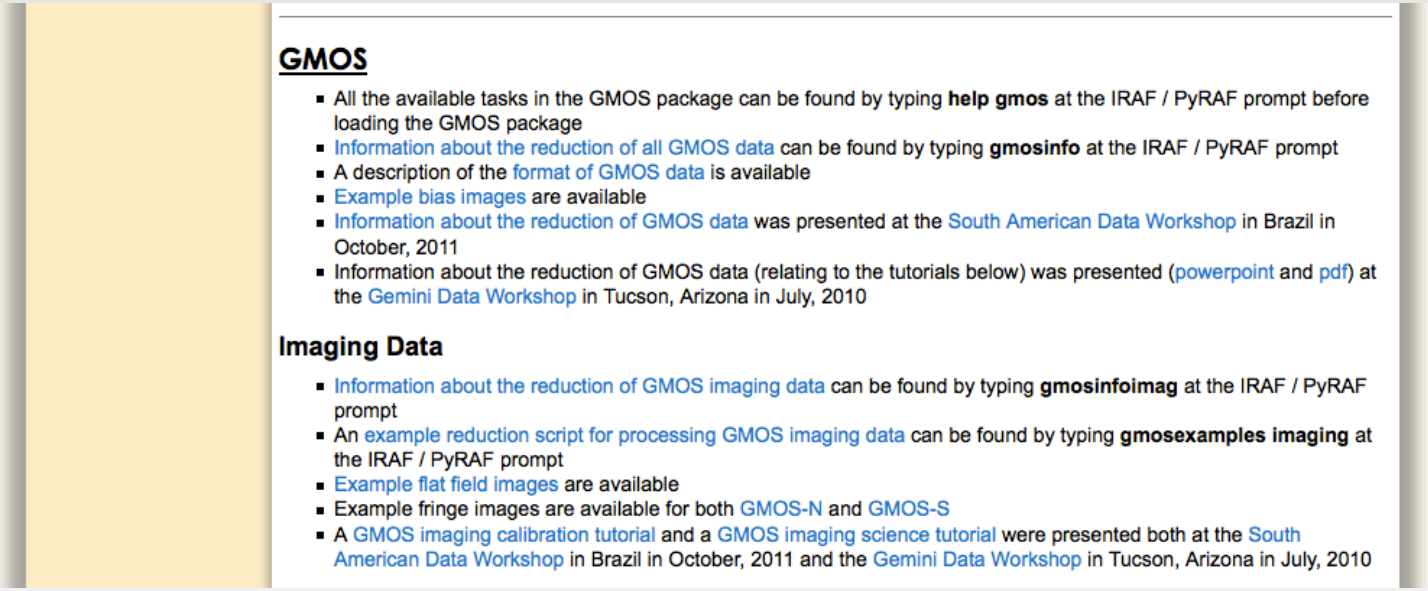
Gemini Guidelines

INSTRUMENT	MODES	PACKAGES
FLAMINGOS-2	imaging longslit	`f2` / `gnirs`
GMOS	imaging longslit MOS IFU	`gmos`
GNIRS	longslit XD IFU	`gnirs`
GSAOI	imaging	`gsaoi`
NIFS	IFU	`nifs` / `gnirs`
NIRI	imaging longslit	`niri` / `gnirs`

Gemini Guidelines

- The Getting Started web page contains information to assist users when processing data obtained with the Gemini telescopes
- `http://www.gemini.edu/sciops/data-and-results/getting-started`



GMOS

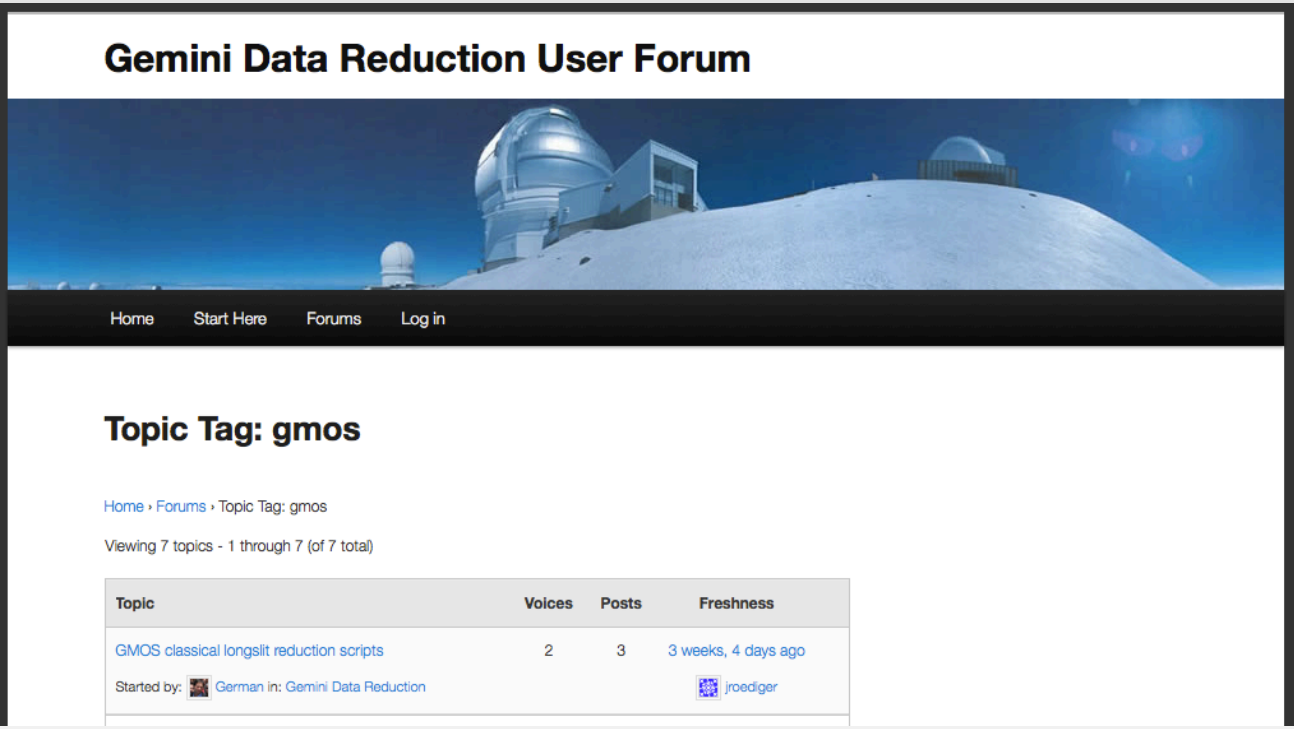
- All the available tasks in the GMOS package can be found by typing **help gmos** at the IRAF / PyRAF prompt before loading the GMOS package
- Information about the reduction of all GMOS data can be found by typing **gmosinfo** at the IRAF / PyRAF prompt
- A description of the format of GMOS data is available
- Example bias images are available
- Information about the reduction of GMOS data was presented at the South American Data Workshop in Brazil in October, 2011
- Information about the reduction of GMOS data (relating to the tutorials below) was presented (powerpoint and pdf) at the Gemini Data Workshop in Tucson, Arizona in July, 2010

Imaging Data

- Information about the reduction of GMOS imaging data can be found by typing **gmosinfoimag** at the IRAF / PyRAF prompt
- An example reduction script for processing GMOS imaging data can be found by typing **gmosexamples imaging** at the IRAF / PyRAF prompt
- Example flat field images are available
- Example fringe images are available for both GMOS-N and GMOS-S
- A GMOS imaging calibration tutorial and a GMOS imaging science tutorial were presented both at the South American Data Workshop in Brazil in October, 2011 and the Gemini Data Workshop in Tucson, Arizona in July, 2010

Gemini Guidelines

- The Gemini Data Reduction User Forum may contain further information related to processing data obtained with the Gemini telescopes (use the topic tags!)
- `http://drforum.gemini.edu/topic-tag/gmos/`



GMOS Imaging Guidelines

- Remember that the Gemini IRAF package includes instrument specific documentation and examples
  - Find out how to reduce GMOS imaging data
    - `gmosinfo`
    - `gmosinfoimag`
  - Follow a GMOS imaging example reduction script
    - `gmosexamples imaging`

Introduction to GMOS

- The GMOS detector is made up of 3 CCDs
  - GMOS detector = 6144 x 4068 pixels
  - Each CCD = 2048 x 4608 pixels
- There are different GMOS detector types:

INSTRUMENT	DETECTOR TYPE	NUMBER OF AMPLIFIERS PER CCD	PIXEL DATA EXTENSIONS IN RAW FITS FILE
GMOS-N (current)	e2v DD	2	6
GMOS-S (current)	EEV	1	3
GMOS-S (coming soon)	Hamamatsu	4	12

Introduction to GMOS

- Pixel scale:
  - GMOS-N = 0.0727 arcsec / pixel
  - GMOS-S = 0.073 arcsec / pixel
- Gap between the CCDs = 37 pixels
- Imaging field of view = 5.5 arcmin x 5.5 arcmin
- Detector characteristics:
  - Good cosmetics, with only a few bad pixels
  - Imaging Bad Pixel Masks (BPMs) are provided in the Gemini IRAF package (in the gmos$data/ directory)

Introduction to GMOS

- Non-linearity correction is not required for GMOS (GMOS is <1% linear up to ~93% full well depth)
- CCD read mode configurations:

READ MODE	AMPLIFIER READ MODE	GAIN MODE
Science	Slow	Low
Acquisition / Bright Object	Fast	Low
Acquisition / Bright Object	Fast	High
Engineering	Slow	High

Displaying GMOS Data

- Use `gdisplay` in the `gmos` package to display GMOS data (set `stdimage` according to binning)
  - `show stdimage`
  - `set stdimage=imtgmos`
    - 6400 x 4644, unbinned and 2x1 binning
  - `set stdimage=imtgmos2`
    - 3200 x 2322, 2x2 and 2x1 binning
  - `set stdimage=imtgmos4`
    - 1600 x 1161, 4x4 binning
  - `gdisplay <filename>.fits 1`

GMOS Imaging Data

- Raw GMOS imaging data will generally consist of:
  - Science frames
    - Offset to account for the gaps between the CCDs
  - Daytime Calibrations
    - Bias frames (for all binnings and read modes)
    - Twilight flat frames (for all filters)
  - Nighttime Calibrations
    - Fringe frames (blank fields, for i and z band only)
    - Photometric standard star frames

GMOS Imaging Data

- Some processed frames are included in the GSA
  - Processed bias frames
  - Processed flat frames
  - Processed fringe frames
- However, these processed frames are **not** overscan subtracted (more on this later)

Basic Reduction Steps

- Create processed bias frame
  - Prepare
  - Overscan subtract
  - Trim
  - Combine

Basic Reduction Steps

- Create processed flat frame
  - Prepare
  - Overscan subtract
  - Trim
  - Bias subtract
  - Combine
  - Normalize

Basic Reduction Steps

- Create processed fringe frame
  - Prepare
  - Overscan subtract
  - Trim
  - Bias subtract
  - Flat divide
  - Object masking
  - Combine

Basic Reduction Steps

- Create processed science frame
  - Prepare
  - Overscan subtract
  - Trim
  - Bias subtract
  - Flat divide
  - Fringe subtract (for i and z band only)
  - Mosaic
  - Align and combine

Preparing GMOS Data

- All raw data must be prepared
  - Raw data is validated
  - Keywords are added to the PHU
    - `OBSMODE`, `NSCIEXT`, `NEXTEND`
  - Keywords are added to / corrected in the pixel data extensions
    - `EXTNAME`, `EXTVER`, `RDNOISE`, `GAIN`
  - Variance and data quality extensions are added, if requested

Overscan Subtraction

- It is recommended to overscan subtract GMOS data
  - The overscan level is expected to drift with time both in absolute value and with respect to each individual amplifier
  - Especially important for faint target spectroscopy
- Note that the processed frames from the GSA are **not** overscan subtracted
  - Don't mix and match data with different processing states
  - Generate the processed frames from the raw data and overscan subtract everything!

Organise the Data

- The data should be grouped by:
  - Filter (except for bias frames)
    - PHU: `FILTER1`, `FILTER2`
  - Region of interest (ROI)
    - PHU: `DETRO*`
  - Binning
    - Pixel data extensions: `CCDSUM`

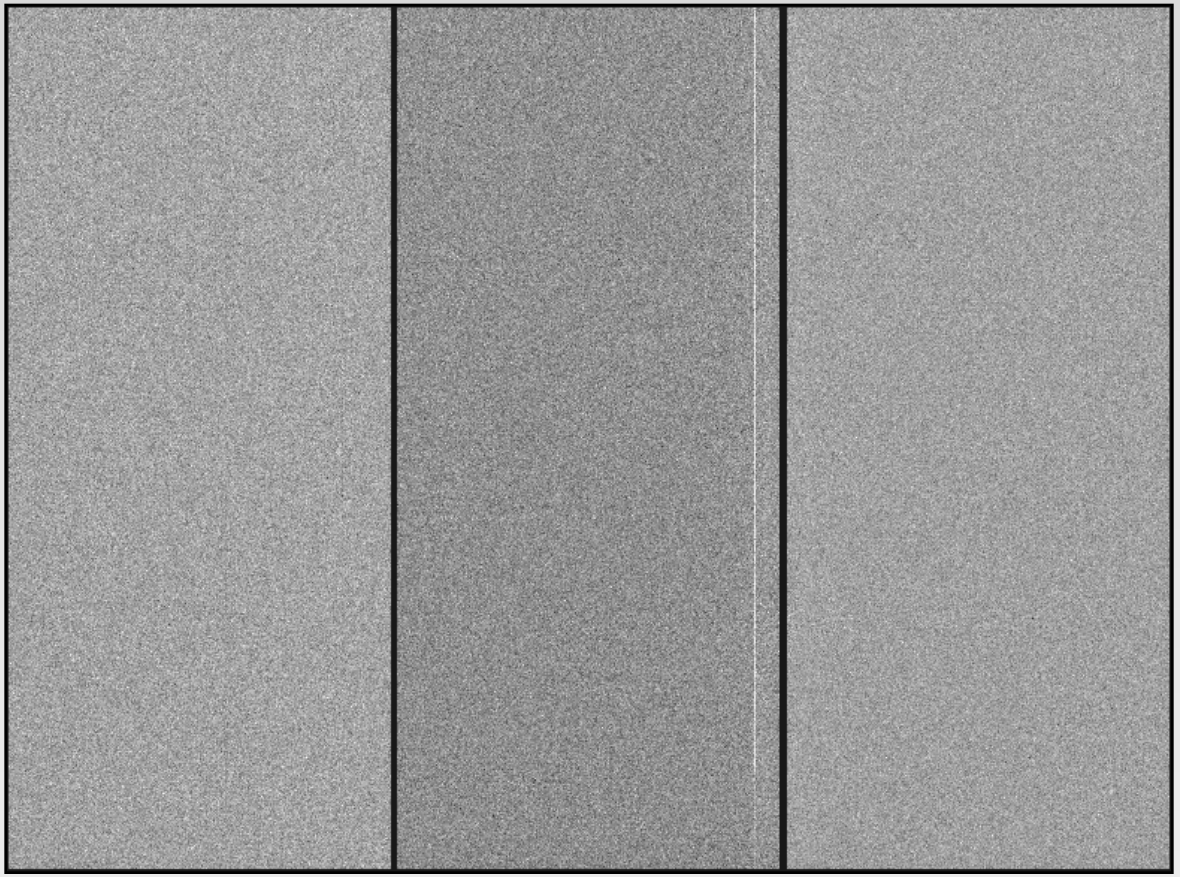
Organise the Data

- The data should be grouped by:
  - Amplifier read mode
    - PHU: `AMPINTEG`
    - Amplifier read mode = slow if `AMPINTEG` == 5000
    - Amplifier read mode = fast if `AMPINTEG` == 1000
  - Gain mode
    - Pixel data extensions: `GAIN`
    - Gain mode = low if `GAIN` < 3
    - Gain mode = high if `GAIN` > 3

Organise the Data

- Use the IRAF task `imhead` or the task `fitsutil.fxhead` to view the header
- Use the IRAF task `hselect` to select keyword values from the header
  - `hselect *fits[<#>] $I,<KEYWORD1>,<KEYWORD2>, yes`
  - values in the list starting with `$` are “special” in IRAF
    - `$I` = name of the current image
- Use the task `gemtools.gemlist` to create files containing a list of filenames of each grouping

Raw GMOS-S Bias Frame



- For more information, see `http://www.gemini.edu/sciops/instruments/gmos/calibration/example-cal-data/bias-images`

Create Processed Bias

- Use the task `gbias` in the `gmos` package
- Prepare, add variance and data quality extensions, specify the location of the raw data
  - `gbias.rawpath="/path/to/raw/data/"`
  - `gbias.fl_vardq=yes`
- Overscan subtract
  - `gbias.fl_over=yes` (default)
- Trim
  - `gbias.fl_trim=yes` (default)

Create Processed Bias

- Combine
  - `gbias.combine="average"` (default)
- Optional:
  - Change the specific region used to determine the overscan value
    - `gbias.nbiascontam` and `gbias.biasrows`
  - Fit the overscan region interactively
    - `gbias.fl_inter=yes`
- For more information, read the `gbias` help file

Create Processed Flat

- Use the task `giflat` in the `gmos` package
- Prepare, add variance and data quality extensions, specify the location of the raw data
  - `giflat.rawpath="/path/to/raw/data/"`
  - `giflat.fl_vardq=yes`
- Overscan subtract
  - `giflat.fl_over=yes` (default)
- Trim
  - `giflat.fl_trim=yes` (default)

Create Processed Flat

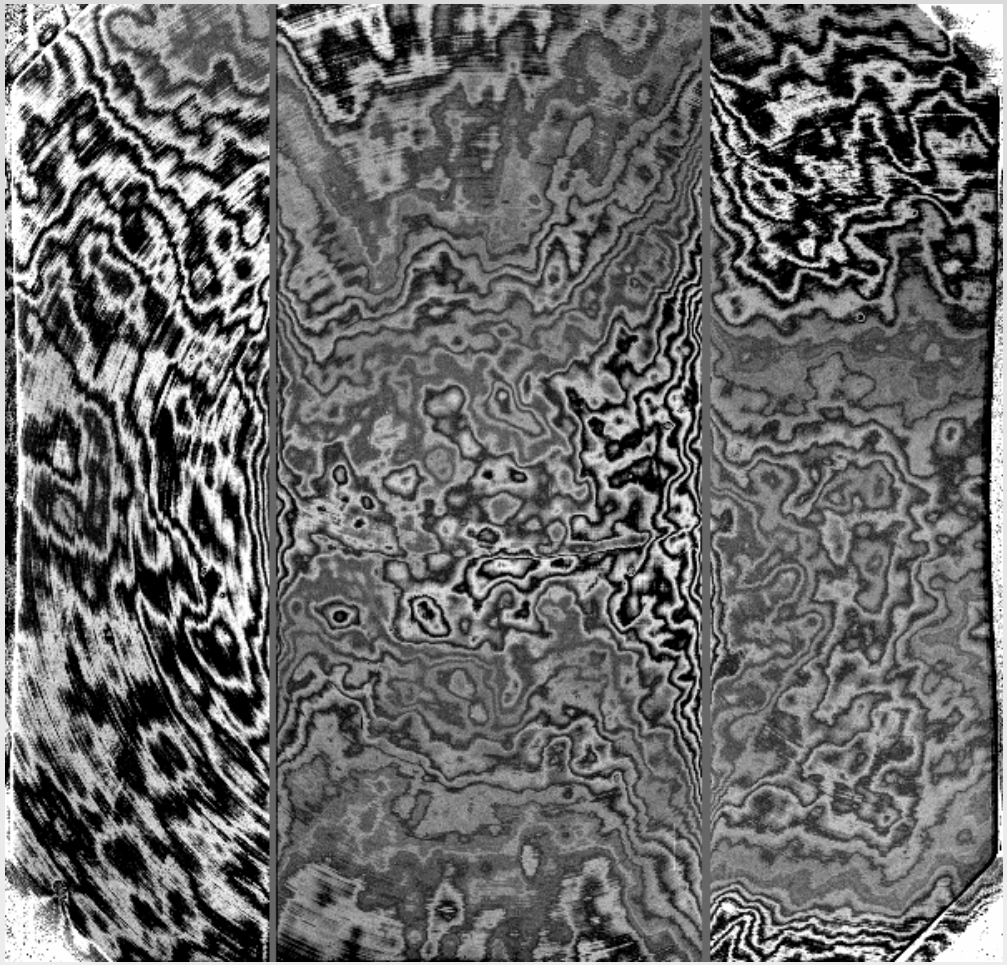
- Bias subtract
  - `giflat.fl_bias=yes` (default)
  - `giflat.bias="<bias_name>.fits"`
- Combine
  - `giflat.combine="median"` (best for twilights)
  - `giflat.fl_scale=yes` (default)

Create Processed Flat

- Normalize
  - `giflat.normsec="default"` (default)
  - The default `normsec` is the section of CCD2:

    `[100/xbin:1800/xbin,100/ybin:4500/ybin]`
- For more information, read the `giflat` help file

GMOS-S Fringe Frame z-band



- For more information, see `http://www.gemini.edu/sciops/instruments/gmos/imaging/fringing`

Create Processed Fringe

- First, use the task `gireduce` in the `gmos` package
- Prepare, add variance and data quality extensions, specify the location of the raw data
  - `gireduce.rawpath="/path/to/raw/data/"`
  - `gireduce.fl_vardq=yes`
- Overscan subtract
  - `gireduce.fl_over=yes` (default)
- Trim
  - `gireduce.fl_trim=yes` (default)

Create Processed Fringe

- Bias subtract
  - `gireduce.fl_bias=yes` (default)
  - `gireduce.bias="<bias_name>.fits"`
- Flat divide
  - `gireduce.fl_flat=yes` (default)
  - `gireduce.flat="<flat_name>.fits"`
- For more information, read the `gireduce` help file

Create Processed Fringe

- Then use the task `gifringe` in the `gmos` package
- Object masking
  - `gifringe.msigma=4.0` (default)
- Combine
  - `gifringe.combine="median"` (default)
- For more information, read the `gifringe` help file

Create Processed Science

- First, use the task `gireduce` in the `gmos` package
- Prepare, add variance and data quality extensions, specify the location of the raw data
  - `gireduce.rawpath="/path/to/raw/data/"`
  - `gireduce.fl_vardq=yes`
- Overscan subtract
  - `gireduce.fl_over=yes` (default)
- Trim
  - `gireduce.fl_trim=yes` (default)

Create Processed Science

- Bias subtract
  - `gireduce.fl_bias=yes` (default)
  - `gireduce.bias="<bias_name>.fits"`
- Flat divide
  - `gireduce.fl_flat=yes` (default)
  - `gireduce.flat="<flat_name>.fits"`
- For more information, read the `gireduce` help file

Create Processed Science

- Then use `girmfringe` in the `gmos` package
- Fringe subtract (for i and z band only)
  - `girmfringe.fringe="<fringe_name>.fits"`
- For more information, read the `girmfringe` help file

Create Processed Science

- Then use `gmosaic` in the `gmos` package
- Mosaic
  - `gmosaic.fl_clean=yes` (default)
- For more information, read the `gmosaic` help file
- Finally, use `imcoadd` in the `gemtools` package
- Align and combine
  - use the default parameters
- For more information, read the `imcoadd` help file