PSICHE tomography documentation

Version 1, 22/03/2017, Andrew King

Introduction

This document explains how to perform a tomography experiment at PSICHE. It explains the steps of an experiment, and gives some trouble shooting tips in case of problems.
This guide focuses on controlling the experiment, recording data, and reconstructing and viewing the results. We assume that the experiment has been set up correctly by the local contact, so you don't need to re-align anything. The aim is that if the control window crashes, or is closed by mistake, or lost, you can get started again.
If you have problems beyond the scope of this documentation, don't hesitate to call either the hall coordinators or the local contact, whose telephone numbers are displayed by the telephone.

Open the control window

The beam line is controlled using Spyc, the SOLEIL Python command line interface. For monochromatic experiments in the experimental hutch, the Spyc session is called MonoTomo. For pink beam experiments in the optics hutch, the session is PinkTomo. In both cases, the window can be opened by double clicking the icon on the desktop (bottom left of the right hand screen). The system will automatically load the Python object **mt** which controls the experiment.
*If everything works correctly, the **mt** object will be automatically configured with the last saved configuration, and the atk panel to display the camera image will open automatically. There is nothing else to configure, so you can start working straight away.*

Initialising the control system

Everything you need for tomography is grouped together in a Python object, usually called **mt** (for "my tomo"). This is automatically initialised when you open Spyc. If, for whatever reason, you have to reload it, it is initialized as follows:

mt = Tomo.Tomo(config='mono')
or
mt = Tomo.Tomo(config='pink')

In this pink beam case, you will be asked to enter the beam energy. This is only for the log file, so if you don't know it doesn't matter.
Once you have done this, most tomography tasks are performed by this object. This means that you need to type **mt.something()...** If you type **mt.** and then hit the **tab** key, Python will list the available methods.

You will need to enter two pieces of information to complete the setup, the experiment name and the detector optic configuration.

The experiment name ensures that all the data directories that you need exist, and that scan parameters are automatically logged in the right file. Your experiment name is usually NAME_MMYY, where NAME is the family name of the proposer, and MMYY the date of the beam time.

mt.setExperiment('King_0116')

You need to enter the detector optic that you are using:

mt.setOptic()

You have the choice of 1x/2.5x/5x/7.5x/10x/20x optics, and simple or tiltable scintillator supports. The method can then position the detector automatically at the nominal focal distance. IF THE DETECTOR IS ALREADY IN FOCUS, DO NOT MOVE! CHOOSE N (THE DEFAULT OPTION)

Display the camera image

To open the display of the camera image:

atk mt

The image is found in the third tab, at the bottom of the window.
Currently, the image is displayed upside down!
Horizontally, it is as if we are the camera, looking into the beam. The figure below gives an idea of the orientations.

Controlling the camera

To put the camera in "live" mode for sample alignment, you can use:

mt.startLive()
mt.stopLive()

To set the camera exposure time (in seconds):

mt.setExpTime(0.1)

Note that the Hamamatsu camera saturates at around 50,000 counts in single acquisition mode.

We can also work in accumulation mode, in which multiple exposures are summed together to improve statistics. In this case, the camera saturates at 50,000 x N, where N is the number of exposures accumulated.

mt.setAccMode() ///could change this to be xN frames, and exposure time is set through setexptime..///
mt.setSingleMode()
If you change modes the atk panel will stop displaying the image. You can close the atk panel, and re-open it with the command **atk mt.**

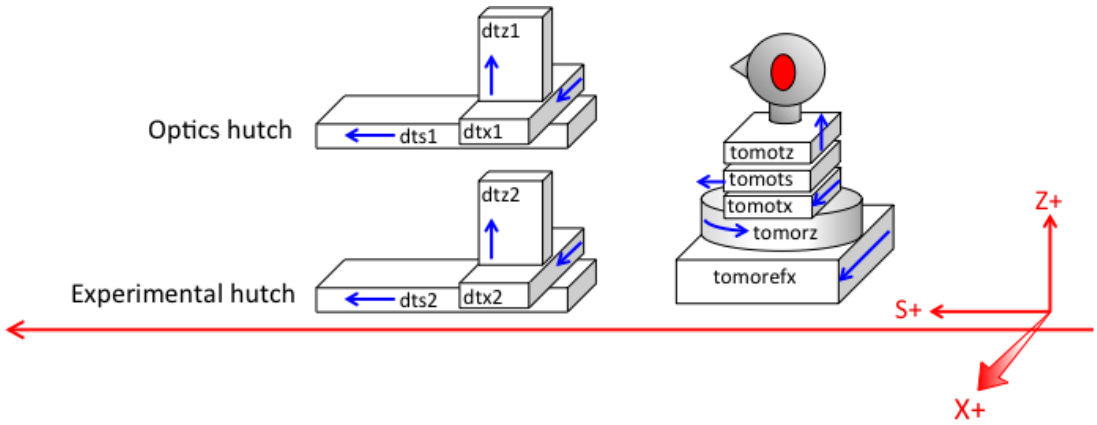
Useful Spyc commands for controlling the beam line

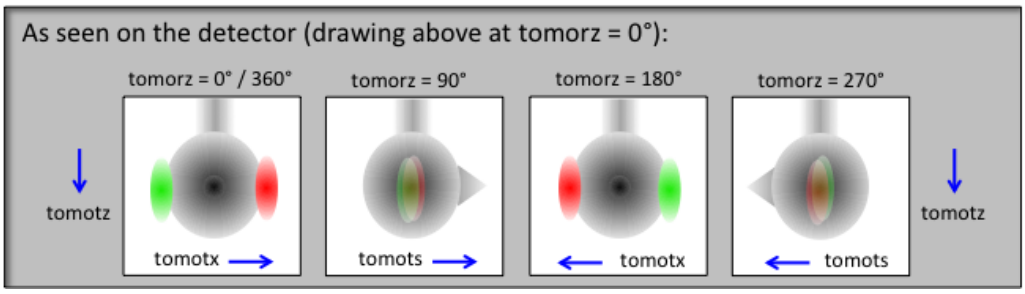
To move motors or open and close shutters. These are standard Spyc commands, so they do not use the **mt** object.

list all motor positions	:	**wa**
list one motor positions	:	**wm motorname**
list several motor positions	:	**wm tomo***
relative movement	:	**dmove motorname increment**
absolute movement	:	**amove motorname position**
control shutters:		
fast shutter (experimental hutch)	:	**fastshutteropen / fastshutterclose**
beam shutter (experimental hutch):		**shopen / shclose**
front end shutter (optics hutch)	:	**feopen / feclose**

Tomography motors

The tomography motors are as drawn here. They are the same regardless of whether the experiment is in the experimental hutch or the optics hutch. The detector motors names are different: **dts1/dtx1/dtz1** in the optics hutch, and **dts2/dtx2/dtz2** in the experimental hutch.





If you work in the experimental hutch and you use the big granite table as a z stage, there are two helper functions to move the table and the detector together. These are: **amovetomotablez** and **dmovetomotablez.** (Note that the command is all one word, not "amove tomotablez")

To help align the sample on the rotation axis at any given rotation angle, there is a helper function **tomoright**. This performs a coupled movement of tomotx and tomots that is perpendicular to the beam:
tomoright 1.5 (note not "dmove tomoright 1.5")

Recording tomography data.

In a normal tomography scan you take reference images of the beam without the sample. The sample is moved out of the beam by the motor tomorefx. This distance is calculated by default based on the field of view of the detector. If you are in local tomography, or have an in-situ environment, you may need to modify the distance. The value is stored in
mt.refDisplacement
To change the value:
mt.refDisplacement = -5.5
…for example.

You should now be ready to set up a tomography scan. To set up the tomography scan parameters:

mt.setScanParameters()

Respond to the prompts. Filenames will be automatically appended with a number to avoid overwriting scans. Normally, the last values that you entered will be remembered as defaults, so you only need to enter the values that you want to change.
mt.showScanParameters() will display the current values.

To collect a dataset:

mt.doTomo()

This will launch an acquisition using the current parameters. There are two different scan macros depending on the acquisition mode of the camera. Single image mode uses the official SOLEIL FlyScan, and accumulation mode uses a homemade system. This is handled automatically, and for the user the only difference is where the data is recorded, and the format of the raw data.

Hopefully, your scan will complete successfully. The next step is to reconstruct the data and view the result.

Reconstruction and viewing results

Reconstructions are performed using the machine PSICHEGPU. To connect to this machine, open a terminal window and type:
gotopsichegpu

Go to your reconstruction directory
cd /psichestockage/experiences/psiche/com-psiche/YOURNAME_XXXX

There are a number of macros that handle the reconstruction of datasets. These are all handled through a single function:
tomodata
The menu should steer you through the options that you need.
The important ones:
s, to select a new dataset. Click into the folder of the dataset you want to analyse, and then wait while the data are preprocessed. You only have to preprocess a dataset once. After a dataset has been preprocessed you can select the dataset later using the option **n.**

To reconstruct and view one slice, use the option **v**. You can choose which slice to reconstruct.

You need to set the correct rotation axis position. This is done with the option **a**. Then you can calculate automatically, scan the axis position, or manually enter a value.

Other options are available. Hit **enter** or **h** to show the different options.

Data and results

Each dataset will be stored in a subdirectory in your reconstruction directory:
/psichestockage/experiences/psiche/com-psiche/YOURNAME_XXXX/dataname

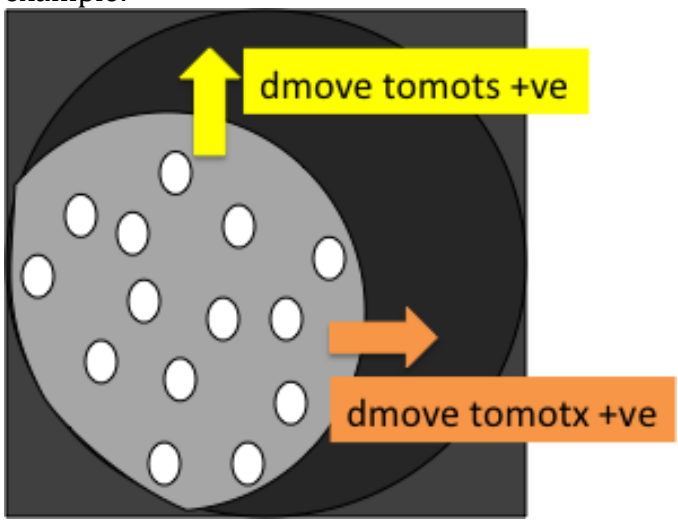
The reconstructions are in .vol format:
/psichestockage/experiences/psiche/com-psiche/YOURNAME_XXXX/dataname/dataname.vol

To viewing data, we use ImageJ. To launch this:
ImageJ-linux64 &

To load in a reconstructed volume, get the dimensions of the volume from the info file. At the commond line type:
more dataname/dataname.vol.info
Then, in ImageJ: File – import – raw. Enter the dimensions. The data type is 32bit real, and you should check the “little endian” option.
///find an hst vol reader for imagej ///

Reconstruction sample position

You can adjust the alignment of your sample using the reconstruction. For example:



Trouble shooting!

Camera is dead – In the camera atk panel with the image, the little coloured flag is gray.
Action: Restart the camera device server.
Open a new terminal window. Type:
vncviewer psiche-pcorca1
This opens a view of the camera PC. Close any open windows. On the desktop there is an icon "**start ORCA device server**". Double click this to start the device server. A terminal window will open.
You should see the flag in the camera atk panel become yellow or green.

Camera is stuck – In the camera atk panel the coloured flag is green, but the image is not updating, and the camera doesn't respond to commands from the Spyc command line.
Action: Use the command **stopORCA** in any spyc terminal. For example, if the MonoTomo or PinkTomo terminal is blocked, you can use the Optics terminal. This should stop the camera, and you should see the flag in the camera atk panel become yellow or green.

Lost the Spyc command window – the window is lost, has disappeared, or has been closed by mistake.
Reopen the command window with the icon on the desktop.
The last saved settings of **mt** will be loaded automatically, and are displayed in the terminal window. In case they are wrong, follow the instructions at the beginning of this document to initialize the **mt** command object.

Monochromatic only – Beam has disappeared. If you open the shutter and put the camera in live mode, the image is dark. If you haven't moved anything, and nothing is blocking the beam (a new, taller sample?) then problem the feedback on the monochromator has failed.
Action: Reset the feedback.
On the **laptop PC, to the left of the desk**…

The software may have crashed. In this case, close the application and try to reopen it using the "PTC Diagnostic" icon. When it opens, make sure that USB is selected, and click OK. An icon I200(1) should appear on the left of the window. If it doesn't appear, close the software, unplug / wait / replug the USB cable. Try again. If it doesn't work, restart the PC (no password required).

Once the software is running and you have the I200 icon, click the icon to open the dialogue. In the tab – Data / PID, make sure that the servo is off (indicator is gray, not green). Click servo to switch off, if necessary.

Make sure that the front end is open (**feopen** in a spyc window)
Click profile. The software will scan the rocking curve of the monochromator, and you will see a profile like this:

Note the value of the minima. The process is to adjust the value in the box DAC (V) while observing the value in the box 1 (see figure). Note that the units of the plot may not be the same as the number displayed. Start from 0. Then increase the value slowly, and observe the increase in flux. The aim is to stop just before the minima, for example at 90%-95% of the minima value. Then click servo to start the feedback. Watch the value in the DAC (V) box. It should be more or less stable… wait a few minutes and see whether the beam is stable. If it is, well done ;-). Otherwise, repeat…

Rotation stage (tomorz) or tomorefx won't move

These stages will switch off if something blocks their movement, or if they are pushed too far out of position (i.e. if you lean on the side of the tomograph…)
In the **Spyc terminal**, taking tomorz as an example:
wm tomorz
this will show the position, and the **State OFF**
seton tomorz
wm tomorz
this will show the position, and the **State ALARM**
amove tomorz XX (where **XX** is close to the current position)
Now it should respond normally

Rotation stage moves, but very slowly

This is usually because a problem has occurred during a scan, and the regular rotation speed has not been restored.
In the **Spyc terminal**:
setspeed tomorz 60 (for 60 degrees / second, or less if appropriate)

FlyScan troubleshooting

The FlyScan is what lets you do a tomogram in ~15 seconds rather than >15 minutes!

Occasionally there are problems and it is necessary to restart the FlyScan server. The following should allow you to get it running again.

In any Spyc terminal, make sure that the camera is stopped:
stopORCA

Open **ASTOR** to manage the device servers
Menu Applications (top left of desktop) **– Tango – Tango Generic Tools – Astor**

Expand the item **PSICHE-Detecteurs**, and double click **psiche-pcorca1**
Right click on **ds_FtpServer/flyscan.1**, and select **Kill** server. The green dot should turn red.
Right click on **ds_FtpServer/flyscan.1**, and select **Start** server. The red dot should turn green.
Note that it is normal that the ds_LimaDetector/Hamamatsu.1 is red!

Expand the item **PSICHE**, and double click **b1406-srv3 (Flyscan acquisition)**
In **Level 2**, you will find the FlyScan devices
Right click on **ds_FlyScanServer/flyscan.1**, and select **Kill** server. The green dot should turn red.
Repeat for the other four flyscan devices
Then, right click on the **ds_FlyScanServer/flyscan.1**, and select **Start** server. The red dot should turn green.
Repeat for the other four flyscan devices.

Now, restart the camera device server, following the instructions above.

Now, look at the **FlyScan GUI.** If you need to open it, type **flyscangui &** in a terminal window.
In the bottom part of the window, select **FSS Logs**. At the bottom left of the window, set Filtered log level to **warning**, and select **Set as minimum log level**

Now, in the Spyc tomo control window, run **mt.setScanParameters()**
Watch in the FlyScan GUI for error messages. If there are no error messages, things are looking hopeful.
If there are error messages… if it is clear which device they refer to, you may be able to restart that device, and then try **mt.setScanParameters()** again.

If all seems well, try a tomo: **mt.doTomo()**