NHSC/PACS Workshop

To the pipelines and beyond !

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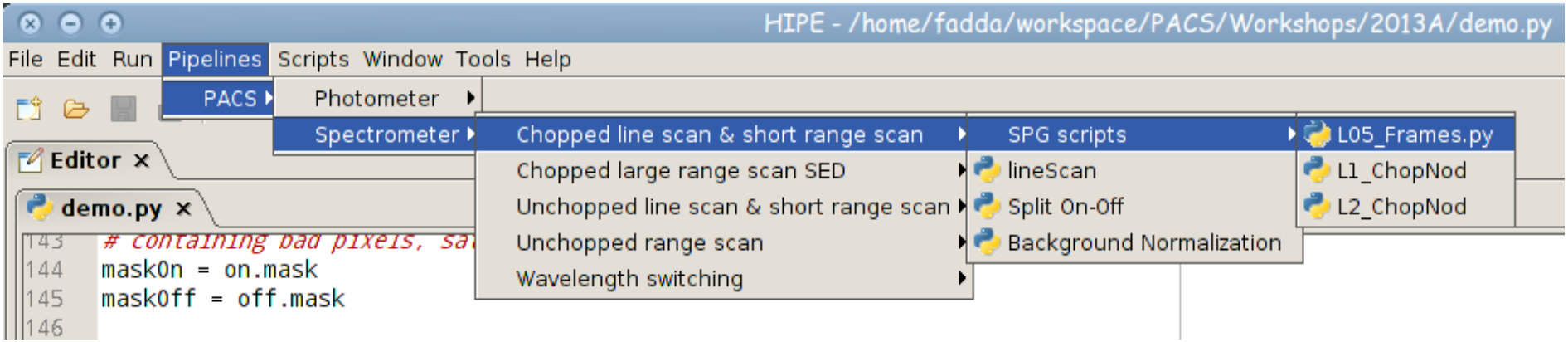
Main steps of the pipelines

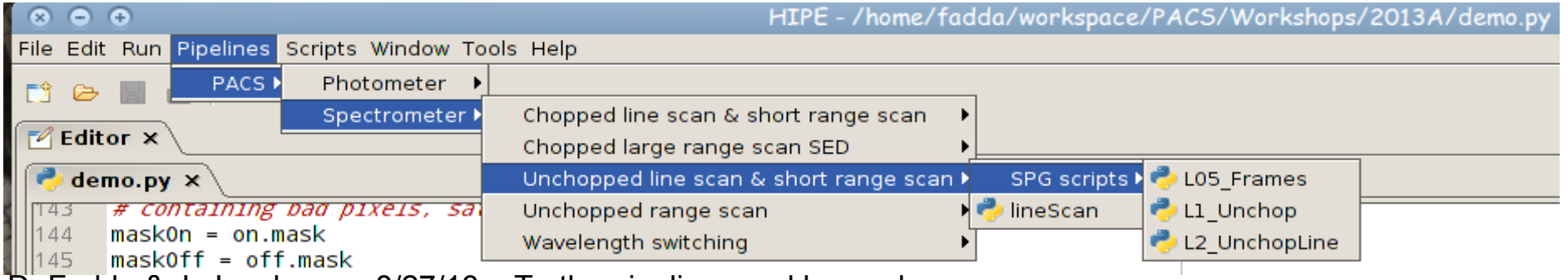
Data are reduced producing different levels of analysis.

LEVEL 0	raw data
LEVEL 0.5	pointing information, signal from digital units to physical units, wavelength added to each pixel
LEVEL 1	compute response from calBlock, apply RSRF and response, flagging of glitches, transient correction, spectral flatfield, transformation in cubes
LEVEL 2	selection of line, difference of cubes (ON and OFF) binning of data and flagging of outliers, spatial projection of data to obtain 3D maps
LEVEL 2.5	In the case of large unchopped scans, 2+ AOR are used so that there is an extra-step.

Interactive pipelines

In HIPE, under the menu *pipelines*, you can find the SPG scripts and the interactive pipelines available for all the different spectroscopic data.
The SPG (standard product generation) scripts are the ones used to populate the HSA archive.





Interactive pipelines

Most of the time, the archival data are already good to go.

If the archival data have been produced with an old version of HIPE or an old calibration, it is advisable to rerun the pipeline to have the best reduction.

In some cases, you will want to go beyond the SPG pipeline. Let's see why.

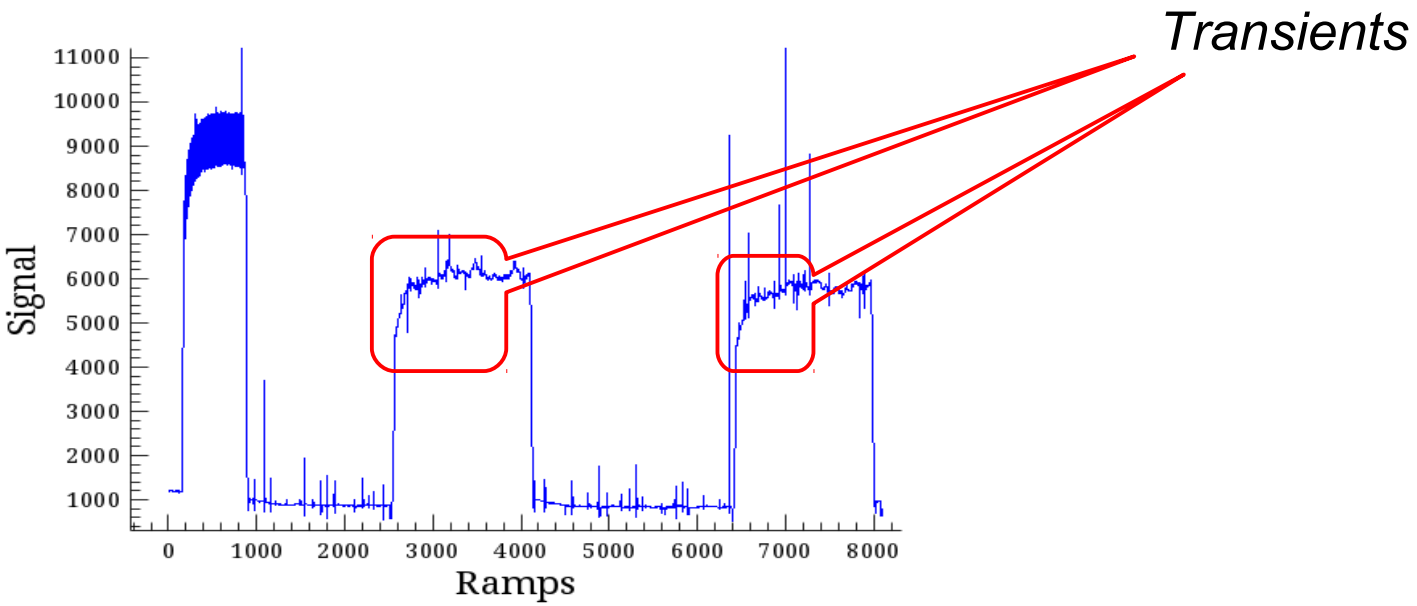
Why going beyond the pipeline ?

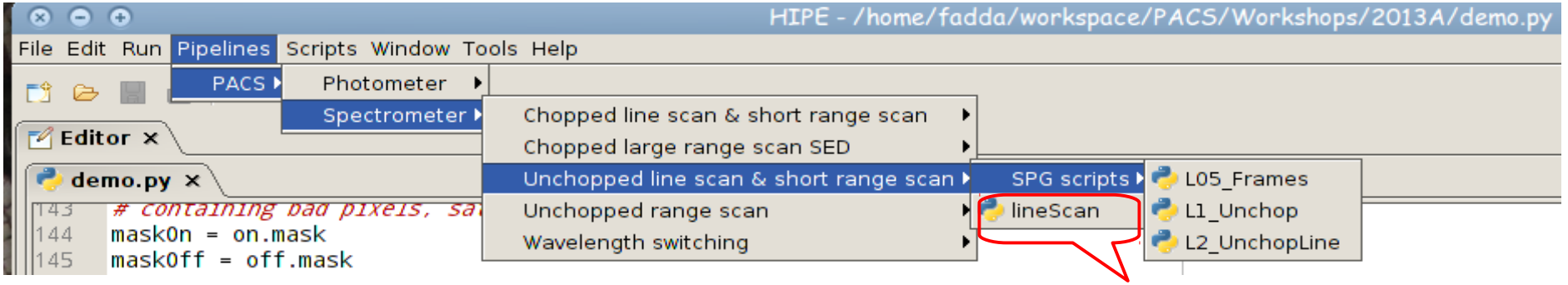
Curiosity:

you are a geek and you know you can do it better !

Why going beyond the pipeline ?

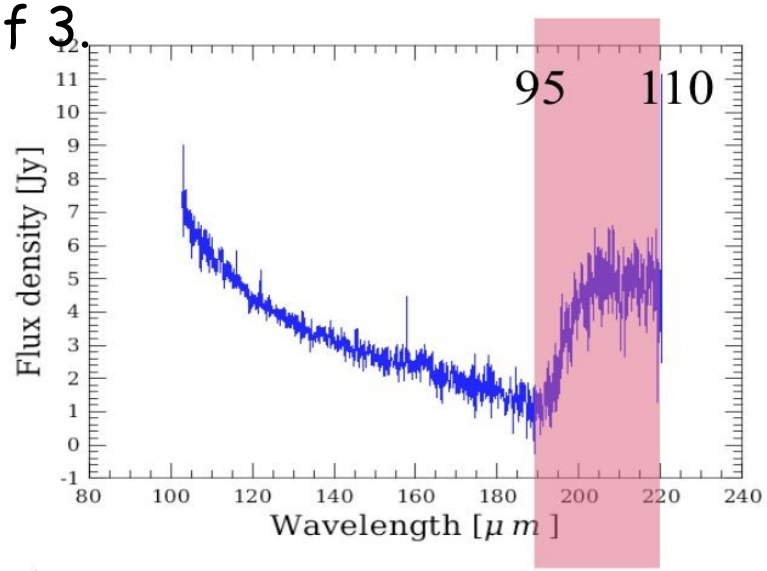
The SPG pipeline is not enough.
Unchopped data. You want to correct the long-term transients





Why going beyond the pipeline ?

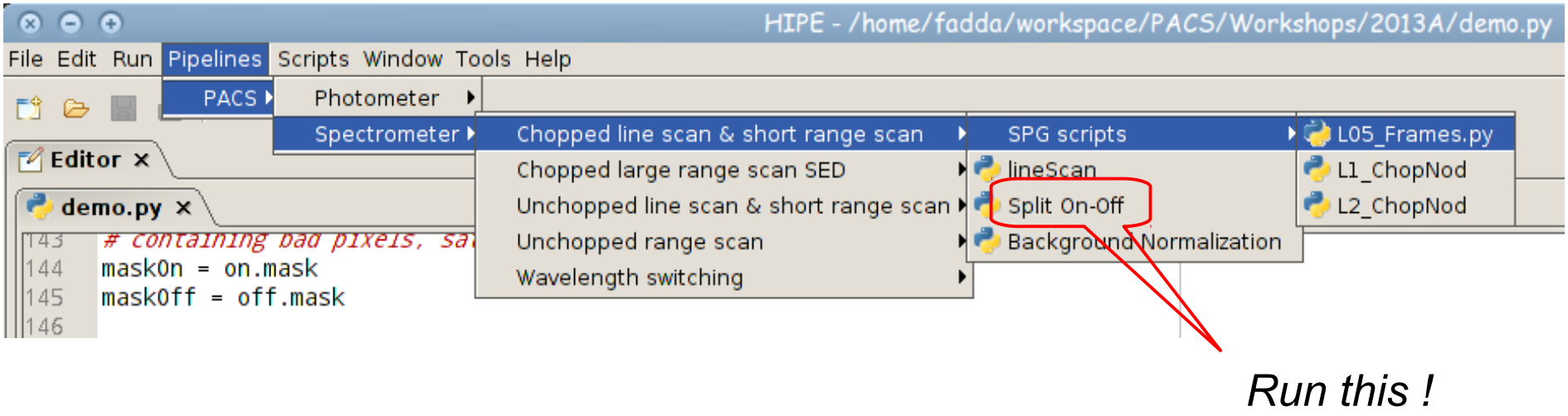
Leak. Your line lies in the region affected by the blue filter leak.
This leak contaminates the 190-220 micron range.
The available RSRF has been obtained without taking this leak into account. As a result, a line flux in this region will be wrong by a factor of 3.



Waiting for the official release of a fixed RSRF, we can provide you a temporary fix. Contact us if needed !

Why going beyond the pipeline ?

Unlucky OFF. You chose an OFF position which contains a source. You want to savage your observation.



Run this !

You can try to run the pipeline by splitting the On and Off observations. There is an interactive pipeline for that. You will find out if the Off is contaminated by lines or it simply a continuum.

Why going beyond the pipeline ?

Get the most out of your data:

The pipeline gives products thought for general usage.
Your data can be better exploited with an interactive pipeline by fixing some parameters.

* You want to explore alternative ways of data reduction, such as "telescope background normalization".

* You want to obtain "drizzled" maps from your raster data.

* You want to directly fit your lines without using cumbersome GUIs which use only rebinned cubes ...

* You want to export some of the data and examine them wit your favorite software.

Multi-threading

When running interactive pipelines, be sure to use the multi-threading option. **This option is only available for the PACS spectrometer** and it will speed-up your reduction by exploiting all the cores of your machine.

Using this option is extraordinarily simple. Just two lines:

```
Configuration.setProperty("herschel.pacs.spg.common.superThreadCount","4")
Configuration.setProperty("herschel.pacs.spg.spec.threadCount","8")
```

Some tasks are threaded. The other ones are naturally threaded by exploiting the slicing of the data.
The **superThreadCount** is used for the general threading, while the **threadCount** is used for the threaded tasks.

Multi-threading

The optimal choice of the threading parameters depends on the number of cores on your machine and the number of slices. Memory is not an issue, because the first part of the pipeline is unthreaded and puts the entire data in memory. When data are sliced, the total memory used is always the same.

An automatic choice is done by putting:

```
Configuration.setProperty("herschel.pacs.spg.common.superThreadCount","0")
Configuration.setProperty("herschel.pacs.spg.spec.threadCount","0")
```

Otherwise, a good choice is to put threadCount equal to the number of cores and superThreadCount equal to the number of slices.

What is in the demo

The demo is organized on an example of unchopped data to show an alternative way of reducing the data.
However, the way of extracting data and fitting lines is applicable to any spectroscopic data.

The demo includes:

a) quick exploration of different levels from archival data
b) reprocess data with interactive pipeline and save products at a certain point of the reduction.
c) display data, also including masks of flagged data
d) save data to analyze them with external software
e) several ways of fitting lines using all the available data
f) alternative ways of reducing unchopped data
g) challenges for the hands-on session