

SAXS1 MAIN COMMANDS

1. Calibrating SAXS1 Beamline

Calibration must be done:

- a) before you start a experiment
- b) when you change your sample holder
- c) after beam injection (it is not mandatory but highly suggested)

Calibration command is:

calibrate

2. Acquisition of your Data

You can either use single acquisition or multiple acquisitions for measuring your sample.

IMPORTANT: You can never have the Pilatus detector counting above 10^6 !

2.1 Single Acquisition

You have your scattering pattern in one single shot.

Single acquisition command is:

acquire samplename t

“**samplename**” is the chosen sample name

t is the exposure time in seconds

The exposure time (**t**) must be less than 400 seconds.

2.2 Multiple Acquisitions

You have several scattering patterns for the same sample.

Multiple acquisitions command is:

acquire samplename t n Δt

“**samplename**” is the chosen sample name

t is the exposure time in seconds

n is the number of frames you want to acquire

Δt is the dead time between exposures in seconds

The total exposure time (**t x n**) must be less than 400 seconds.

The dead time (**Δt**) must be greater than 0.2 seconds.

For closing the shutter between measurements, use a dead time (Δt) greater than 6 seconds.

If the dead time (Δt) is greater than 6 seconds, the program will run on **LT** mode. In this mode, the shutter will close between measurements and the exposure time of **each acquisition (t)** can be **400 seconds** at most.

The table below resumes the program operation for each mode.

Mode	t(s)	n	Δt(s)
Single	$t \leq 400$	-	-
Multi	$t \times n \leq 400$		$0,2 \leq \Delta t < 6$
LT	$t \leq 400$	any	$\Delta t \leq 6$

2.3 Results

Multiple image acquisition will generate a numerical suffix representing the image made. The first image will be named **samplename_0000.tif**, the second one **samplename_0001.tif** and so on. The program generates 2 image files, one normalized with the relative efficiency (**samplename_norm.tif**) and one without (**samplename.tif**). The relative efficiency is generated during the calibration and is the ratio between the bean intensity before and after the empty sample holder, it is appended to the saxspar file during calibration. The *_norm* suffix is added after the number suffix. So the normalized first image from a multiple acquisition experiment will be named **samplename_0000_norm.tif**.

All the data collected is appended to the end of the **saxspar file**. It is named **saxspar#####.txt**, where ##### represents the user proposal number. If it is an acquisition on **LT mode** the data will be displayed as:

Expositions number:

Time between expositions:

Date of the experiment:

Time	Current	Archive	t(s)	I0	IT	IT*Er	Attenuation
.
.
.

In any other mode, the data will be as:

Expositions number:

Time between expositions:

Start time of the first image:

Archive	t(s)	I0	IT	IT*Er	Attenuation
.
.
.

Where Time represents the hour, minute and second the image was made.

Current represents the current at the ring at the time the image was made in mA.
Archive represents the name of the image file whose data is from.
t(s) represents the exposition time of that image in seconds.
I0 is the photon count measured before the sample.
IT is the photon count measured after the sample.
IT*Er is the photon count measured after the sample, corrected by Er (Relative Efficiency) factor.
Attenuation is the result from $I_0/(IT*Er)$ which indicates how much the sample attenuated the beam.

3. Integrating your Data

The integration of your scattering data depends on how you have acquired your data.

3.1 For Single Acquisition

If you have acquired your scattering pattern in one single shot, the integration command is:

```
cake_plot samplename_norm.tif emptyname_norm.tif
```

Alternatively, if you want to see your scattering curve as a log x log plot, you have to type “-l” at the end of the sentence, as shown below:

```
cake_plot samplename_norm.tif emptyname_norm.tif -l
```

3.2 For Multiple Acquisitions

If you have acquired your scattering patterns by using multiple acquisition command, the integration command is:

```
mcake_plot samplename_0001_norm.tif emptyname_norm.tif
```

where “**samplename_0001_norm.tif**” is the first file of your multiple acquisition series and “**emptyname_norm.tif**” is the scattering pattern of which you want to subtract your data.

4. Plotting your Data

4.1 Plotting your Scattering Curves

You can plot one or more scattering curves which were already reduced. It (or they) must be a “**.dat**” file extension.

Moreover, you can also chose to plot a log x linear or log x log style.

For a log x linear plot, the command is:

```
plot samplename_norm_minus_emptyname_norm.dat
```

Alternatively, if you want to see your scattering curve as a log x log plot, you have to type “-l” at the end of the sentence, as shown below:

```
plot samplename_norm_minus_emptyname_norm.dat -l
```

You can plot several scattering curves at the same time. For doing that, you have to:

1) type the names of all samples that you want to plot in sequence, like below:

```
plot samplenameA_norm_minus_emptyname_norm.dat
    samplenameB_norm_minus_emptyname_norm.dat
    samplenameC_norm_minus_emptyname_norm.dat
    ...
```

2) type strategically names of your samples by using “*” since “*” means all words and possible combinations that you have into your folder like exemplified below:

```
plot samplename*_norm_minus_emptyname_norm.dat
```

In this case, you are going to plot all scattering curves for those samples which have samplename followed by some identification like “samplenameA”, “samplenameB” and “samplenameC”.

4.2 Plotting your Scattering Images

You can plot one scattering image of the Pilatus detector at a time. It must be a “.tif” file extension. The command is:

```
plottif samplename.tif
```

5. Data Average

If you want to make the average of some scattering curves the command is:

```
avg samplename*.dat
```

In this case the script will do the average of all scattering curves that start with “samplename” and end with “.dat”.

In case of degradation of your sample, in a series of images of the same sample, you can use the same script to use the best curve until some point in **q**, and make the average of all scattering curves for greater values of **q**. For this procedure, the command is:

```
avg bestsample.dat # samplename*.dat
“bestsample.dat” is the best sample for lower q
# is the limit point in q
```

“**samplename*.dat**” are the scattering curves you want to do the average

6. Solid Sample Holder (PASMI)

In case you are using the solid sample holder, PASMI, to move the sample the command is:

pasmi #

is the position of your sample

The order of the positions is shown below:

- 1
- 2
- 3
- 4
- 5
- 6
- 7

7. Safety Manuals Links

Safety Job Instructions:

https://wiki.Inls.br/mediawiki/images/f/f4/LNLS-SGT-IT-001_R00_SAFETY_JOB_INSTRUCTION_AT_LNLS.pdf

LQU Training (in portuguese):

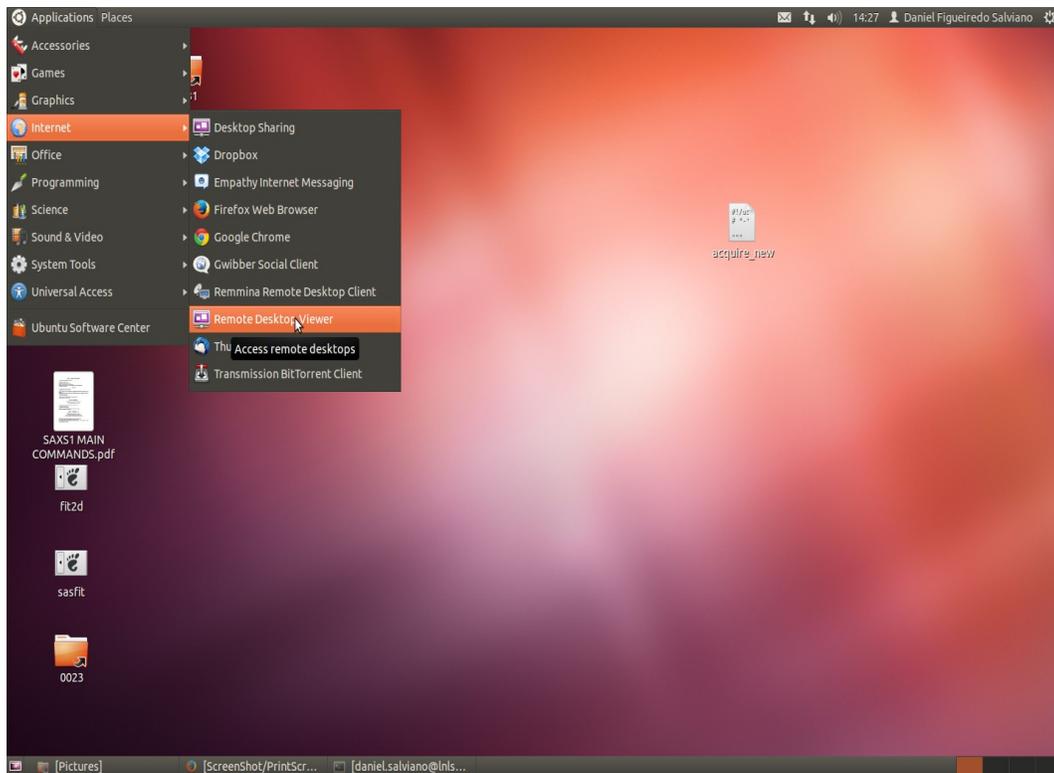
<https://wiki.Inls.br/mediawiki/images/f/f7/LQOUTRAINING.pdf>

Safety User's Training

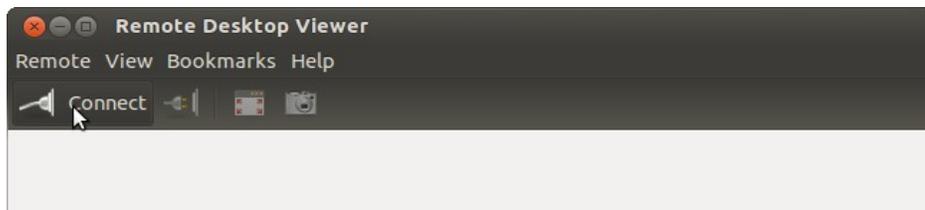
https://wiki.Inls.br/mediawiki/images/c/cd/Apostila_usuarios-_Treinamento_de_seguran%C3%A7a-port-19-02.pdf

8. Connecting via VNC

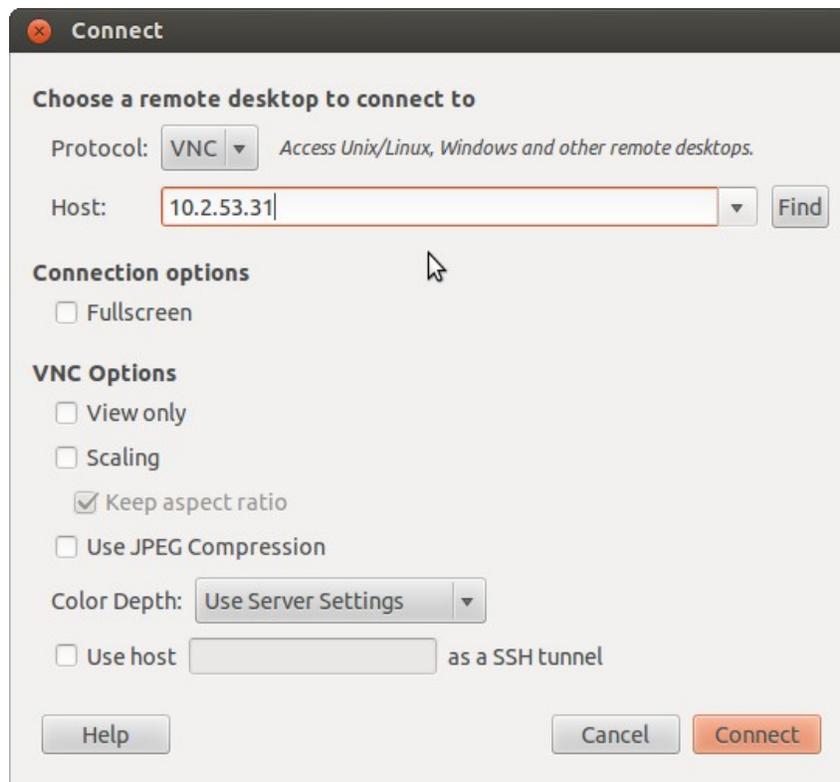
- At the top left of the Desktop screen go to Applications > Internet > Remote Desktop Viewer



- Click on *Connect*



- Change Protocol to VNC
- Type *10.2.53.31* at Host



➤ Enter with the Password: "saxsI"