



PIG 12

High Level Interface

Jose Enrique Ruiz – IAA / CSIC
Gammapy Coding Sprint
Erlangen - July 15th 2019

$\gamma \pi$

1

2

3

4

Pull requests 18

Label issues and pull requests for new contributors

Now, GitHub will help potential first-time contributors discover issues labeled with [help wanted](#) or [good first issue](#)

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Filters is:pr is:open

Labels 20

Milestones

- 18 Open ✓ 1,530 Closed
- Add GTI union ✓ feature
- PIG 16 - Gammapy package structure ✘ pig
- PIG 14: uncertainty estimation ✘ pig
- PIG 12 - High-level interface ✘ pig
- PIG 13 - Gammapy dependencies and distribution ✘ pig
- PIG 9 - Event sampling ✘ pig

PIG 12 - High-level interface #2219

Open cdeil wants to merge 3 commits into [gammapy:master](#) from [cdeil:pig-12](#)

Conversation 3 Commits 3 Checks 6 Files changed 1 +141 -0

cdeil commented on 6 Jun

This PR contains first ideas for a high-level interface for Gammapy.

Developing this is one of the projects on our roadmap (see [here](#)) that so far hasn't seen much discussion or developments.

Wrapping and scripting the existing working examples in the tutorials:

Changes from all commits File filter... Jump to... 0 / 1 files viewed Review changes

```

141 docs/development/pigs/pig-012.rst
...
1 + ... include: ../../references.txt
2 +
3 + ... _pig-012:
4 +
5 + ****
6 + PIG 12 - High-level interface
7 + ****
8 +
9 + * Author: José Enrique Ruiz, Christoph Deil, Axel Donath, Regis Terrier
10 + * Created: June 6, 2019
11 + * Accepted: tbd
12 + * Status: draft
13 + * Discussion: 'GH 2219'_
14 +
15 + Abstract
16 + ====
17 +
18 + We haven't started yet on the 'High level interface in the Gammapy roadmap'_
19 + project, but to have something for Gammapy v1.0 in October, we need to start
20 + this work very soon.
21 +
22 + The high-level interface should be easy to use and allow users to do the most
23 + common analysis tasks and workflows quickly. It would be built on top of the
24 + existing Gammapy code-base, first on its own, but likely starting to develop
25 + it would inform improvements in code organisation throughout Gammapy.
26 +
27 + There are two main snf not exclusive options:
28 +
29 + - Develop a set of simple CLI tools within the scope of the 'Gammapy command line interface'_.
30 + - Use a config-file driven approach to run a less flexible analysis via orchestrated workflows.

```

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20c7714

None yet

0.13

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PIG 12 - High-level interface

- Author: José Enrique Ruiz, Christoph Deil, Axel Donath, Régis Terrier
- Created: June 6, 2019
- Accepted: tbd
- Status: draft
- Discussion: [GH 2219](#)

Abstract

We haven't started yet on the [High level interface in the Gammapy roadmap](#) project, but to have something for Gammapy v1.0 in October, we need to start this work very soon.

The high-level interface should be easy to use and allow users to do the most common analysis tasks and workflows quickly. It would be built on top of the existing Gammapy code-base, first on its own, but likely starting to develop it would inform improvements in code organisation throughout Gammapy.

There are two main snf not exclusive options:

- Develop a set of simple CLI tools within the scope of the [Gammapy command line interface](#).
- Use a config-file driven approach to run a less flexible analysis via orchestrated workflows.

The first option is what [Fermitools](#) and [ctools](#) already use, where each tool is simple/atomic enough to allow users to inspect the output results before taking a decision on how to run and set the parameter values for the next tool.

The second option is what is implemented in [Enrico](#), or HAP in HESS. It involves basic orchestrated analysis workflows using a set of input parameters that the user provides via a configuration file. We would need to define a structured syntax for declaration and orchestration of parameters and tasks (probably using YAML format) and also provide config files as templates for users.

Achieving a stable high-level interface with one or both of these options would allow us to continue improving the Gammapy code-base without breaking user-defined workflows or recipes based on CLI tools.

PIG 5 - Gammapy 1.0 Roadmap

- Author: Axel Donath (editor), Régis Terrier & Christoph Deil
- Created: September 28, 2018
- Accepted: January 31, 2019
- Status: accepted
- Discussion: [GH 1841](#)

High-level interface

Implement a config-file based high level analysis interface (e.g. as used in [fermipy](#)) and command line tool. It gives access to limited, pre-scripted standard analysis workflows. Alternatively the high level analysis interface could generate pre-filled Python scripts or notebooks, that can be edited and executed by users.



What is a High Level Interface ?

An **interface** to access and run most common Gammapy **tasks and workflows**

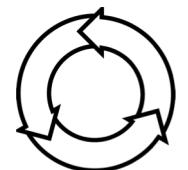
Built on top of existing Python API which will be hidden under the hood

Interface / Working methodology

- Easy to use for those using a **commands-in-terminal** approach
- Provide means to build → run **simple workflows based on configuration files**

Tasks and Workflows / Granularity / Iterative Fine-Tuning

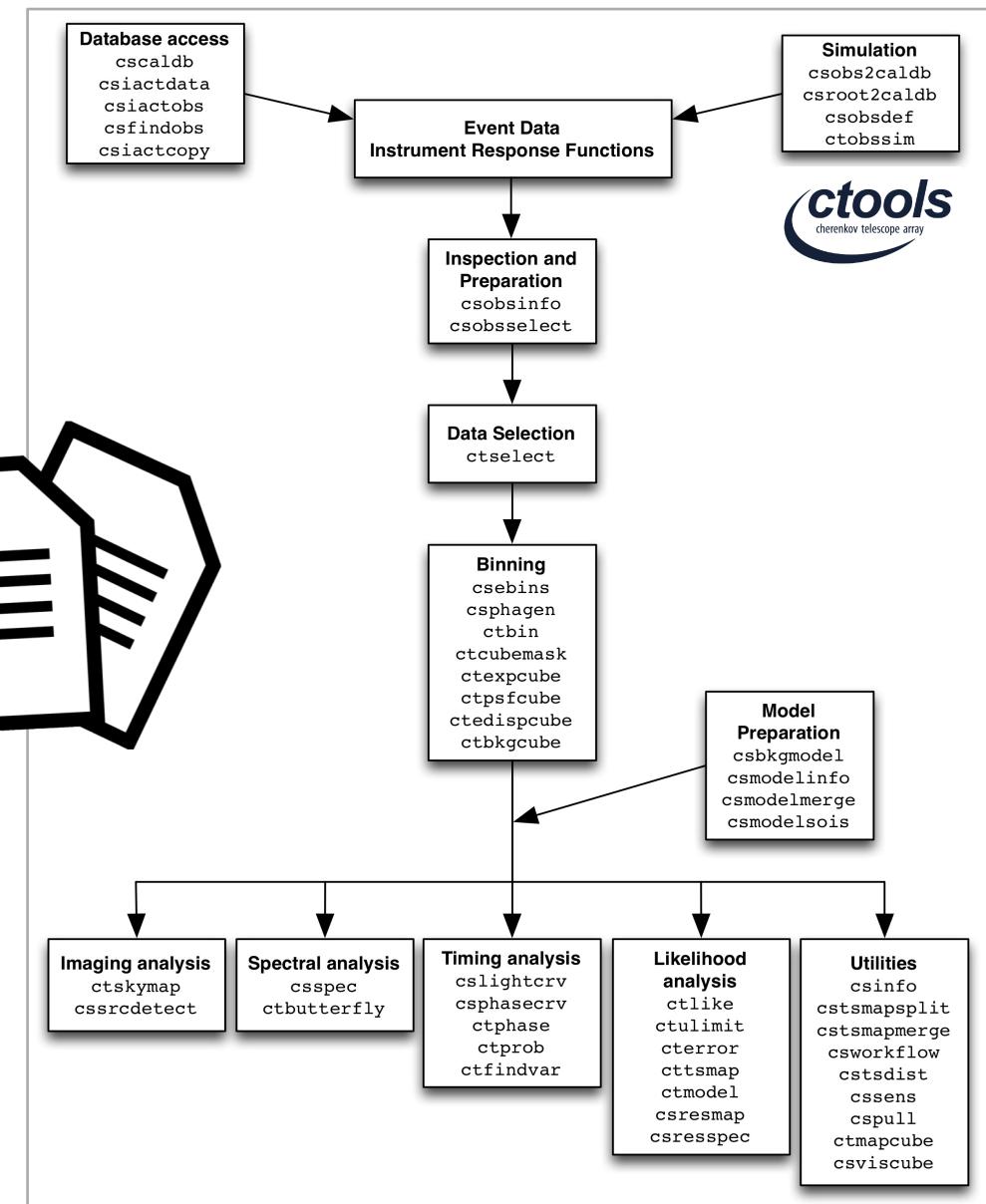
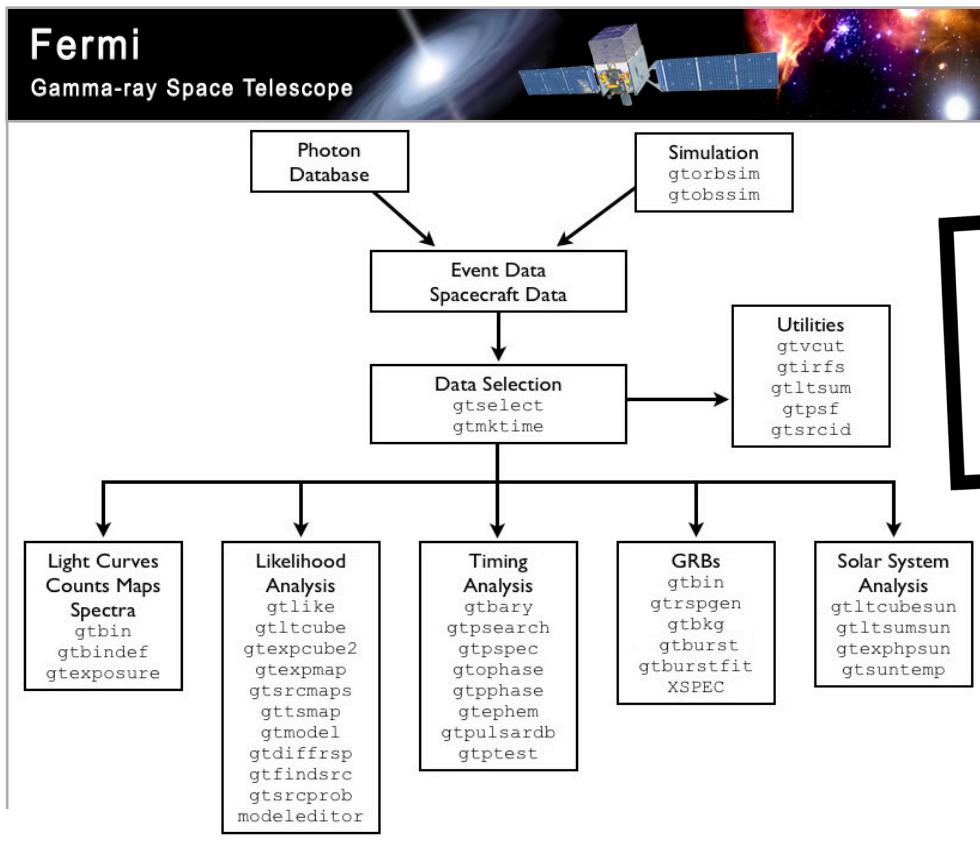
- **Atomic tasks** that need visual inspection of results for the user to take follow-up decisions
- Simple common workflows to get a **rough estimated result** of i.e. data reduction (map, spectrum,..), model fitting, spectral points, light curves, imaging, source detection, etc...



CTA will likely run an automated analysis of all data providing quicklook products

What do others have ?

Command Line Tools



H.A.P - H.E.S.S. Analysis Program

What do others have ?

Config files + Python API

 Fermipy <https://fermipy.readthedocs.io/en/latest/quickstart.html>

Configuration files are used in Python analysis scripts written by the user to build the workflow and run it executing the Python script.

```
from fermipy.gtanlaysis import GTAnalysis

gta = GTAnalysis('config.yaml',logging={'verbosity' : 3})
gta.setup()

# Free Normalization of all Sources within 3 deg of ROI center
gta.free_sources(distance=3.0,pars='norm')

# Free all parameters of isotropic and galactic diffuse components
gta.free_source('galdiff')
gta.free_source('isodiff')

# Free sources with TS > 10
gta.free_sources(minmax_ts=[10,None],pars='norm')

# Fix sources with TS < 10
gta.free_sources(minmax_ts=[None,10],free=False,pars='norm')

# Fix sources with 10 < Npred < 100
gta.free_sources(minmax_npred=[10,100],free=False,pars='norm')
```



```
data:
    evfile : ft1.lst
    scfile : ft2.fits
    ltcube : ltcube.fits

binning:
    roiwidth   : 10.0
    binsz      : 0.1
    binsperdec : 8

selection :
    emin : 100
    emax : 316227.76
    zmax   : 90
    evclass : 128
    evtype   : 3
    tmin    : 239557414
    tmax    : 428903014
    filter   : null
    target   : 'mkn421'

gtlike:
    edisp : True
    irfs  : 'P8R2_SOURCE_V6'
    edisp_disable : ['isodiff','galdiff']

model:
    src_roiwidth : 15.0
    galdiff   : '$FERMI_DIFFUSE_DIR/gll_iem_v06.fits'
    isodiff   : 'iso_P8R2_SOURCE_V6_v06.txt'
    catalogs  : ['3FGL']
```

What do others have ?

Workflow Configuration

Enrico <https://enrico.readthedocs.io>

1. Create configuration file

```
enrico_config Myconfig.conf <answer a few questions like the position of your target>
```

2. Create XML file for sky model

```
enrico_xml Myconfig.conf
```

3. Run likelihood analysis for full spectrum

```
enrico_sed Myconfig.conf
```

4. Compute Lightcurve or TSMap

```
enrico_lc Myconfig.conf  
enrico_tsmap Myconfig.conf
```

5. Plot results

```
enrico_plot_sed Myconfig.conf (plot the SED)  
enrico_plot_lc Myconfig.conf (plot the lightcurve)  
enrico_plot_tsmap Myconfig.conf (generate a fits file for the TS map)
```

```
[target]-  
... name = PG155+113  
... ra = 238.92935  
... dec = 11.190102  
... spectrum = PowerLaw2  
... redshift = 0.5  
... ebl_model = 4  
... fit_tau = no  
[space]-  
... xref = 238.92935  
... yref = 11.190102  
... rad = 10.0  
... binsz = 0.1  
... coordsys = CEL  
... proj = AIT  
... phibins = 0  
[file]-  
... spacecraft = ~/myanalysis/FT2.fits  
... event = ~/myanalysis/data.list  
... xml = ~/myanalysis/XML_model.xml  
... tag = MyTag  
[time]-  
... tmin = 239557417.0  
... tmax = 256970880.0  
... file = ""  
... type = 'MET'  
[energy]-  
... emin = 200.0  
... emax = 300000.0  
... enumbins_per_decade = 10  
[analysis]-  
... # General analysis options
```



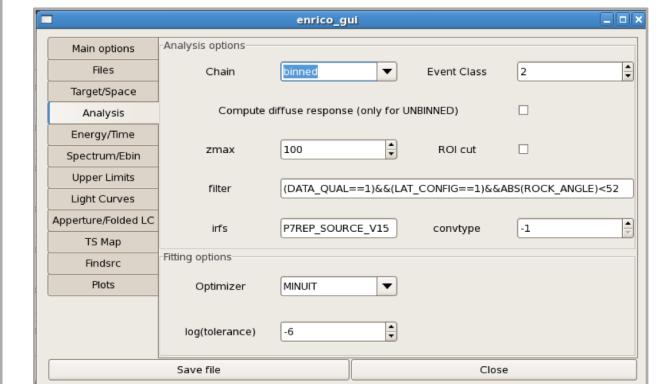
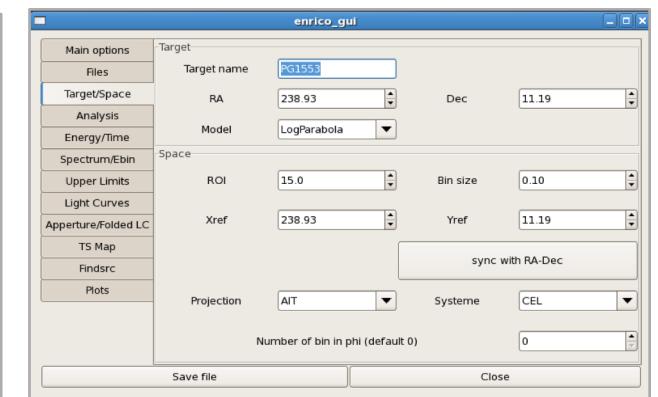
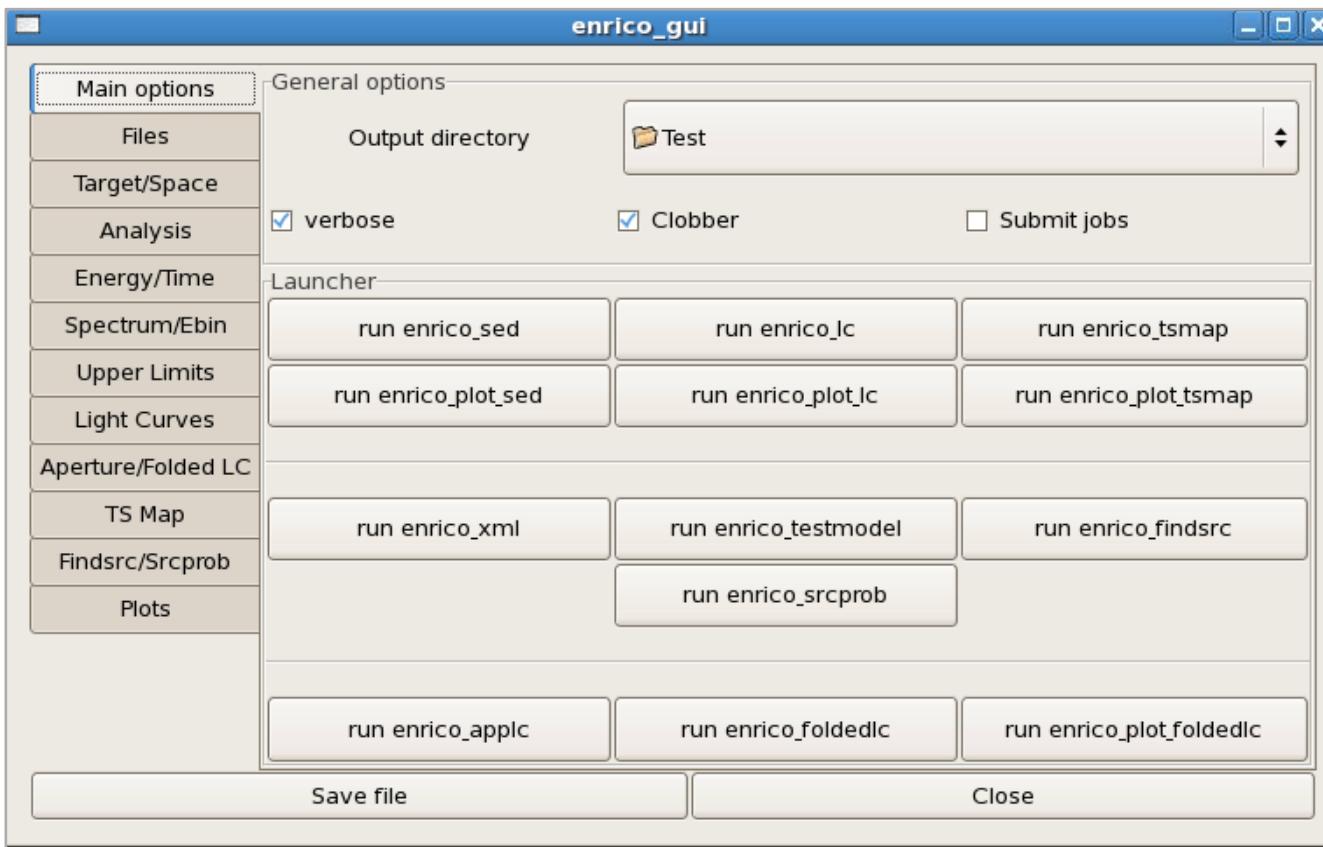
What do others have ?

Workflow Configuration

Enrico

<https://enrico.readthedocs.io/en/latest/gui.html>

GUI to build config file and run commands





What do others have ?

Workflow Configuration

```
# ===== #
# csworkflow class #
# ===== #
class csworkflow(ctools.cscript):
    """
    Executes an analysis workflow.

    The ``csworkflow`` script executes an analysis workflow defined in an
    XML file.
    """
```

csworkflow.py 
cherenkov telescope array

Command line tools (`tools`)



ctapipe https://cta-observatory.github.io/ctapipe/ctapipe_api/tools/index.html

- Based on Python Traitlets framework
- Options for the command-tools may be specified in the command line or in a *config file*
- Config file formats supported JSON or Python

Also provides a framework to develop command line tools from Python classes.



What do we have ?

Command Line Interface

- Small set of tools for an embryonic CLI
- Developed with **Click** placed in `gammify.scripts`
- Only `gammify image` may be potentially needed in a data analysis process

<https://docs.gammify.org/0.12/scripts/index.html>

```
$ gammify --help
Usage: gammify [OPTIONS] COMMAND [ARGS]...

Gammify command line interface (CLI).

Gammify is a Python package for gamma-ray astronomy.

Use `--help` to see available sub-commands, as well as the available
arguments and options for each sub-command.

For further information, see https://gammify.org/ and
https://docs.gammify.org/

Examples
-----
$ gammify --help
$ gammify --version
$ gammify info --help
$ gammify info

Options:
--log-level [debug|info|warning|error]
Logging verbosity level.
--ignore-warnings
Ignore warnings?
--version
Print version and exit.
-h, --help
Show this message and exit.

Commands:
check    Run checks for Gammify
download Download datasets and notebooks
image    Analysis - 2D images
info     Display information about Gammify
jupyter Perform actions on notebooks
```

Jupyter notebooks

- ~25 tutorials /recipes in notebook format

Python scripts

- Very few scripts and all need to be fixed and readapted

High-level analysis Python Classes in API

- SpectralAnalysisIACT
- LightCurveEstimator
- FluxPointEstimator
- SigmaVEstimator

Granularity



What should we do?

Develop a set of simple CLI tools

- Start prototyping with a small subset that could be extended as use-cases for analysis recipes are identified.
- Provide well established classes and code-structure to build the tools.

Use a config-file driven approach to run a less flexible analysis via orchestrated workflows

- First inspection /quicklook analysis via automated workflows.
 - Provide **templated configuration files** for user editing.
 - Skeleton **parametrized jupyter notebooks** filled and executed under the hood → pretty execution reports.
- Format for declaration of parameters /values: YAML, JSON, others..
Structured syntax for workflow building and orchestration of tasks.



<https://github.com/nteract/papermill>

YAML files for declaration of parameters /values

Use cases design

- In which cases is serialization needed?

Development framework

- Take advantage of existing code set-up for CLI tools in `gammapy.scripts` `$ click_`
- Other frameworks i.e. Python-Fire <https://github.com/google/python-fire>
- **ctapipe tools**



Related activities / PIGs

Improving the code-base without breaking workflows/recipes made with High Level Interface

not stable API $\not\Rightarrow$ not stable High Level Interface

PIG 6 Observations handling

PIG 7 Models

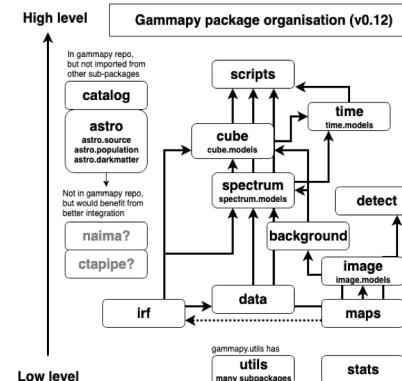
PIG 8 Datasets

PIG 10 Regions

PIG 11 Lightcurves

PIG 14 Uncertainties

PIG 16 Gammapy package structure



Future PIG Provenance / Structured logging



Seamless tracking and recording of software actions.

In the form of **structured** log files.

Provenance metadata model.



Enhanced inspection and **forensic studies** of the research analysis process.

Improving reproducibility and reuse by the community.