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Basic tutorial - How to use quick_tomo

QuickTomo by Alessio d'Acapito
Tutorial by Alice Decombe & Alessio d'Acapito

Welcome to the Quick_tomo v0.2 tutorial! This tutorial is intended for use on your own system.

Quick_tomo is a tomography image processing pipeline made for complete beginners or for quick image processing for quality check of your sample in the tomograms. Preprocessing is handled by Scipion, alignment and reconstruction of the tomograms are made with AreTomo following a recipe that is tested to work on any type of cryo-ET data.

I. Installation and getting everything ready

To install

```
cd ~
git clone https://github.com/alessiodacapito/quick_tomo.git
```

This git includes

- This tutorial
- The pre-digested Scipion workflow
- The tested and running Aretomo executable (compiled for cuda 10> yourCuda >13)
- The Quick_tomoV0.2 script

You will also need a working scipion installation with the following plugins:

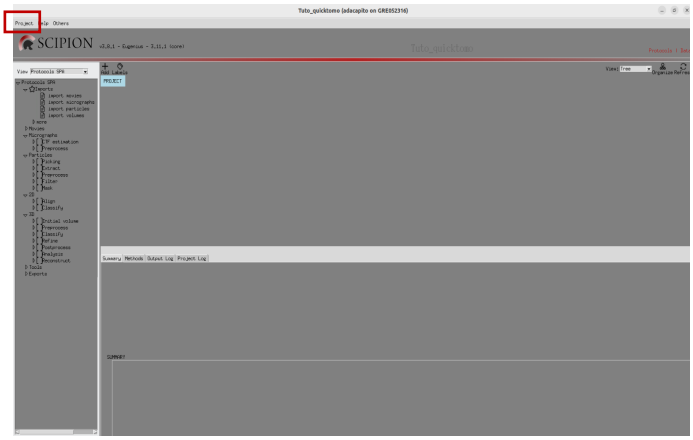
- Ctffind4
- Imod
- MotionCorr

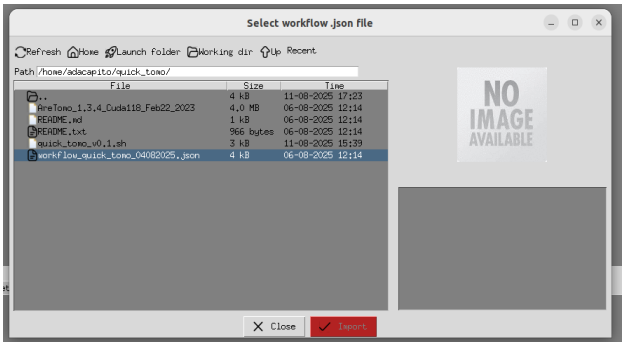
If you are lucky enough to work with SBGrid, the installation of scipion already meets all the requirements.

Now you are ready to go!

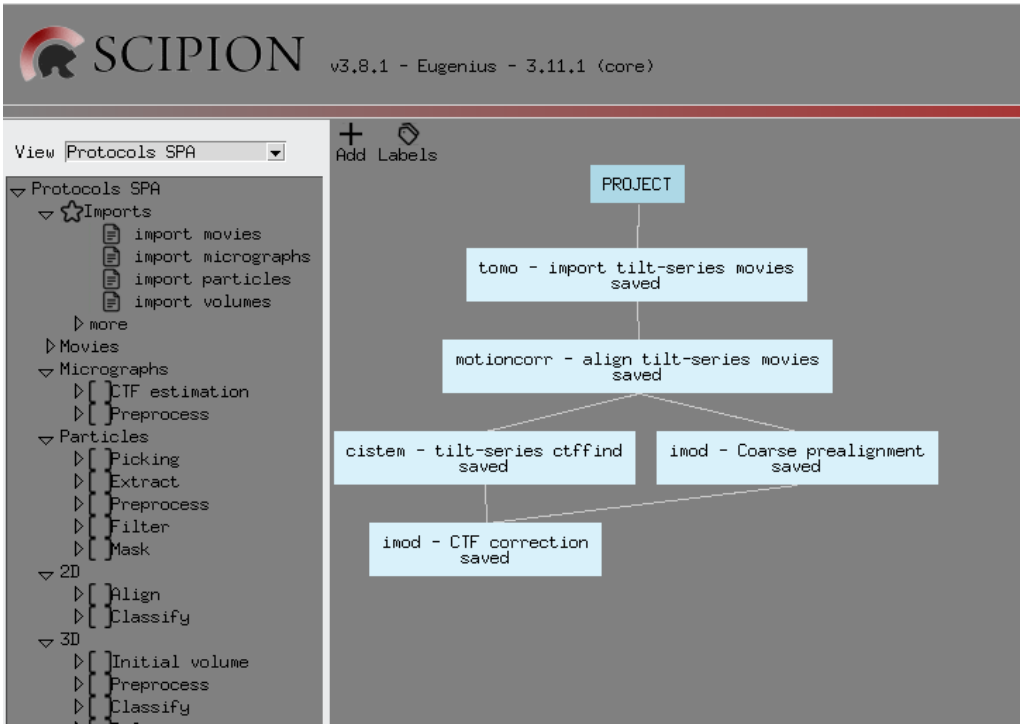
II. Preprocessing with Scipion

Launch scipion. Create your project in the location of your choice. **Make sure you take note of this exact path, you will need it for later**. Once the new project is open, import the quick_tomo workflow_quick_tomo_04082025.json by going into on Project → Import workflow

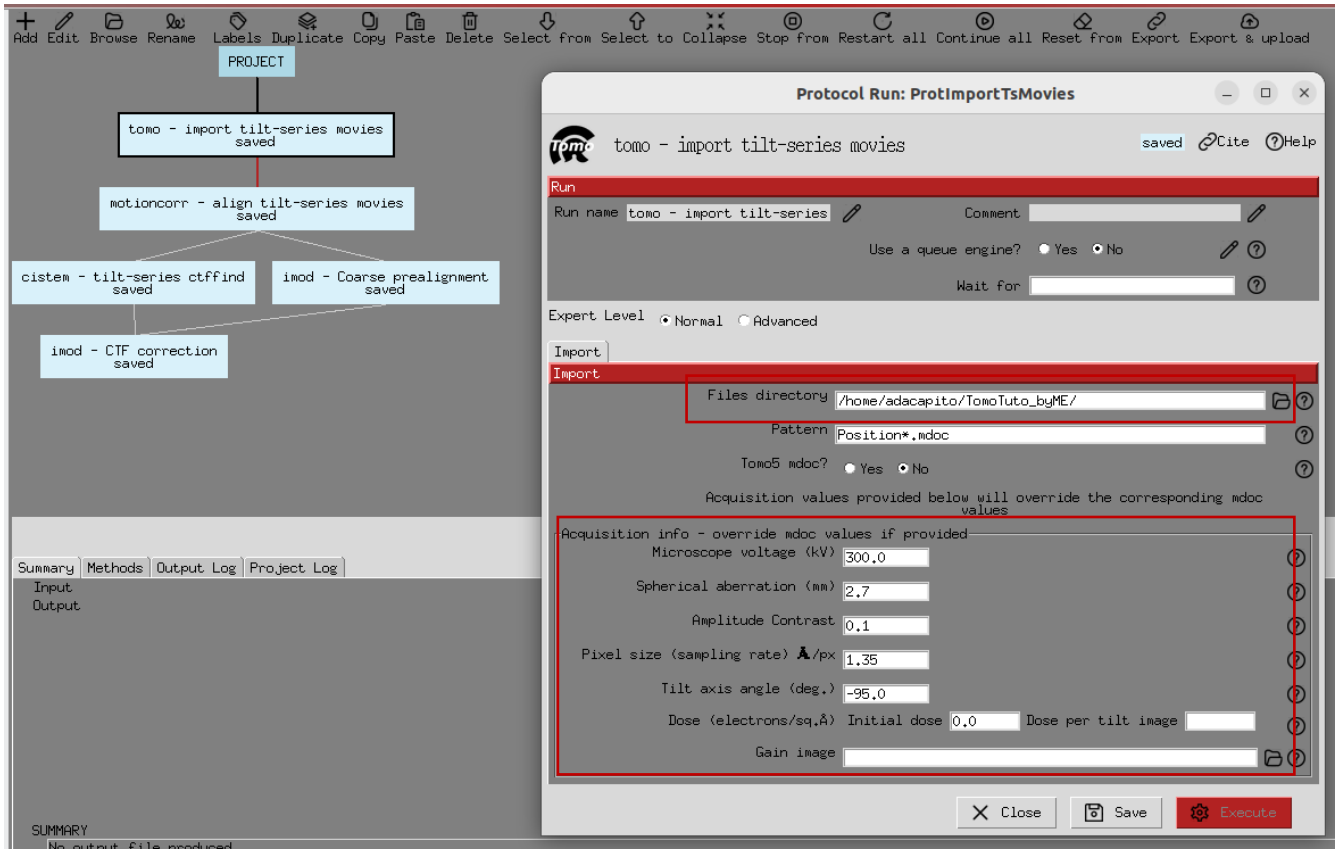




If the workflow is imported correctly, you have the preprocessing tree ready.



Double click on tomo-import tilt-series and wait, this can take few seconds to open.



Now let's fill in a bunch of info:

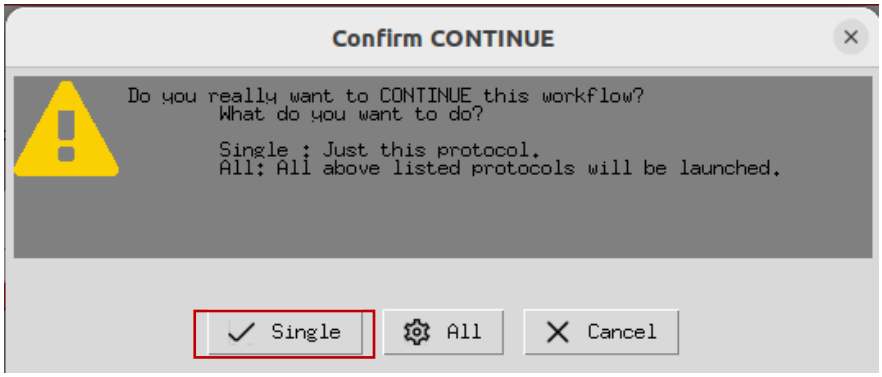
- location of your raw data (tiffs and mdocs should be in the same directory).
- Voltage
- Pixel size
- Tilt axis angle (specific to the microscope, ask your local contact for this info), but usually -95.0 works
- Gain ref (.gain file given by your local contact)

All parameters you leave empty will be filled up based on the mdoc metadata. It is good practice to fill up all the parameters that you know to avoid errors that could be present in the mdoc files.

IMPORTANT : always tick NO to "Tomo5 mdoc?"

Once everything is filled up, hit Execute.

Always click on Single when the following window opens:

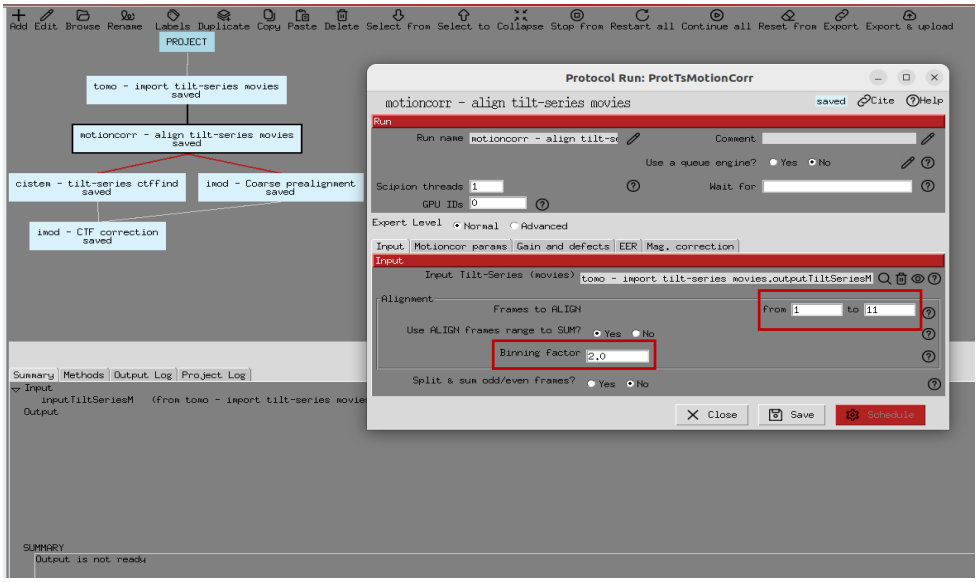


When it's done the job will appear in green. You can refresh the screen sometimes (button at the top right of the Scipion screen).

Now, let's start motion correction.

Open the job by double clicking on motiocorr.

Leave the binning factor on 2, it is good practice in tomography to bin by two at this step as we don't need (and will not reach here) high resolutions.

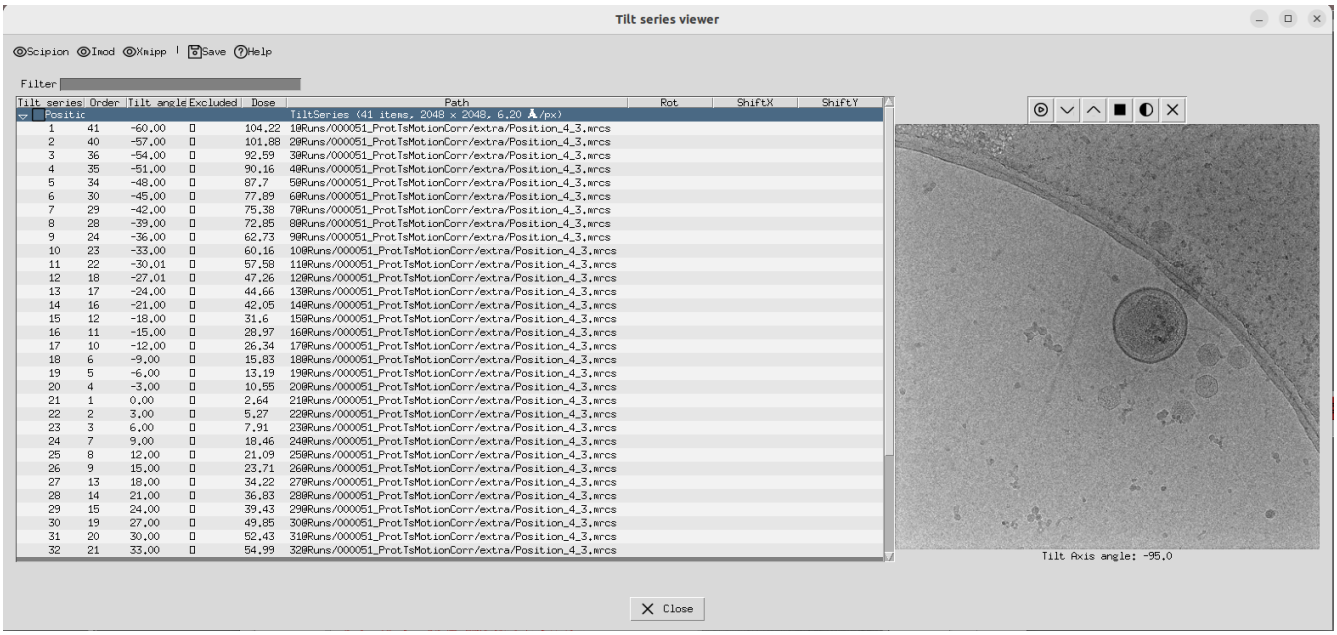


Change Frames to ALIGN from 1 to 0 for the program to take into account all the frames.

Execute. This process takes time.

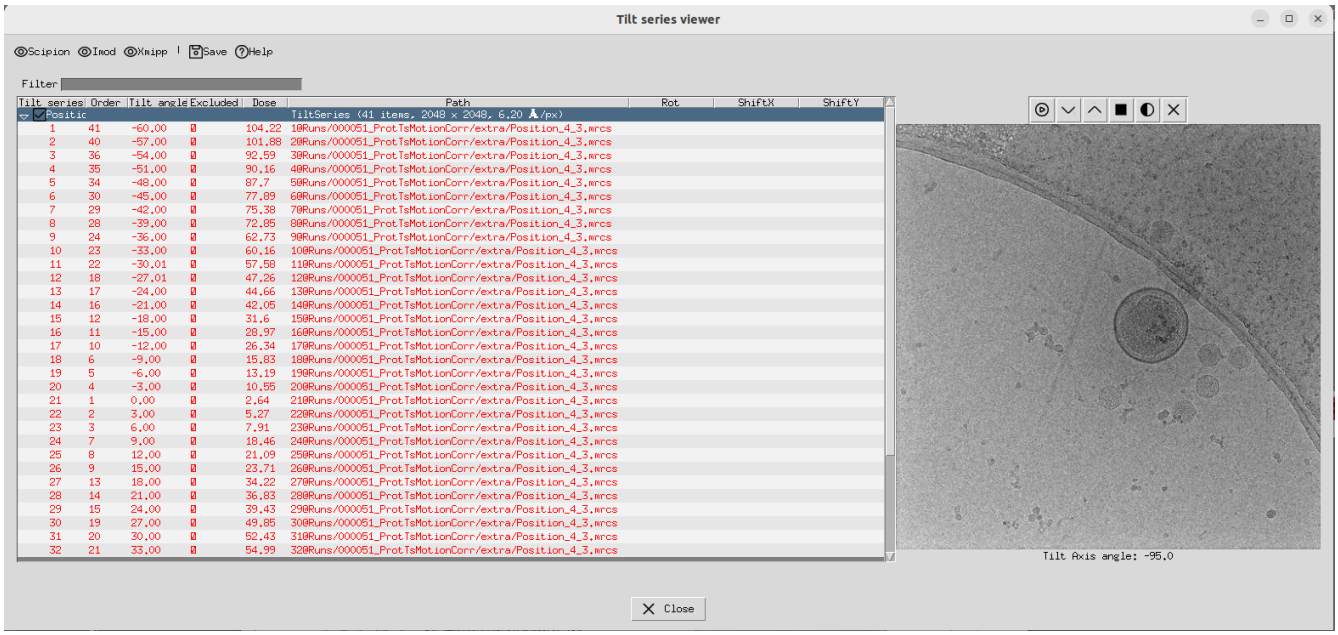
When it's done (blue panel becomes green) it's time for manually checking for bad tilt series and dark images. This step is crucial for quality tomography image processing and should not be skipped for any reason, look at your data it's beautiful.

Click on Analyze Results (middle right of the main screen).
A window opens, click on the eye icon after "Display full frame aligned tilt series". This leads you to this screen:

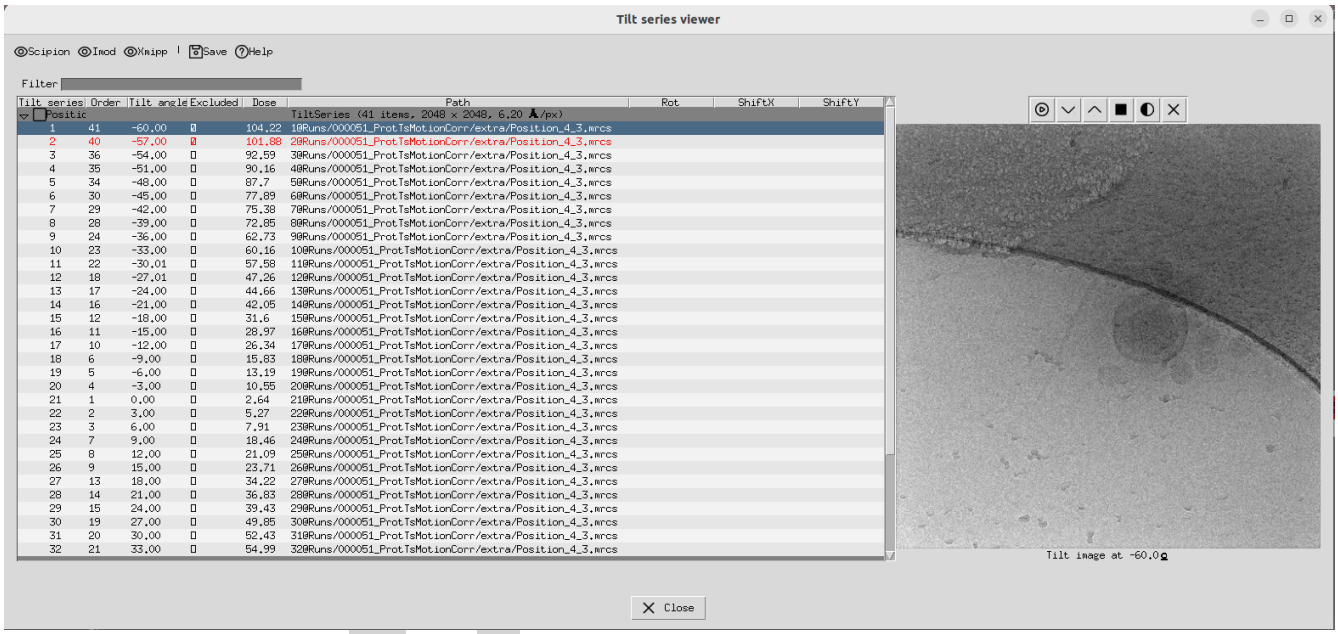


There you can check every position and every frame in it. Good practice is to exclude single tilts that are abnormally shifted as well as dark images, as this will help for automated alignment of the tilts.

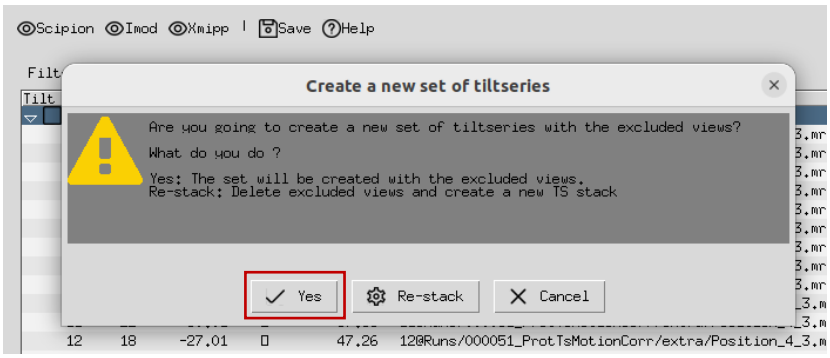
To exclude a full tomogram tick in the box near the position:



To exclude one frame or more tick the “Excluded” box:



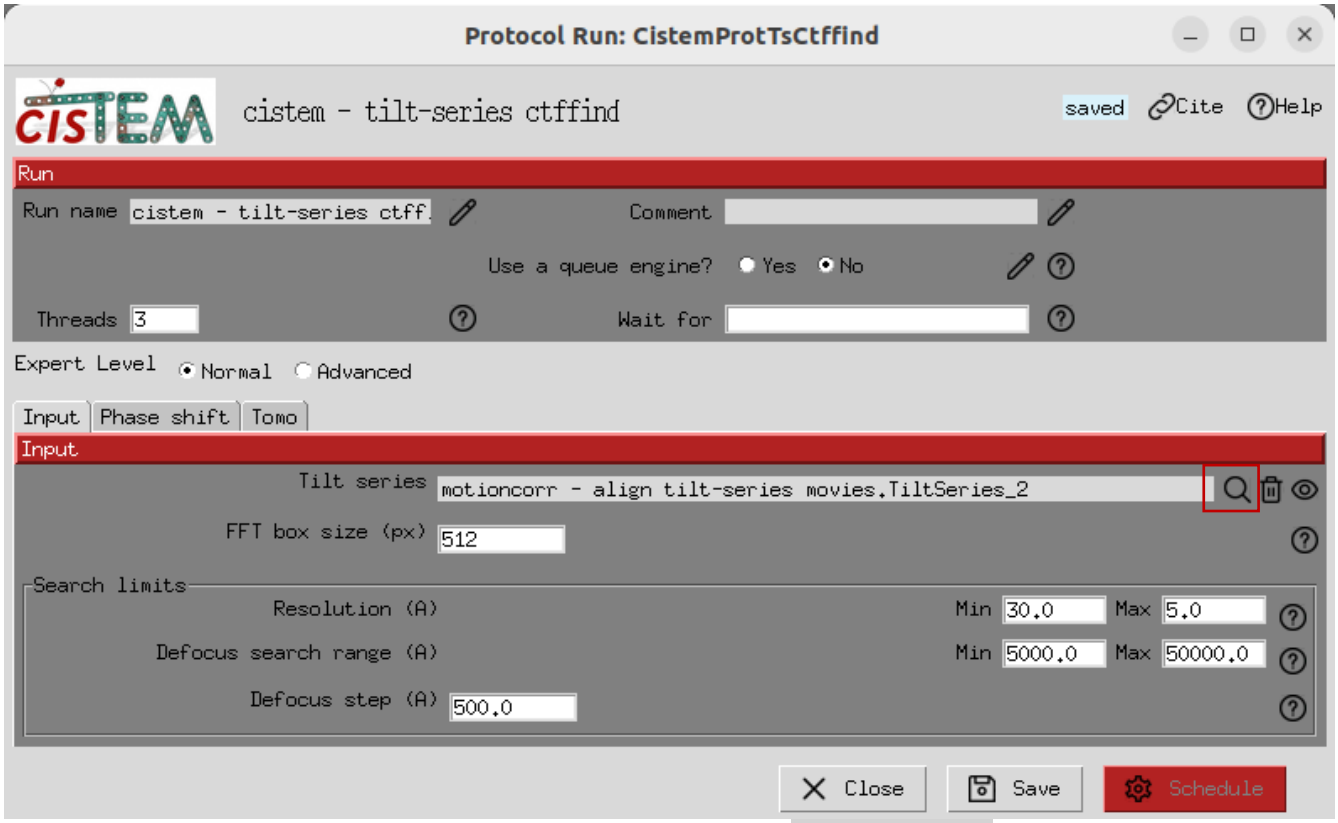
When you are done, click on Save, then Yes.



At this point, be sure you have a message in red saying the files are being written one by one, then close both windows. This will save a second set of tilt series that is called TiltSeries_2. Check in the log that

this set was created and has indeed the number of tilt series that you expect. This can take a few minutes depending on your system.

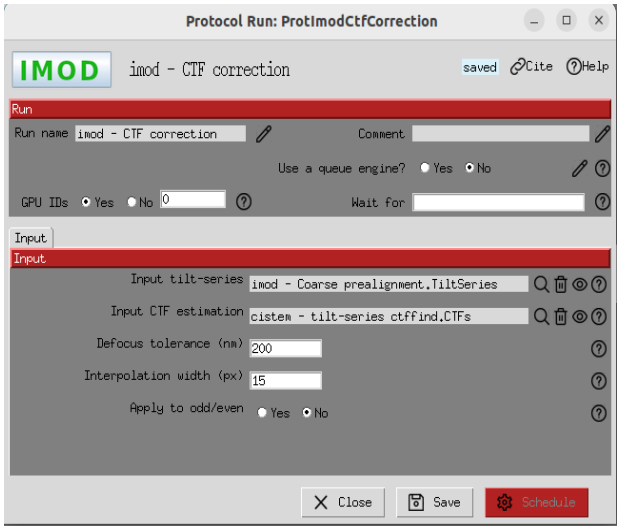
Double click on cistem-tilt-series-ctffind:



Make sure that the TiltSeries_2 series file exists by clicking on the magnifying glass.
Execute.

Double click on imod-Coarse prealignment and leave everything as it is and Execute. This step will pre-align your tilt series. This is a non-mandatory step that could be skipped but usually improves a lot the final result.

When the two last jobs are complete, run the last one: imod-CTF correction.



Execute without changing the presets unless you have good reasons for it.

When everything is green, your data is done preprocessing and you are ready to run quick_tomo !

III. Reconstruction of the tomograms with Quick_tomo

On a terminal go to your quick_tomo location and launch the quick_tomo script.

Newer features include:

- Choice of the binning factor
- Create odd/even half tomograms in order to train your favorite denoising software

```
cd ~/quick_tomo
./ quick_tomo_v0.2.2.sh
```

The scrip is going to need:

- Your data path (the path to your Scipion project that that you have of course saved from before)
- Your chosen output directory
- You binning factor
- If you want half tomograms

The script is going to work its magic. For each tomogram the script shows you the path it found the data in and what it is doing.
A wheel for elapsed time runs, on my system (NVIDIA GeForce RTX 2070 super) reconstruction of one single tomogram takes approximately 2min.

For the nerds out there, this is basically what quick_tomo does:

- It fetches ctfcorrected tilt series from Scipion and runs AreTomo (v1.3.4) with the following arguments (the famous secret sauce)

-AlignZ 250 *# AlignZ is critical, for me 250 works on everything*
-VolZ 1400 *# VolZ is the z size of your tomo. It can be adjusted by changing the code if needed*
-FlipVol 1 *# to have tomos in the right orientation*
-Wbp 1 *# because I hate how SART reconstruction look like (and you should too)*
-DarkTol 0 *# because you have already removed all dark images, of course you did!*

Once it's finished, check your tomograms with your favorite software.
If you don't know where to start we recommend **3dmod** (if you are new, you can start here https://bio3d.colorado.edu/imod/doc/3dmodguide.html), but other software as **Napari** (get the BLIK plugin for tomography data handling https://napari-hub.org/plugins/blik.html) or **bshow** work as well.

Here you go, enjoy your tomograms!

IV. Conclusion and contact

Thanks for reading and using quick_tomo.

If you have any issue or comment with this tutorial or the workflow itself or if you want to suggest new features, please contact me at adacapito@ibs.fr .