

Fermi Science Tools hands-on session: the Crab Nebula

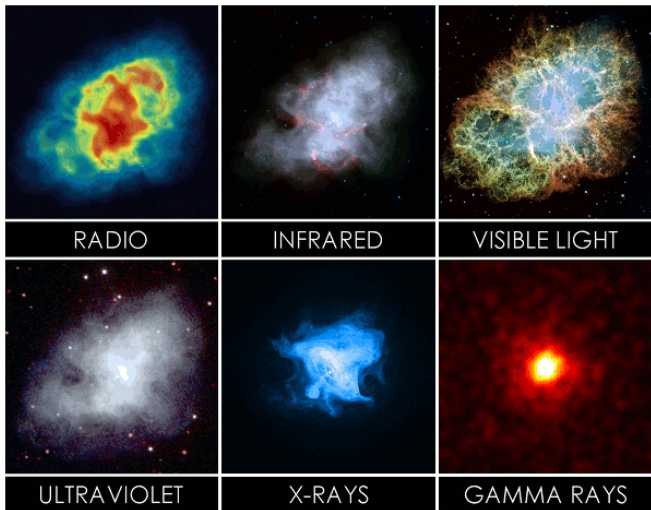
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SEXTEN CENTER
FOR
ASTROPHYSICS

The main character: Crab



We will analyze the Crab nebula during the flare of March 2013

Mayer et al. ApJ, 775, L37 2013, <https://arxiv.org/abs/1308.6698v1>

Outline of the hands-on

- Data download: already done!
- Selection of data with `gtselect`
- Phase unfolding with TEMPO2
- Off-phase selection to isolate the nebula: again `gtselect`
- IRF creation: `gtltcube` and `gtexpmap`
- Model creation: `make3FGLxml.py`
- Diffuse sources contribution: `gtdiffrsp`
- Likelihood analysis: `gtlike`
- SED building (done tomorrow by Michele): Python wrappers of the Fermi Tools

Some useful links

- Overview of the tools and documentation for each executable:
<https://fermi.gsfc.nasa.gov/ssc/data/analysis/scitools/overview.html>
- Detailed explanation of Fermi LAT data analysis:
<https://fermi.gsfc.nasa.gov/ssc/data/analysis/documentation/Cicerone/>
- For the nebula selection:
https://fermi.gsfc.nasa.gov/ssc/data/analysis/scitools/pulsar_gating_tutorial.html
- For the likelihood analysis:
https://fermi.gsfc.nasa.gov/ssc/data/analysis/scitools/likelihood_tutorial.html

Data download

Use the LAT Data Server:

<https://fermi.gsfc.nasa.gov/cgi-bin/ssc/LAT/LATDataQuery.cgi>

LAT Photon, Event, and Spacecraft Data Query

Object name or coordinates:	<input type="text" value="Crab"/>
Coordinate system:	<input type="text" value="J2000"/>
Search radius (degrees):	<input type="text" value="30"/>
Observation dates:	<input type="text" value="56346.0, 56369.5"/>
Time system:	<input type="text" value="MJD"/>
Energy range (MeV):	<input type="text" value="100, 500000"/>
LAT data type:	<input type="text" value="Photon"/>
Spacecraft data:	<input checked="" type="checkbox"/>
<input type="button" value="Start Search"/> <input type="button" value="Reset"/>	

Before anything else...

- To use the Fermi Science tools, remember to source the right script in the home directory of the Virtual Machine:

```
$ source fermitools_heasoft.sh
```

Selection of data

- `gtselect` is used to cut on parameters, usually energy and time
- A particular event class and event type can be chosen
- More on `gtselect`:
<https://fermi.gsfc.nasa.gov/ssc/data/analysis/scitools/help/gtselect.txt>
- Example:

```
$ gtselect evclass=128 evtype=3
```

and then you enter the `gtselect` prompt
- Also, selection of Good Time Intervals (GTI): use `gtmktime`
- Always check your cuts with `gtvcut`!

Data inspection: count maps

- To inspect the data, `gtbin` is provided
- It can bin the data into a count map which can be opened with `ds9`

Phase unfolding

- At this point, you need the Crab pulsar ephemerides, a plain text file containing the properties of the pulsar
- For each event in the data, we must assign a phase to create the pulsar light curve
- For phase assignment we will use the Fermi TEMP02 plugin, which adds a column called PULSE_PHASE to the event fits file
- Example:

```
$ tempo2 -gr fermi -ft1 events.fits -ft2 spacecraft.fits  
-f Crab_ephem.par -phase -graph 0
```
- The light curve can be produced with `fv`

Pulsar removal

- Once we have the pulsar light curve, we have to select the so called off-pulse region, where the pulsar is not pulsing
- When we found the off-pulse, we can cut on the PULSE_PHASE to isolate the nebula contribution
- Example:

```
$ gtselect evclass=128 evtype=3 phasemin=0.5 phasemax=0.9
```

and then you enter the `gtselect` prompt
- After pulsar removal, we can create a new count map and compare it with the one where the pulsar is still there
- From here, the standard likelihood analysis can start. **BUT: since we cut off events from the data, we will have to scale the final fluxes by the fraction of data we removed**
- Example: phase cut 0.5 – 0.9 \Rightarrow scale factor = $1/0.4 = 2.5$

Exposure map calculation

- Exposure map calculation: `gtl1cube` and `gtexpmap` (in this order)
- `gtl1cube`: creation of the livetime cube
- `gtexpmap`: creation of the exposure map
- LAT team recommendation: 10 energy bins per decade, source region larger than the ROI
- **NOTE: if you change any of your cut in energy, time, zenith or others, you will have to run `gtl1cube` and `gtexpmap` again**

Model creation

- The likelihood analysis needs an input model
- A model contains the spectral informations about all the point and extended sources in the source region
- To those, we must add the galactic diffuse and extragalactic isotropic contributions (provided by the LAT team), which can be downloaded from:
<https://fermi.gsfc.nasa.gov/ssc/data/access/lat/BackgroundModels.html>
- The model is contained in a XML file
- If you have few sources, you can create the XML file by hand
- For hundreds sources, a python script is provided, called `make3FGLxml.py`
- This tool can be found at:
<https://fermi.gsfc.nasa.gov/ssc/data/analysis/user/>

Model creation with make3FGLxml.py

- Use example:

```
$ python make3FGLxml.py gll_psc_v16.fit event.fits -o input_model.xml  
-G gll_iem_v06.fits -g gll_iem_v06 -I iso_P8R2_SOURCE_V6_v06.txt  
-i iso_P8R2_SOURCE_V6_v06
```

- This will create an output XML which we are going to inspect
- We have to add two extended sources, so we should download the following file:
https://fermi.gsfc.nasa.gov/ssc/data/access/lat/4yr_catalog/LAT_extended_sources_v15.tgz
- More options for make3FGLxml.py can be found with the command:

```
$ python make3FGLxml.py -h
```

or

```
https://fermi.gsfc.nasa.gov/ssc/data/analysis/user/readme\_make3FGLxml.txt
```

Diffuse sources response calculation

- When modeling a source, it can happen (as in Crab's case) that some diffuse (extended) sources are present
- In this case, the response of these sources must be computed properly
- The tool to perform this job is `gtdiffrsp`
- If this computation is not done at this stage but with `gtlike` (see next slide), it will take long every time, so better to split the jobs

Likelihood minimization with gtlake

- Now the likelihood \mathcal{L} must be computed: gtlake is what we need
- The likelihood is built starting from the source model we created and the Maximum Likelihood estimators are found
- Two likelihood methods are provided: UNBINNED and BINNED
- We will use the UNBINNED, mostly suitable for short time observations
- Run gtlake like this:

```
$ gtlake refit=yes plot=yes sfile=Output_model.xml
```
- It will take some time...
- **NOTE: at the end of the likelihood analysis you get the best parameters which describe your data according to your model, not the best model. You could find a better representation of your data with a different model!**