Rewriting the DCT pre-processing pipeline

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Diffraction Contrast Tomography (DCT)

A short introduction

What is it?

- Acquire 2D images from different angles
- Acquire transmitted and diffracted beam
  (notice: the acquisition area is larger than the beam)
- Identify and group diffraction spots by grain
- Reconstruct the grains individually

How is it different than XCT?

- Reveals 3D grains orientation and shape
- Allows to build digital models of the sample
- Enables new experiments; e.g.: visualize slip bands

Figure 1: DCT setup (simulation). Credits: Wolfgang Ludwig.

↑ click

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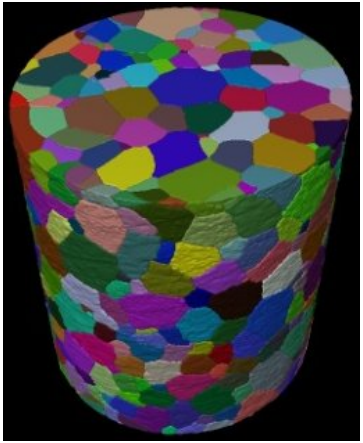

Figure 2: Reconstructed volume with individual grains segmented (different colors). Credits: Wolfgang Ludwig.

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Pipeline: from acquisition to 3D reconstruction

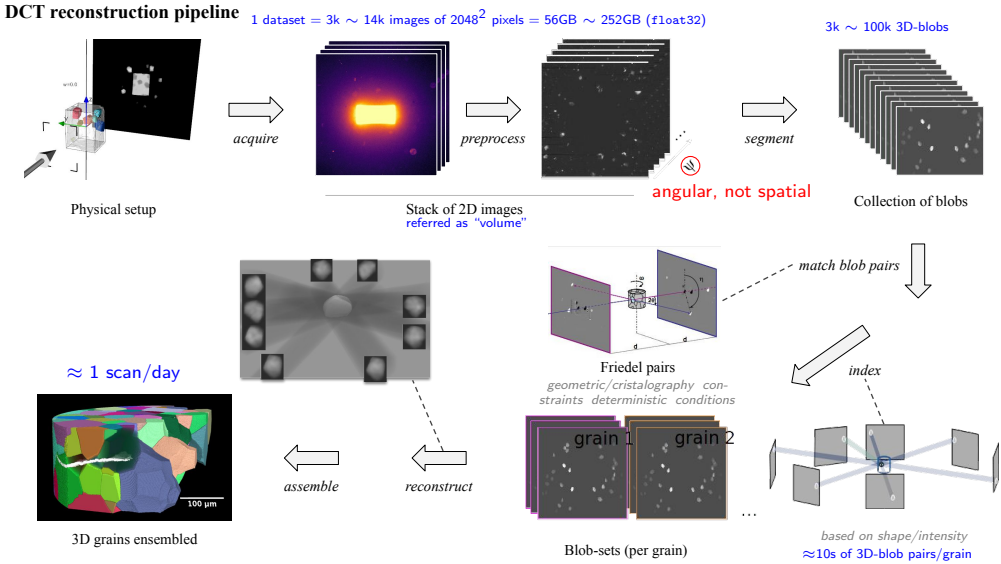
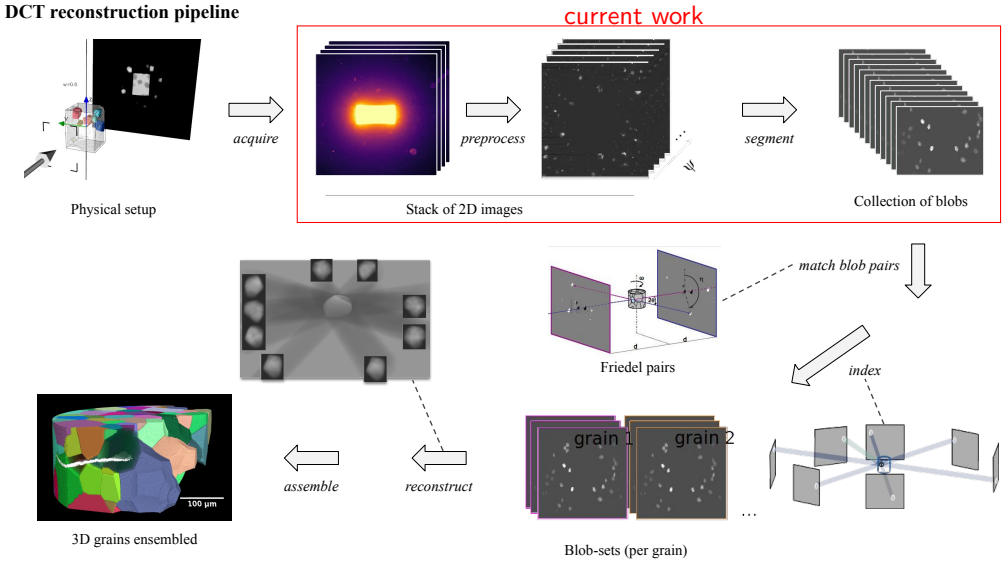


Figure 3: Main steps in DCT's reconstruction pipeline

Pipeline: from acquisition to 3D reconstruction



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Preprocessing

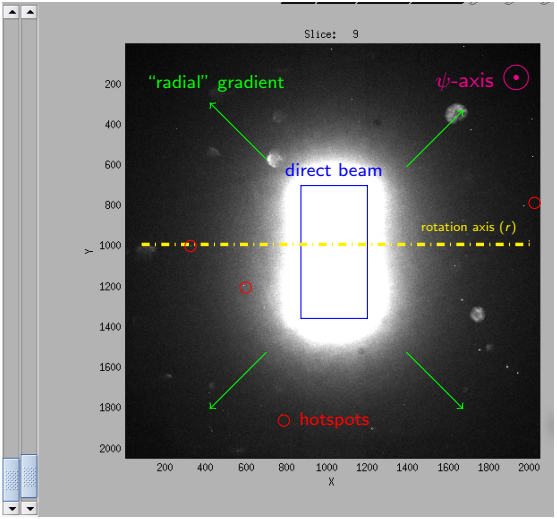
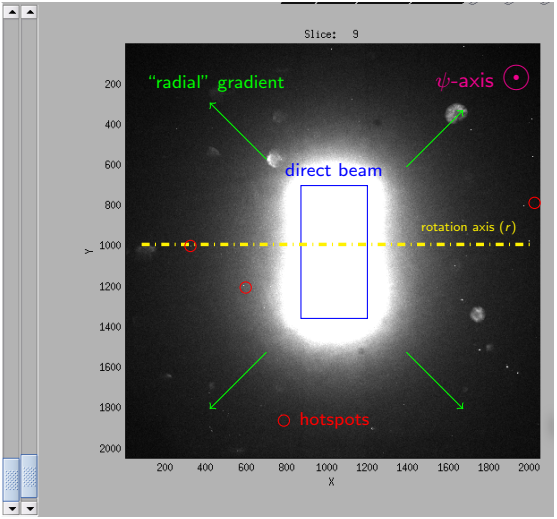


Figure 4: Raw acquisition

Image characteristics

- 4 sensors grid
- source intensity oscillates
  i.e. beam intensity variation over ψ
- beam/blobs brightness 2 scales apart
- blobs closer to r are ψ-longer

Preprocessing



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Preprocessing steps

- subtract the offset
- (optional) normalize by the margin's average
- subtract a per-pixel ψ-wise moving median
  i.e. 1D moving median on 2048^2 positions
- 2D median filter (per frame)

Preprocessed image

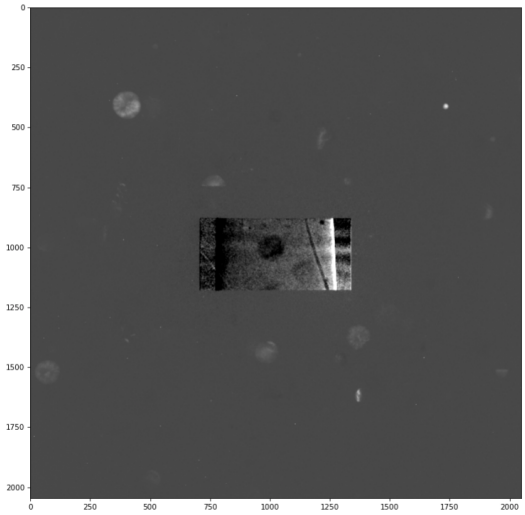


Figure 5: Preprocessed image

Segmentation

Double threshold in *3D*

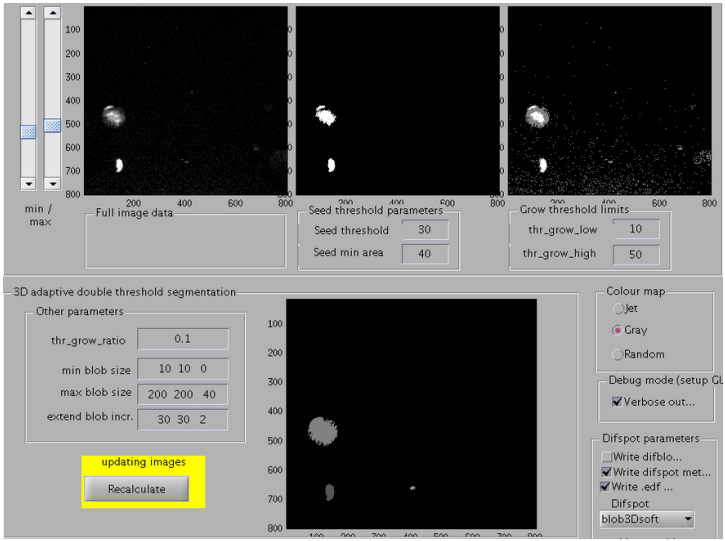


Figure 6: Double threshold interface

- threshold the image
- find all connected regions

for each connected region

- find the local maximum value M
- the local threshold is τM

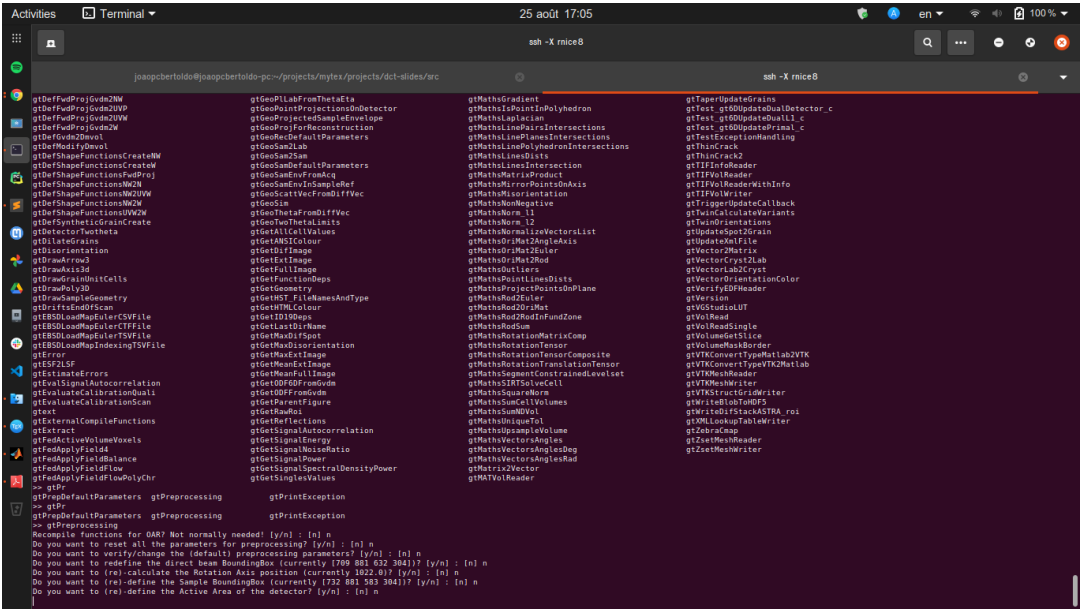
  $\tau \in [0, 1]$ is the tolerance parameter
- from M's location, get a BB[a] of size $2 \times bb_{max}$

  $bb_{max} \in \mathbb{R}^3$ is the maximum BB parameter
- threshold the BB with τM and get its connected component c
- keep it if $bb_{min} <= c <= bb_{max}$

[a] bounding box

Metamorphosis

Before



Metamorphosis

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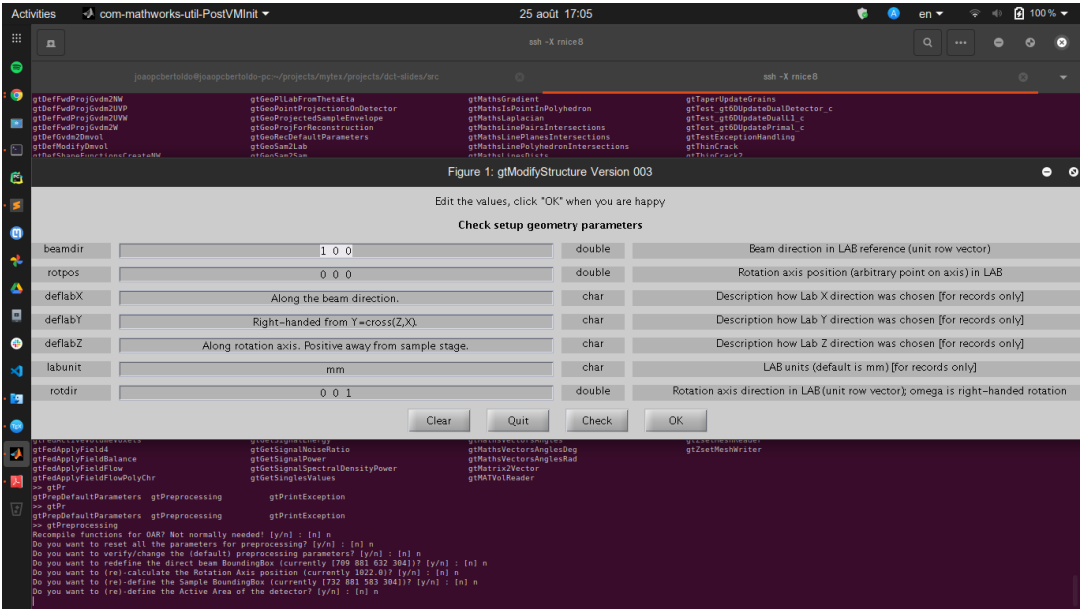


Metamorphosis

Before

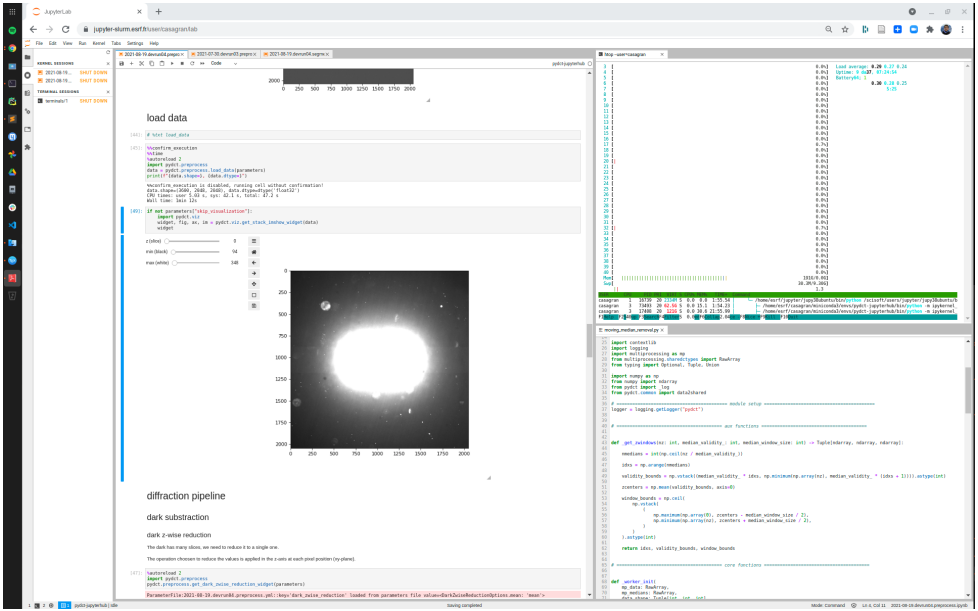
- MATLAB
  - → paid
  - → window-based application (ssh -X...)
  - → pipeline "spread" over several files/functions
  - → user types commands
  - → parameters in `.m` file
  - → compiled
  - → command line interface + windowed interfaces
  - → backend vs. fronted
  - → dependency on file/folder naming convention

Now

- Python
  - → free, open-source
  - → IPython/JupyterLab-based application
  - → pipeline in Jupyter Notebooks
  - → notebook guides the user
  - → parameters in `YAML` files (human-readable)
  - → interpreted
  - → notebooks with functions and widgets
  - → code as software
  - → user-configurable URLs (path + hdf5 link)

Metamorphosis

After



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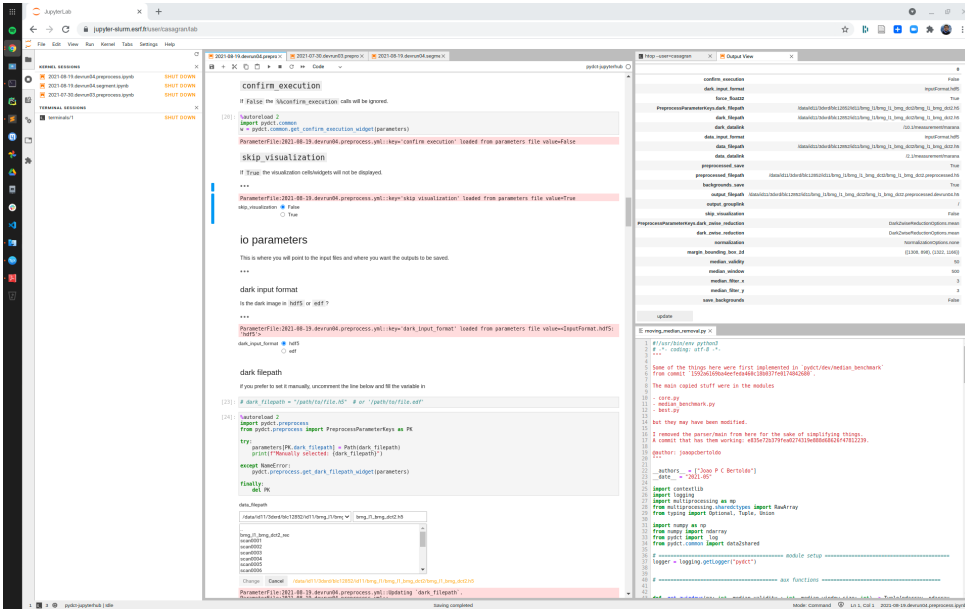

Metamorphosis

Before

- EDF files
  - → ESRF-specific format
  - → 1 volume = 3600 files
  - → metadata in yet other files

Now

- HDF5 files
  - → generic format
  - → 1 volume = 1 file
  - → metadata in the same file

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- Parallelized on several machines
  - → OAR (job config files, management)
  - → network communication
  - → repeated io-operations

Now

- HDF5 files
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- Parallelized on a single machine's cores
  - → Python's native library `multiprocessing`
  - → no network transfer
  - → shared memory space

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  - → 8 machines

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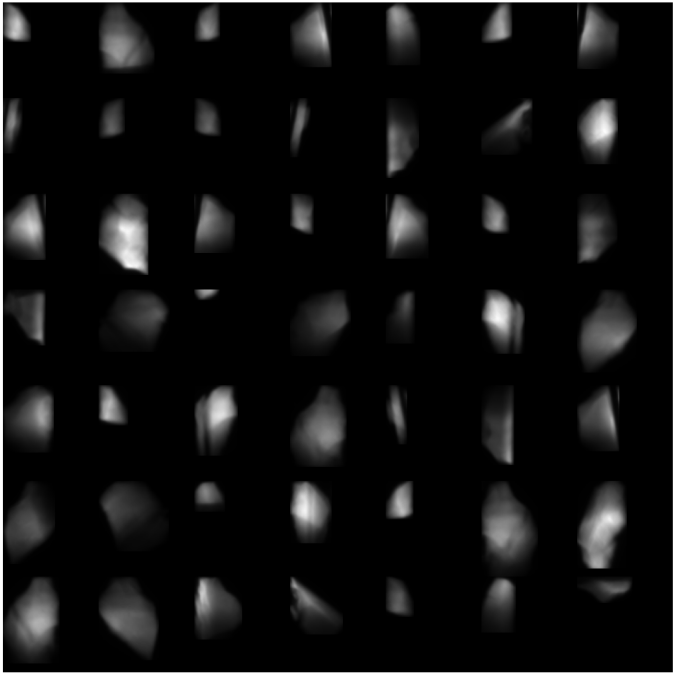
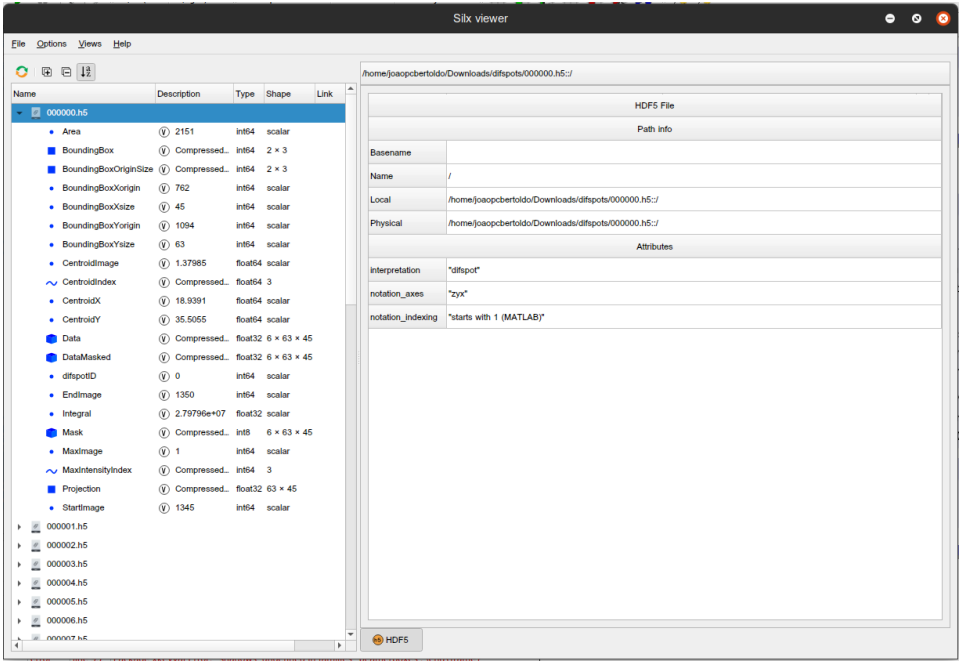
Results

- Installed and used in Psyché during an experiment
- Kenza's material (AD730) processed with `pydct`

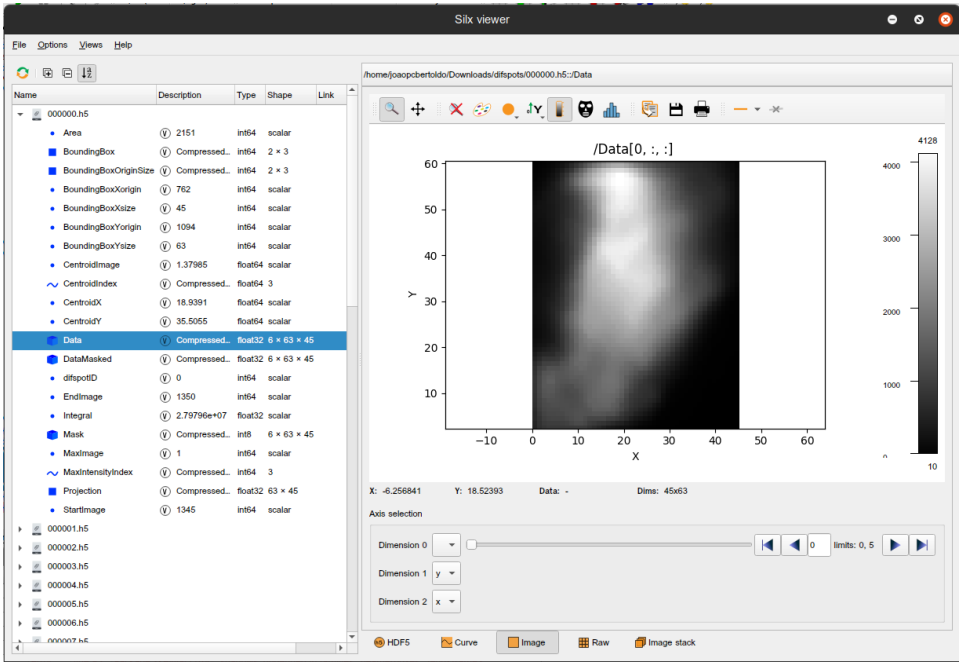
Difspot



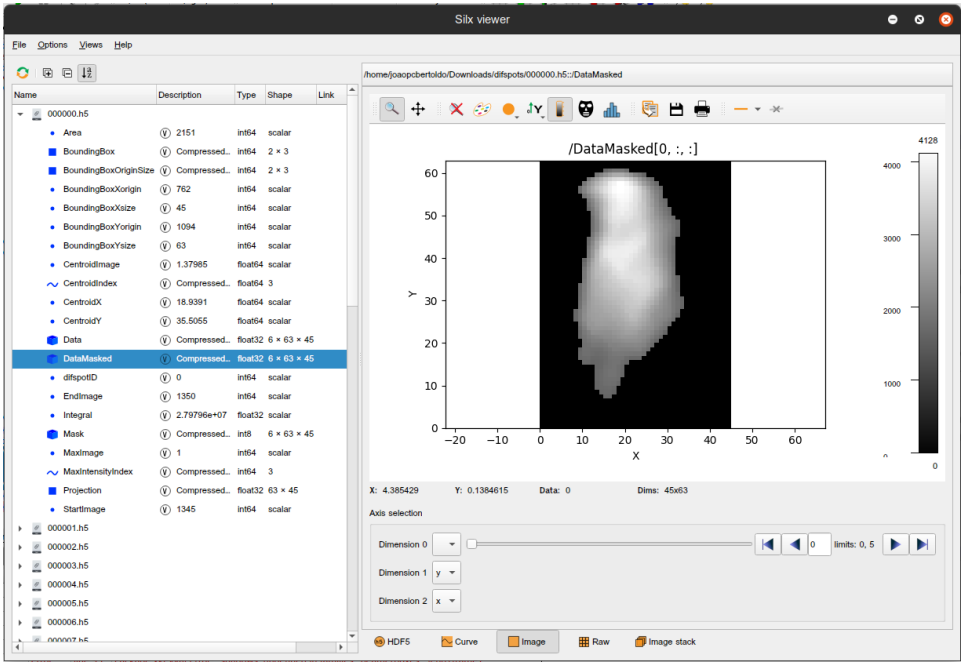
Difspots from AD730



Difspots from AD730



Difspots from AD730



Thank you!

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Segmentation

Double threshold in 1D

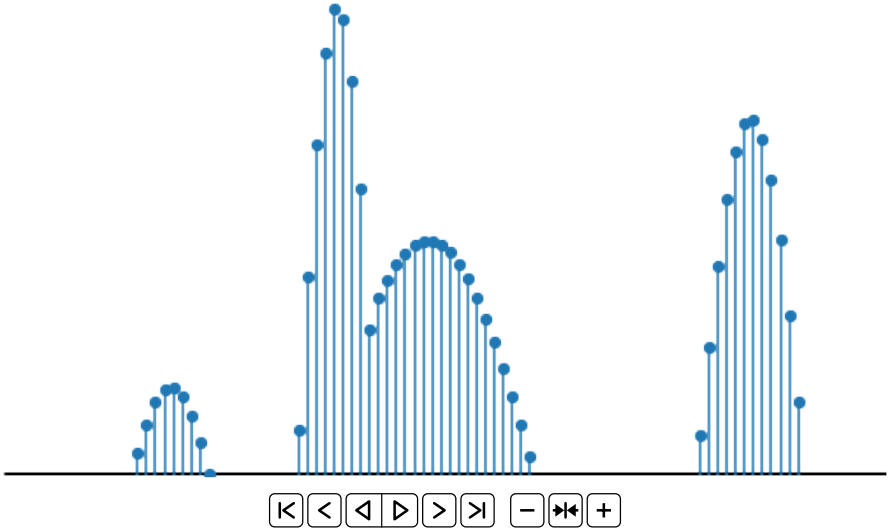

Figure 7: double thsrehold illustration