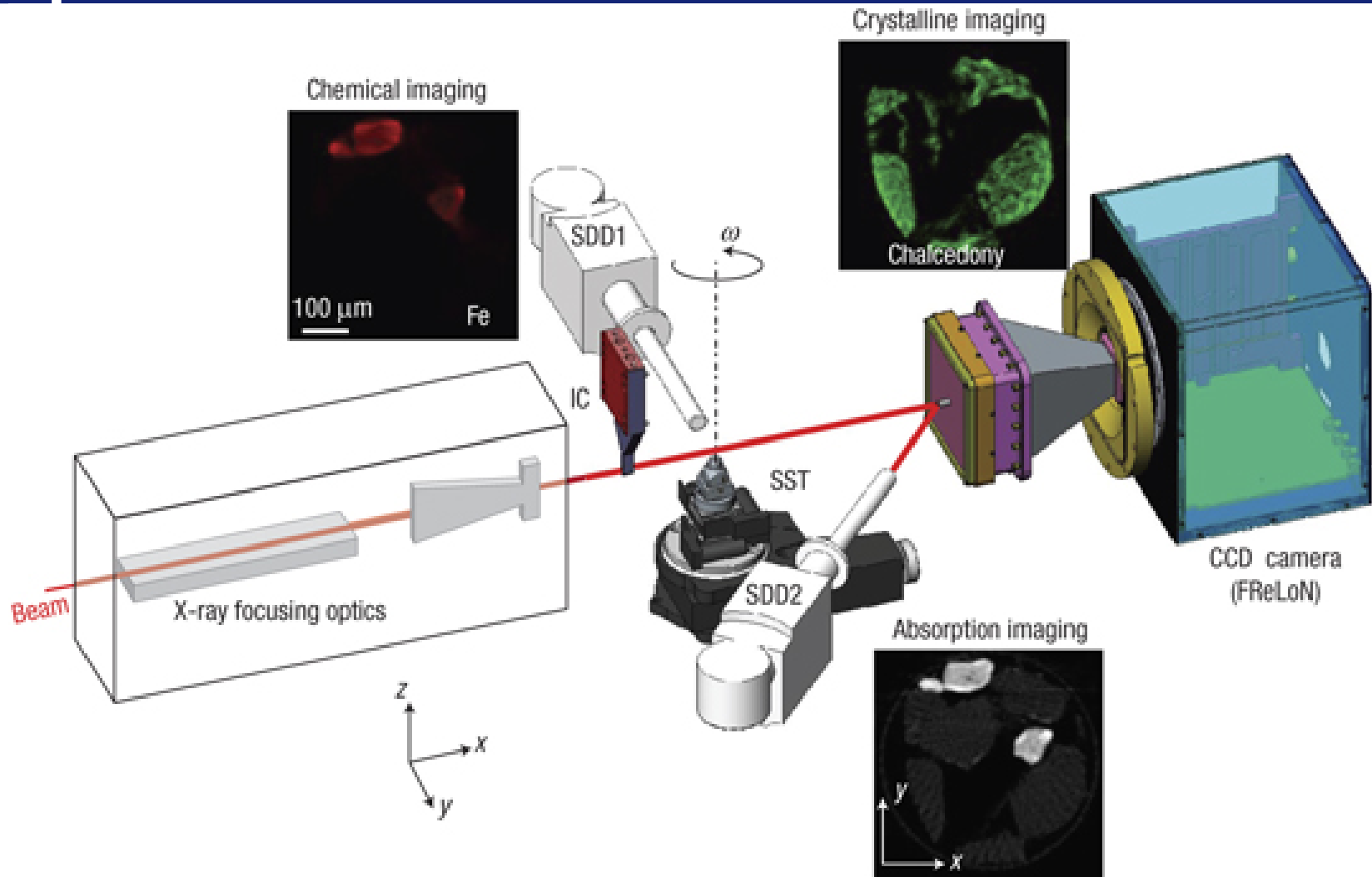


The European Synchrotron

Imaging with diffraction data ...  
on the high-energy beamline for materials engineering

- **Introduction:  $\mu$ XRD-CT and PDF-CT**
- **Presentation of the ID15 @ESRF**
- **Acquisition scheme**
- **Hardware**
- **Software**
- **Conclusions**
- **Acknowledgments**

# Micro X-Ray diffraction contrast tomography

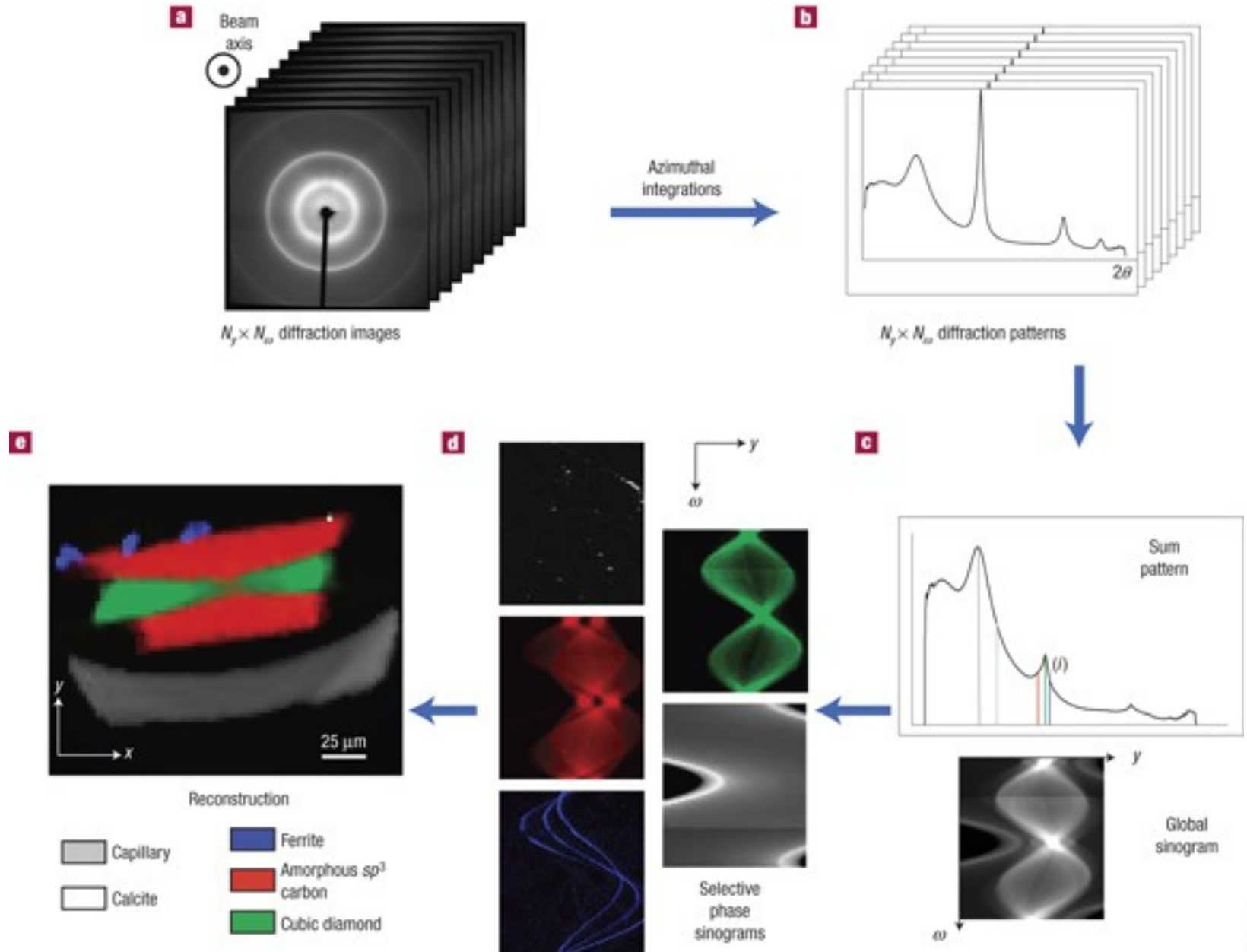


Probing the structure of heterogeneous diluted materials by diffraction tomography

Pierre Bleuet, Eléonore Welcomme, Eric Dooryhée, Jean Susini, Jean-Louis Hodeau & Philippe Walter

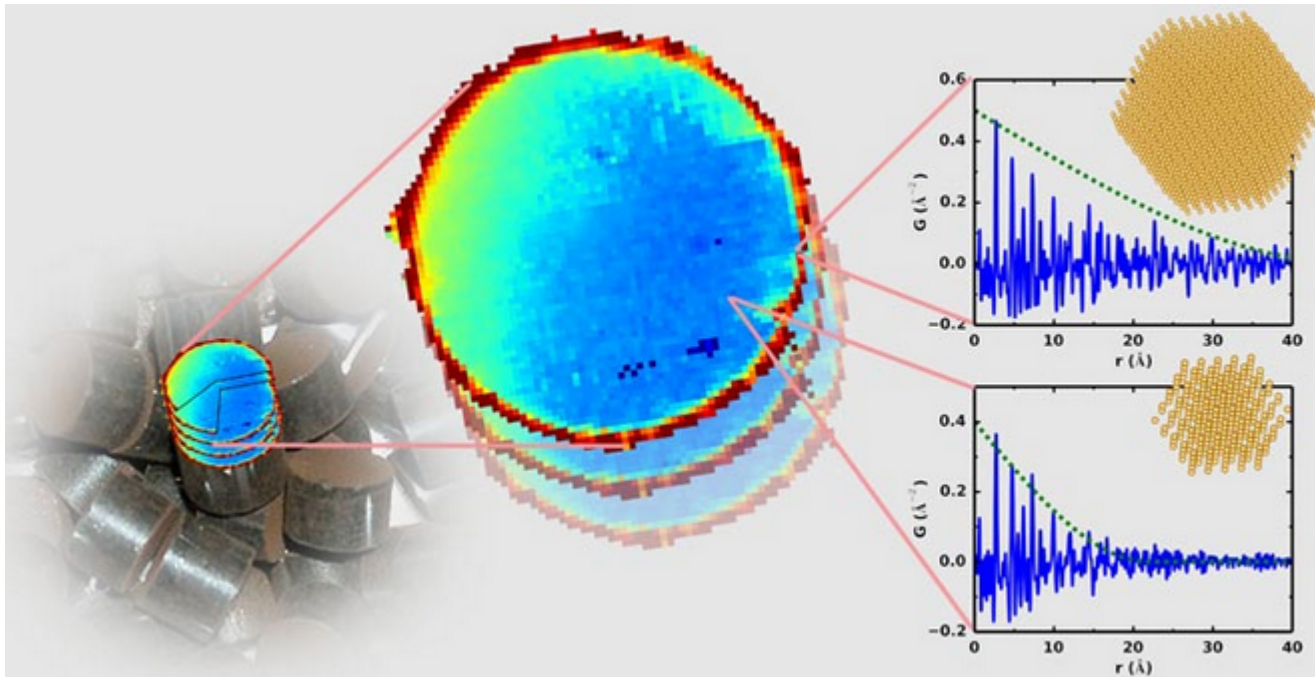
Nature Materials 7, 468 - 472 (2008) doi:10.1038/nmat2168

# diffraction contrast tomography: data processing



# Pairwise Distribution Function – Contrast Tomography

- **Extention of the PDF tools from S. Billinge to amorphous phases**
- **Combined to  $\mu$ XRD-CT**



Pair distribution function computed tomography

Simon D. M. Jacques, Marco Di Michiel, Simon A. J. Kimber, Xiaohao Yang, Robert J. Cernik, Andrew M. Beale & Simon J. L. Billinge

Nature Communications 4, Article number: 2536 (2013) doi:10.1038/ncomms3536

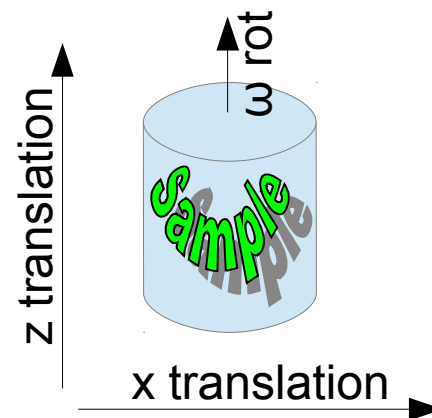
- **High energy materials beamline: 20 - 750 keV**
- **Beam size ~ 1 $\mu$ m**
- **Applications**
  - Solid state chemistry
  - Catalysis
  - In-situ experiments
  - Metallurgy
- **Techniques**
  - energy dispersive diffraction
  - powder diffraction
  - pair-distribution function analysis
  - diffraction contrast tomography

- **Strategy:**

- 6 → 600  $\omega$ -steps
- 100 → 1000 x-steps
- 100 → 1000 z-steps
- Nyquist suggests:

$$\omega\text{-steps} = x\text{-steps} * \pi / 2$$

The fastest scan can be  $\omega$  or x depending on the experiment  
the number of z steps is adapted depending on available time



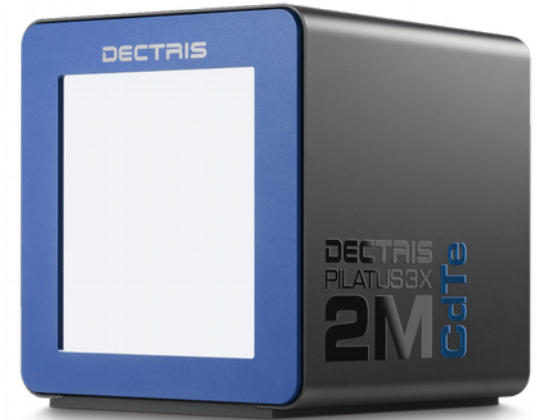
- **The target for data processing is 1000<sup>3</sup> datasets**

Each image is multi-mega-pixel, ~ 10 Mbyte/image

- **The raw dataset represents: 10 Pb (10 000 Tera Bytes !)**

- ESRF has currently only 4PB of storage

- **Well known electronics:**
  - 2.4 Mpix images
  - 250 Hz acquisition speed
  - >55% efficiency up to 100 keV
- **Used on many protein diffraction beamlines**
- **Well interfaced in LimA**
  - But never used continuously at full speed ...
- **Allows large  $\mu$ XRD-CT scans within a week:**
  - $N_z = 400$ ,  $N_x = 400$ ,  $N_\omega = 600$
  - 100 million files
  - 230 Tera-Bytes of compressed data
  - 800 Giga-Bytes after azimuthal integration :-)



... until now

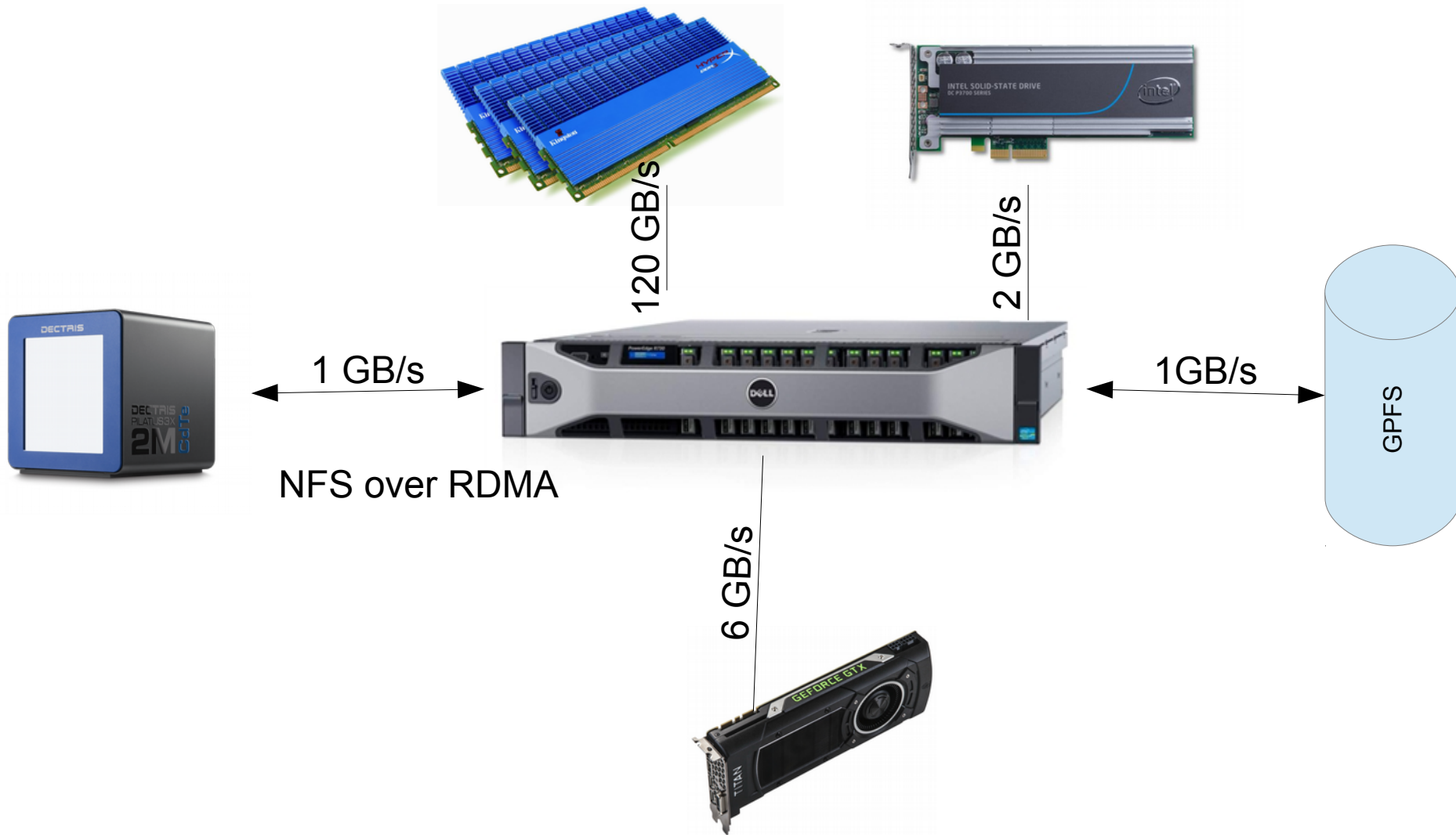


- **Pilatus3 2M detector PC interconnect:**
  - ONE 10GB fiber link out
  - Maximum transfer rate: 1 Gb/s
  - NFS over RDMA is needed
- **Image size and bandwidth needed at 250Hz**
  - 10 Mbyte raw data → 2.5 Gb/s
  - 2.4 Mbyte CBF data → 0.96 Gb/s
  - LZ4 compression gives variable image size → discarded

CBF compression scheme (4x) is used to start with ...

- **Standard dual socket server (Dell R730)**
  - 2 sockets, 3.4 GHz hexacore processors
  - 128GB of memory
- **Network interconnect**
  - 2x 10Gbit ethernet link
    - **To the detector (NFS over RDMA server)**
    - **To the central storage (GPFS client)**
  - 4x 1Gbit link
    - **Commands & normal NFS**
- **Local storage:**
  - Fast SSD interfaced in PCI-e (NVMe), 2TB
  - Disks, 2TB extensible to 24 TB
- **Local GPU computing**
  - Nvidia Titan-X

# General layout



250 Hz ↔ 1 GB/s ↔ 4 ms/image

- BLISS
- DAHU
- PyFAI
- FABIO
- SILX

Click icon to add picture

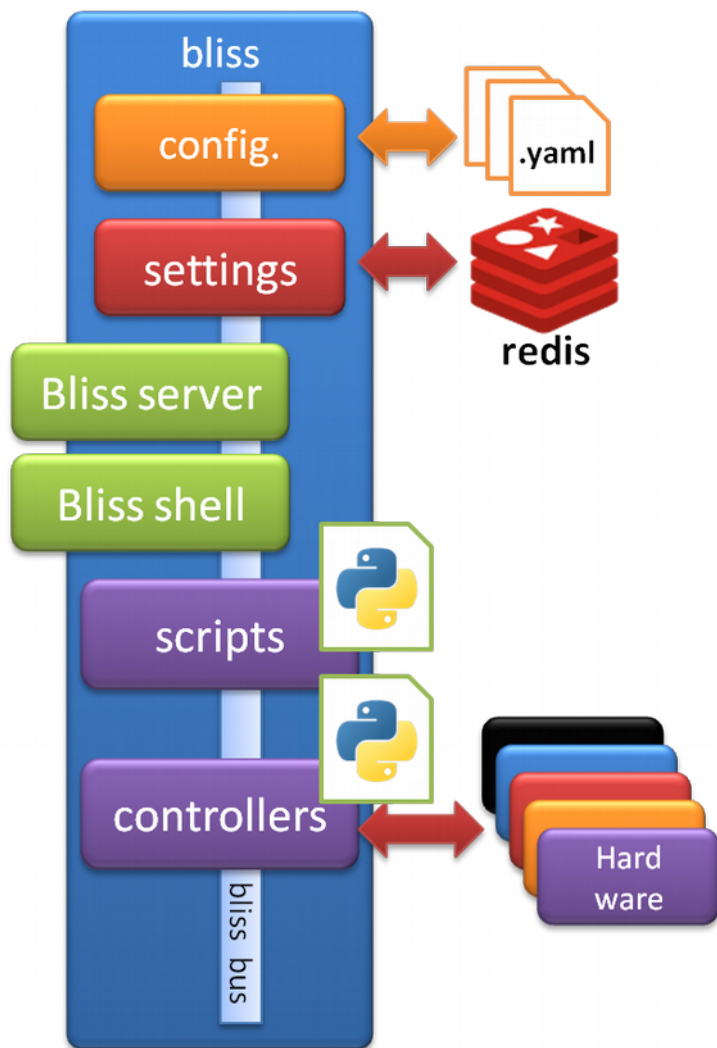


The spec replacement project  
Started Dec 2015

*In development*

Alpha version running on:

- MASSIF
- ID15 & ID31



- Python control library
- Configuration
- Communication
- Hardware control
  - motion, temperature, ...
- Data recorder
- Scan engine
- Shell + GUI(s)
- Tango Bliss Server

Bliss Server



```

couthinho@bcu01ctrk:~$
Welcome to the bliss shell on ID31

Using sixc session

>>> umv(mock_bb, 20)

mock_bb
20.0000

>>> wa()
Current Positions (user, dial)

mock_bb  mock_hg  mock_ho  mock_lb  mock_rb  mock_tb  mock_vg
-----  -
20.00000  0.00000  0.00000  0.00000  0.00000  0.00000  20.00000
20.00000  0.00000  0.00000  0.00000  0.00000  0.00000  20.00000

>>> ascan mo
mock_bb mock_lb mock_vg move
mock_hg mock_rb mock_vo
mock_ho mock_tb monkey
    
```

```

Terminal
Welcome to "spec" Release 6.04.01
Copyright (c) 1987-2016 Certified Scientific Software
All rights reserved

(Portions derived from a program developed at Harvard University.)
(Linked with BSD libedit library for command line editing.)

Using "/users/blissadm/spec/debtan6/spec.d"
for auxiliary file directory (SPECED).
Faking a state named "esrf".
Using your state file from /dev/esrf.

Getting configuration parameters from "SPECED/spec/config".

Type h changes for info on latest changes.
Browse to http://www.certif.com for complete documentation.

Reading file "SPECED/site.mac".
Reading file "/users/blissadm/local/spec/macros/ID00setup.mac" (level 2).

Doing SETUP.
Reading file "SPECED/setup".
Reading file "SPECED/spec/setup".
bliss info: 'spec' session configured with 'ID00/bliss/spec'

62.SPEC> b_run wa()
Current Positions (user, dial)

mock_bb  mock_hg  mock_ho  mock_lb  mock_rb  mock_tb  mock_vg  mock_vo
-----  -
35.00000  0.00000  0.00000  0.00000  0.00000  -1.00000  34.00000  -18.00000
0.00000  0.00000  0.00000  0.00000  0.00000  0.00000  34.00000  -18.00000

62.SPEC>
    
```



ESRF - ID31 configuration application

ID 31 ESRF - ID31

Files Objects Instruments

Apply Apply & Update TANGO server

Name: icek314  
Controller: M20M  
Host: icek314  
Port: 3000

Name	Unit	Steps p/ unit	Velocity (unit.s <sup>-1</sup> )	Acceleration (unit.s <sup>-2</sup> )	Backlash (unit)	Low limit (unit)	High limit (unit)
srot	deg	400	5	20	0.1	-1000	1000
sby	mm	200	5	20	0.1	-1000	1000
sbz	mm	200	5	20	0.1	-1000	1000
sx	mm	-100.0	5.0	20.0	0.1	-1000.0	1000.0
mz	mm	200	5	20	0.1	-1000	1000
oy	mm	250.0	1.5	20.0	0.1	-1000.0	1000.0
oyaw	deg	4000.0	0.2	20.0	0.1	-1000.0	1000.0
oz	mm	20000.0	0.1	4.0	0.1	-20.0	20.0
opitch	deg	400.0	5.0	20.0	0.1	-1000.0	1000.0
say2	mm	-200	2	8	0.1	-1000	1000
camt	deg	200.0	2.0	20.0	0.1	-1000.0	1000.0



## Dahu is a lightweight plugin based framework...

... technically a JSON-RPC server over Tango written in Python

- **The *dahu* server executes jobs**

- Each job lives in its own thread.
- Each jobs execute one plugin
- The job is responsible for de/serializing JSON string coming from Tango

## Plugins are Python classes or functions

- Plugins are dynamically loaded from python modules
- Plugins have a single input and output: *simple* dictionaries.

- **Jobs can be re-processed offline**

- **Lightweight means limited overhead:**

- 1  $\mu$ s for a dummy plugin execution
- 150  $\mu$ s for a dummy job
- 300  $\mu$ s when called from Tango (old figures, sorry)





## On the server side:

### Define the function (in `demo.py`):

```
import pyFAI, fabio

def integrate_simple(poni, image, curve)
    ai = pyFAI.load(poni)
    img = fabio.open(image).data
    ai.integrate1d(img, 1000, filename=curve)
    return {"out_file":curve}
```

### Create the plugin:

```
from dahu.plugin import plugin_from_function

plugin_from_function(integrate_simple)
```

## On the client side:

```
import PyTango, json

dahu = PyTango.DeviceProxy("dau/dahu/1")

plugin = 'demo.integrate_simple'

inp = {'poni': 'example.poni',
       'image': 'example.tif',
       'curve': 'integrated.dat'}

jid = dahu.startJob([plugin,
                    json.dumps(inp)])
```

- **Reprocess one/multiple job from the command line:**

```
dahu-reprocess job_description_1234.json
```

**runs jobs sequentially on the computer**



- **Library for accessing diffraction images**
  - Fruit of the Fable collaboration (2007-2009)
  - Supports most detectors format, including CBF and HDF5
  - Now integrated as part of the *silx* project

- **Changed of license:**  → 
  - No more enforcement to publish modifications
  - More open towards industry
  - Compatible with the policy for *silx*

- **Simple profiling:**

```
%timeit data = fabio.open("/nvme/test.cbf").data
```

**10 ms/image just for reading one image**

- **Advanced profiling:**

- Total time: 30ms

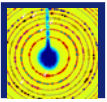
- **15 ms for byte-offset decompression**
- **10 ms for MD5 hash calculation**
- **1 ms parsing the CIF structure**
- **1 ms for reading the file**

- **Solutions:**

- Skip the checksum verification
- Use a pool of decompressor thread, optimum: 6 readers

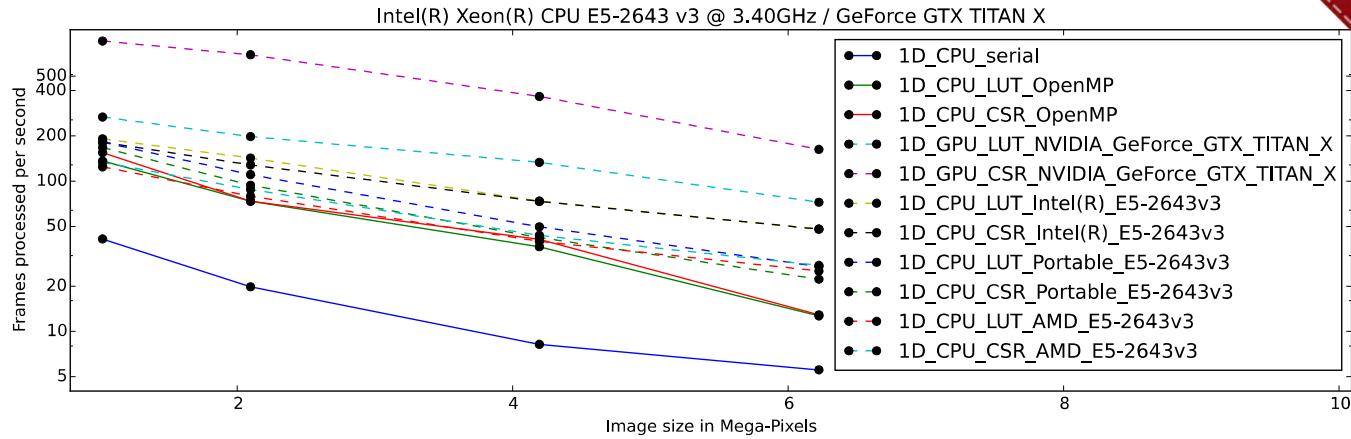
- **Better solutions**

- Implement the byte-offset decompression on GPU → Far from trivial

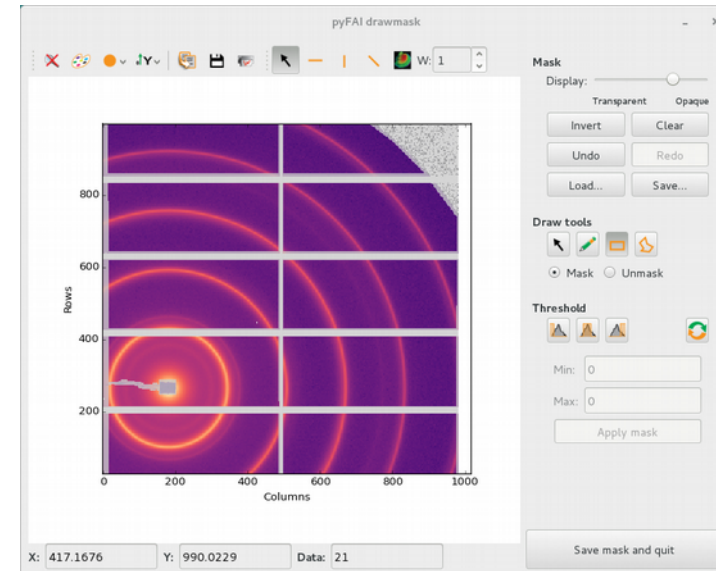


# PyFAI: fast azimuthal integration

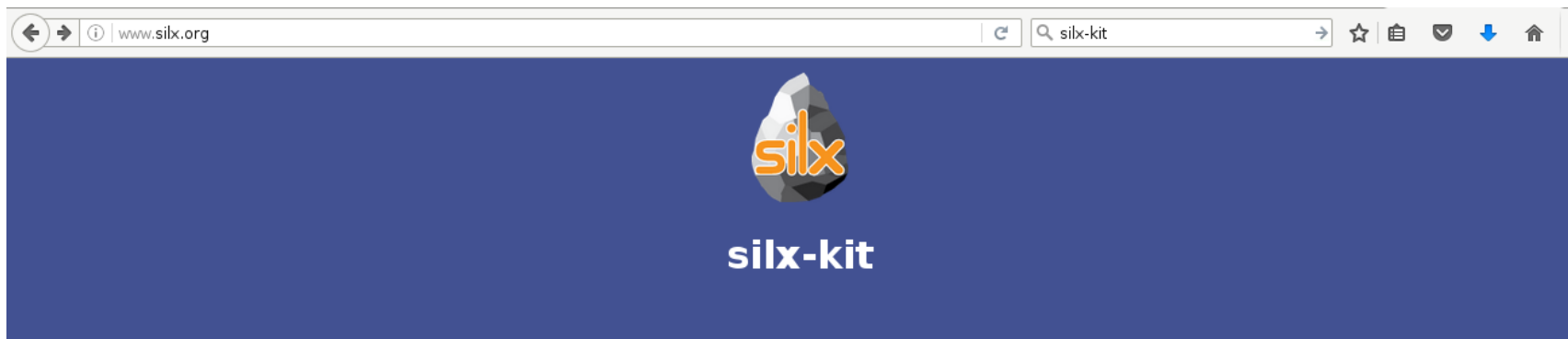
Fork me on GitHub



- ~2 ms processing per image
- Graphical user interface in preparation
  - Will rely on silx for the GUI
  - Mask tools already using *silx*
- Version 0.13 planned in the coming weeks
- May change license as well



# silx-kit: join efforts, share the maintenance



## silx

Scientific Library for  
eXperimentalists



### Resources

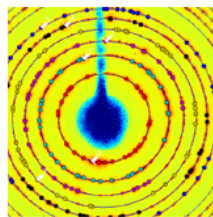
- [silx on GitHub](#)
- [Wheels and source on PyPi](#)
- [Installation instructions](#)

### Documentation

- [Latest release](#)
- [Nightly build](#)
- [v0.3.0](#)
- [v0.2.0](#)
- [v0.1.0](#)

## pyFAI

Fast Azimuthal Integration in  
Python



### Resources

- [pyFAI on GitHub](#)
- [Wheels and source on PyPi](#)
- [Installation instructions](#)

### Documentation

- [Latest release](#)
- [Nightly build](#)

## FabIO

I/O library for images produced by  
2D X-ray detector



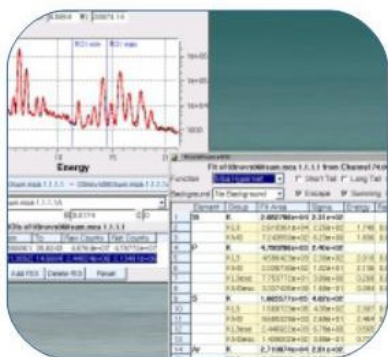
### Resources

- [FabIO on GitHub](#)
- [Wheels and source on PyPi](#)
- [Installation instructions](#)

### Documentation

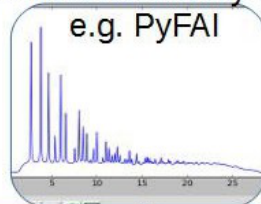
- [Latest release](#)
- [Nightly build](#)

Mainly Pierre Knobel ...

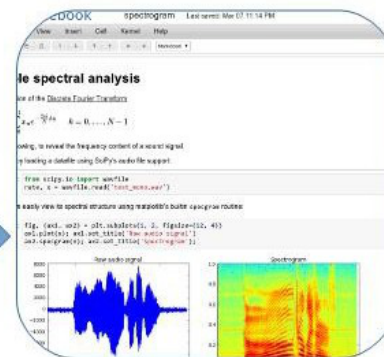


Standard Apps e.g.  
PyMCA, PyDIF  
... and Valentin Valls

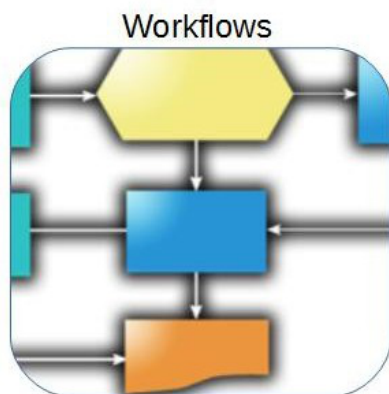
Mainly Jérôme Kieffer  
Online data analysis  
e.g. PyFAI



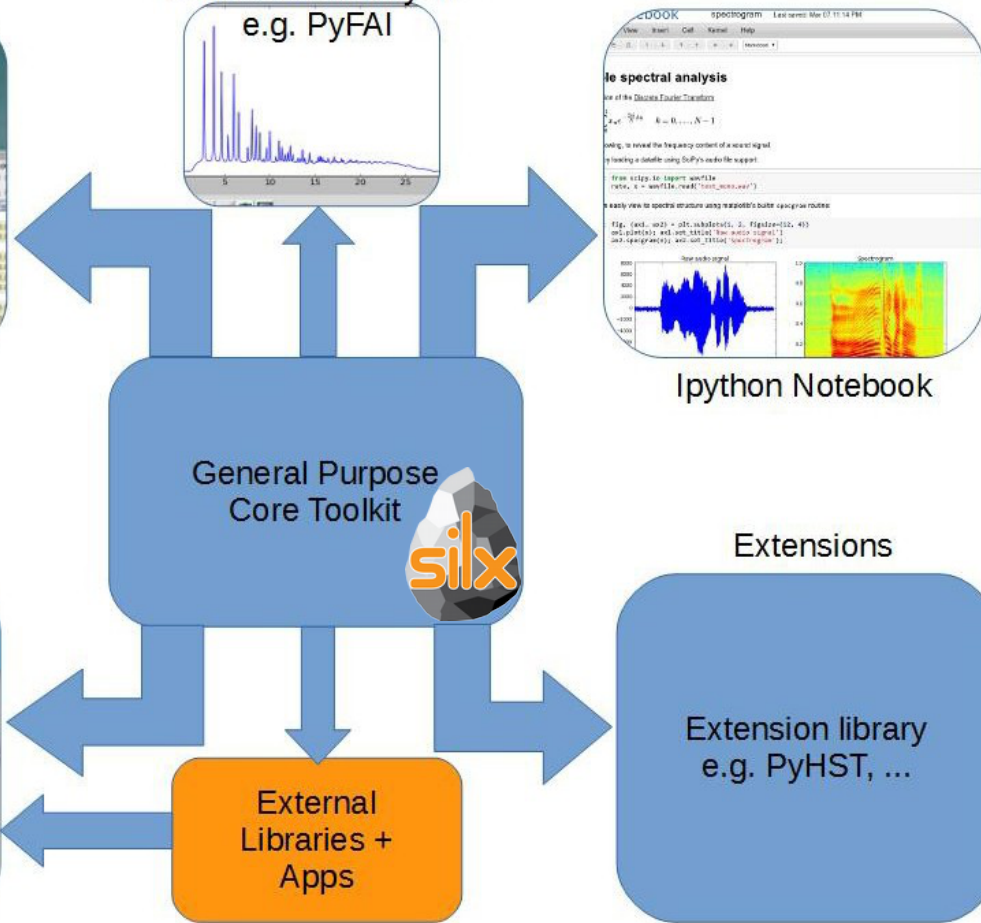
Mainly Thomas Vincent



IPython Notebook



Mainly Henri Payno





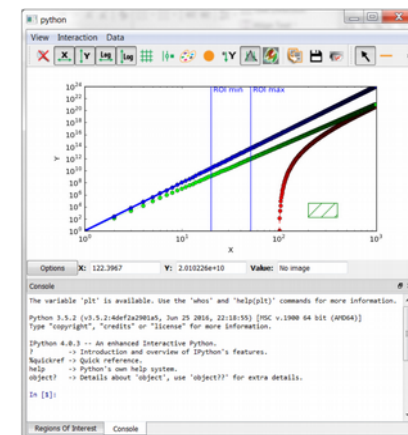
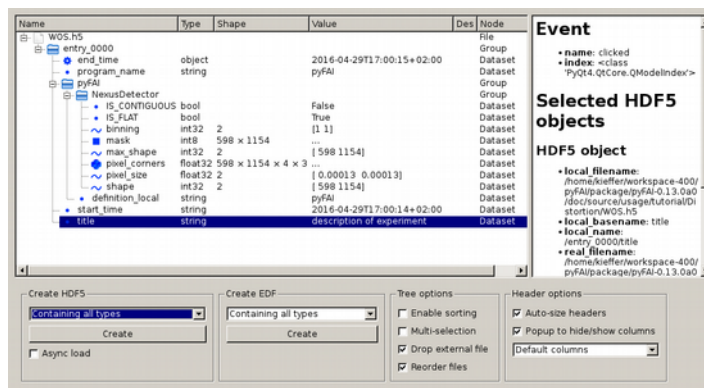
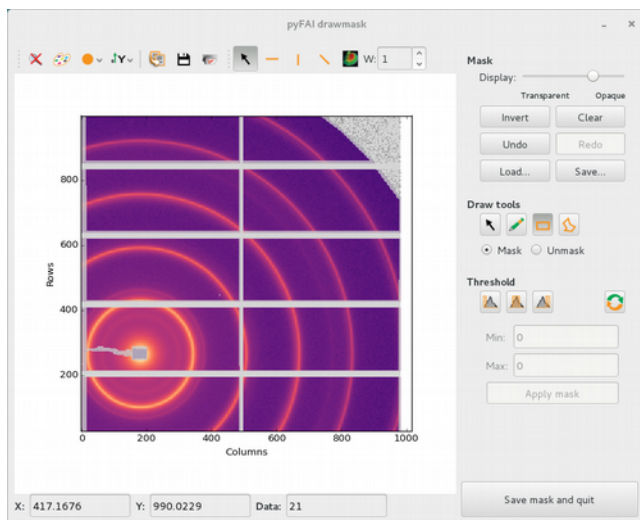
# Management of the *silx-kit* project

- **Public project hosted at github**  
<https://github.com/silx-kit/silx>
- **Continuous testing**  
Linux, Windows and MacOSX
- **Nightly builds**
  - Debian packages
  - RPM on target
- **Weekly meetings**
- **Quarterly releases**
- **Code camps before release**
- **Continuous documentation**

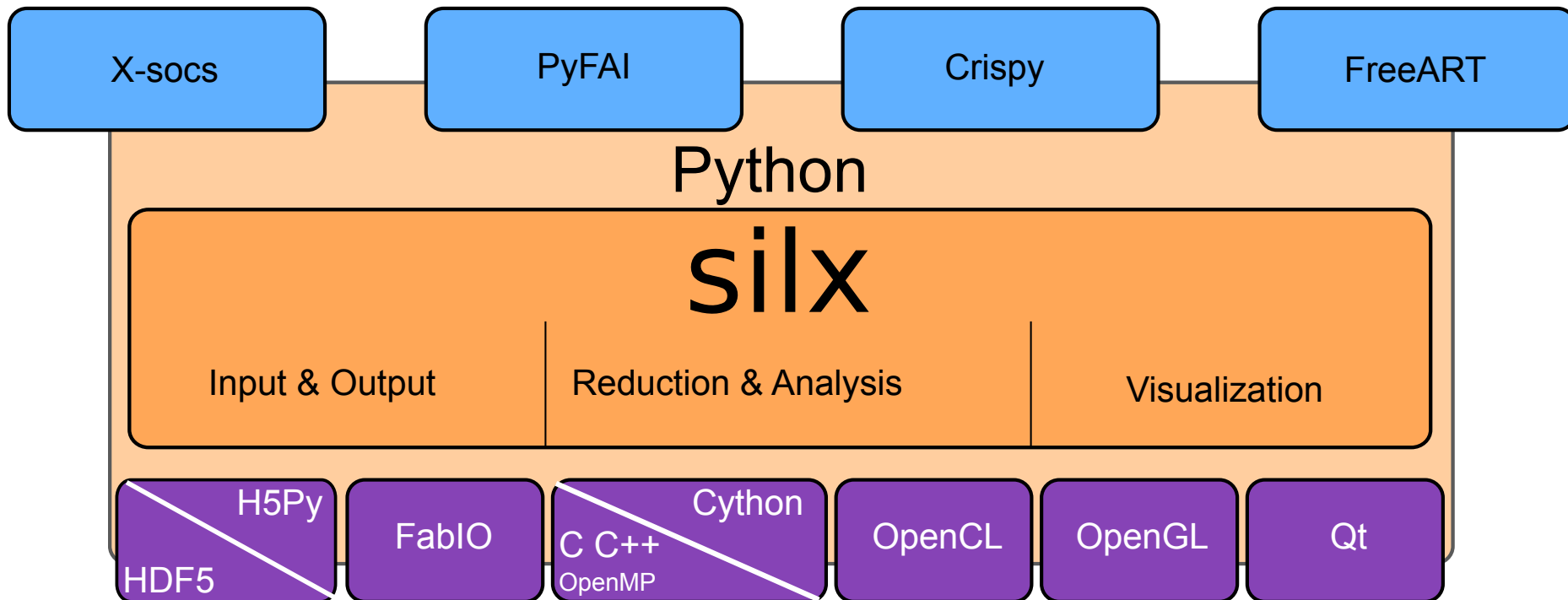
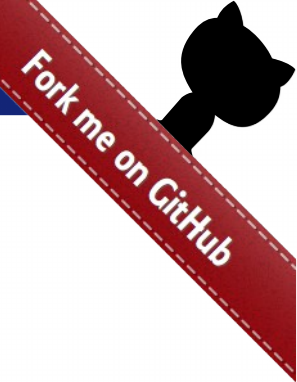
<http://www.silx.org/doc/silx/>



- **A toolbox for data analysis programs**
  - A uniform way to access data: a la HDF5
  - Common reduction routines (histogram, image alignment, fit)
  - A set of advanced widgets for:
    - **Browse spec, images, HDF5 files**
    - **Plot curves and fit**
    - **Display images, profiles, draw masks**
- **Resources: ~3 FTE over 6 persons**
- **Available everywhere: Linux, MacOSX, Windows**







- One of the most challenging experiment on the engineering point of view
- Very high data-rate, big-data on the radar
- 18 month of work for engineers from:
  - **The ID15-beamline (Marco, Gavin, Thomas)**
  - **The beamline control unit (Seb, Manu, Tiago, Alejandro)**
  - **The computer services (Gabi, Benoit)**
  - **Under the coordination of Jens Meyer**
- The data reduction will be performed on:
  - **CPU for decompressing the images (6 threads)**
  - **GPU for azimuthal integration**
  - **180 Hz achieved in production like mode but:**
    - Multiple bunches of data can be parallelized
    - 300Hz have been achieved on test computer
  - **Data may be exported in HDF5 (or not)**

- **ID15:**
  - Marco Di Michiel
  - Gavin Vaughan
- **Data scientists:**
  - Vincent Favre-Nicolin
  - Marius Retegan
- **Computing services:**
  - Benoit Rousselle
  - Gabriele Förstner
- **Beamline control unit**
  - Jens Meyer
  - Sébastien Petitdemange
  - Tiago Coutinho
  - Matias Guijarro
- **Data analysis unit**
  - V. Armando Solé
  - Thomas Vincent
  - Valentin Valls
  - Henri Payno
  - Pierre Knobel
  - Damien Naudet