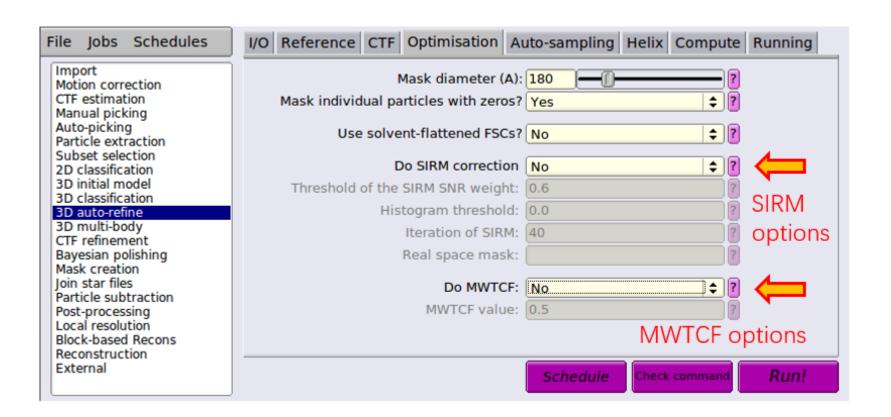
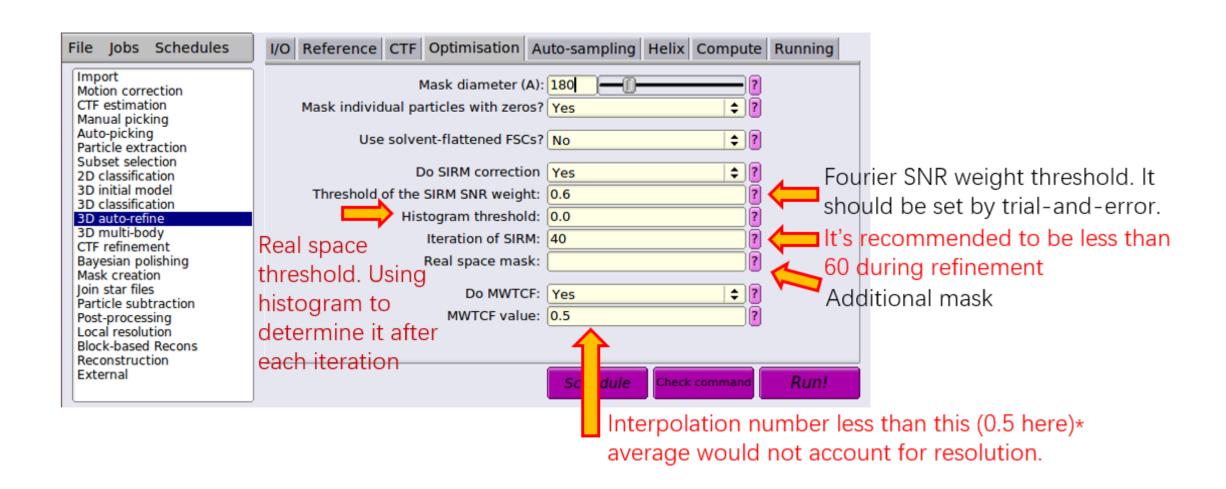
https://github.com/homurachan/SIRM\_RELION

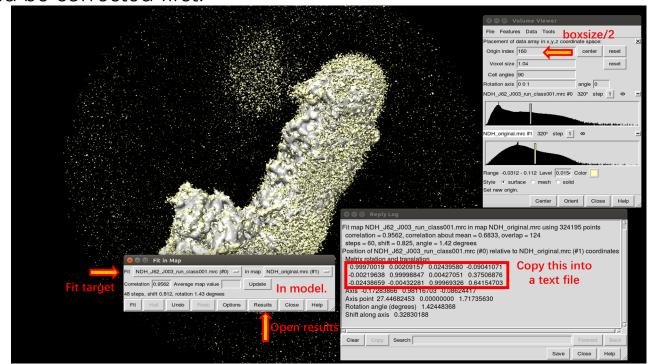
1. Triggering SIRM correction during 3D auto-refine



## 1. Triggering SIRM correction during 3D auto-refine



- 2. Validation, Compare the results between RELION and CryoSPARC
- 1. Convert the cryoSPARC .cs file into the RELION .star file. Recommend to use the csparc2star.py from pyem package.
- I suggest to use `relion\_star\_handler --i input.star --o output.star` that convert the output star into RELION 3.1ver
- 2、Refine utilizing SIRM-RELION
- 3. Normally, the reconstructions between cryosparc and relion would have a small rotation difference. Should be corrected first.



Use "Validation\_preprocess\_read\_relion\_star\_rotate\_accordingto\_chimera\_fitting.py" to correct.

More details: https://github.com/homurachan/Block-based-recontruction/wiki/How-to-fit-block-into-original-map

```
E:\>type J003.txt
                          0.02439808 -0.09048470
 0.00218999
              0.99998850
                          0.00426617
                                        0.37514684
-0.02438890
            -0.00431832
                           0.99969322
                                        0.64161460
E:\>python ./read_relion_star_rotate_accordingto_chimera_fitting.py
<input star> <chimera txt> <pixel size> <output star> <output INT translation txt>
E:\>python ./read_relion_star_rotate_accordingto_chimera_fitting.py J003.star J003.txt 1.04 J003_fit.star INT.txt
Is relion3.0? = 0
              0.00208527 0.02439808]
              0.9999885
             -0.00431832 0.9996932211
```

#### 4. Validation

We only need to correct the starfile that you want to use for SIRM correction. Let's call it relion\_rotted.star. The results from cryoSPARC named cs\_refine.star. Run the 'Validation\_compare\_cryoSPARC\_and\_relion.py' script.

python Validation\_compare\_cryoSPARC\_and\_relion.py relion\_rotted.star cs\_refine.star "Angluar threshold" "n for C-n symmetry" "validation\_result.star"

The "angular threshold" is the maximum allowed orientation difference in deg. If larger than this threshold, the particle would be recognized as a bad one and move to the other file.

Normally, the recommended value of "angular threshold" is 2~3 for small proteins. It can also be inferred from the reported angle accuracy from RELION. Multiply that value by ~3 is generally good, but you should always try before actually use.

The "n for C-n symmetry" is designed to expand the asymmetric unit into the whole sphere. I found that even applied symmetry, sometimes the starfile from cryoSPARC is the whole sphere, which caused problems for calculation. Please check the orientational distribution graph from cryoSPARC.

#### 4. Validation

```
72
           for i in range(mline,len(instar line)):
73
               if(instar line[i].split()):
                   imagename=str(instar line[i].split()[IMG index])
74
75
                   image serial=int(imagename.split('@')[0])
76
                   image filename tmp=cryosparc filename (imagename)
77
                   image filename=""
78
                   cryosparc2relion serial.append([])
                   cryosparc2relion imagename.append([])
79
                   cryosparc2relion line.append([])
81
                   for mm in range(0,len(image filename tmp)):
                       image filename+=image filename tmp[mm]
82
83
                       image filename+=" "
                   cryosparc2relion serial[len(cryosparc2relion serial)-1]=image serial
84
                   cryosparc2relion imagename[len(cryosparc2relion imagename)-1]=image filename
                   cryosparc2relion line[len(cryosparc2relion line)-1]=i
86
87
           print("Finish reading part1")
89
           orirelion serial=[]
           orirelion imagename=[]
90
           orirelion line=[]
91
           for i in range(mline2,len(oristar line)):
92
               if(oristar line[i].split()):
93
94
                   imagename=str(oristar line[i].split()[ori IMG index])
                   image filename tmp=cryosparc filename (imagename)
95
                   image serial=int(imagename.split('@')[0])
96
```

It should be noted that these two "cryoSPARC\_filename" at Validation\_compare\_cryoSPARC\_and\_relion.py need to be assessed before use.

If your rlnImageName is cryoSPARC like, which includes random serial at the front of the filename, use the cryoSPARC\_filename function. Otherwise use the relion\_filename function instead.

## 4. Validation

The outputs are three files. "validation\_result.star" stores the angular changes of each particles. It IS NOT the actual star.

validation\_result.star\_lessthan\_"threshold"\_change\_line.star is the validation picked results. The orientation information is from the FIRST input star of the script. So if you want to keep the results from cryoSPARC, put that cs\_refine.star at the front. However, in our tests, the results from SIRM-RELION are generally better.

The other file: validation\_result.star\_largerthan\_"threshold"\_change\_line.star stores the dropped particles.

## Summary:

- 1. Refine the same dataset with cryoSPARC and RELION
- 2. Fix the rotation difference between two software
- 3. Set an angular threshold. It removes the particles whose angular changes are larger.

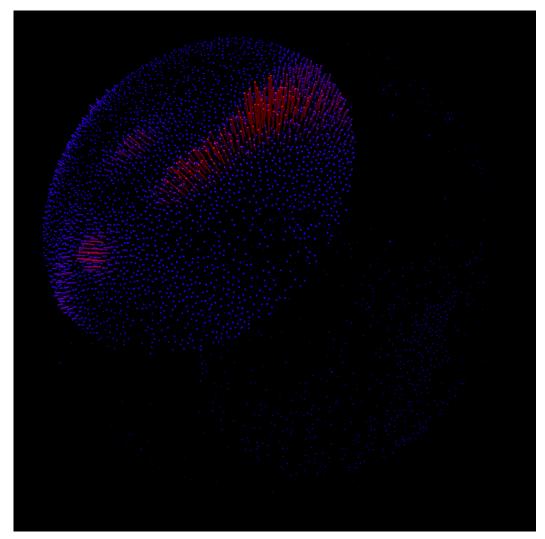
The Mask-Picking process is normally performed AFTER the Validation process. Assuming we choose "validation\_result.star\_lessthan\_"threshold"\_change\_line.star".

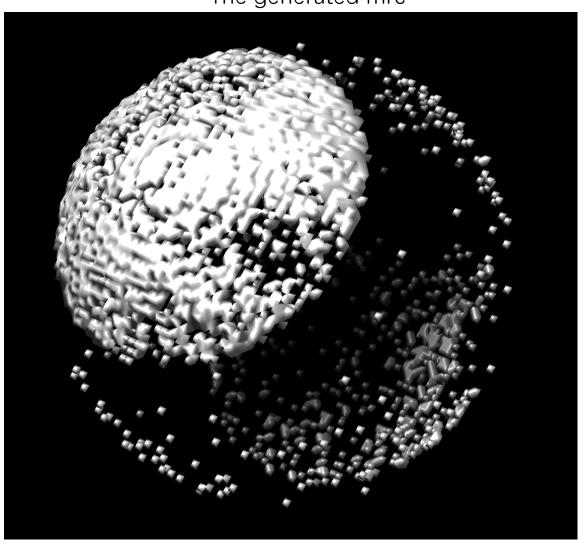
- 1、utilize `relion\_star\_handler` from SIRM-RELION to generate BILD from this star. `relion\_star\_handler --i validation\_result.star\_lessthan\_"threshold"\_change\_line.star --o test.bild --write\_bild`. It can be followed by --bild\_angle\_step and --bild\_radius which are shown on the "Write bild options".
- 2. Use the MaskPicking\_step1\_read\_relion\_bild\_produce\_mrc.py to generate 3D mrc from the BILD file. Require to install numpy and mrcfile.

`python MaskPicking\_step1\_read\_relion\_bild\_produce\_mrc.py test.bild 0.9375 "mrc\_radius" test.bild.mrc

The "mrc\_radius" in in pixel and should not be larger than 80, or the next few steps would be painfully slow.

The BILD The generated mrc

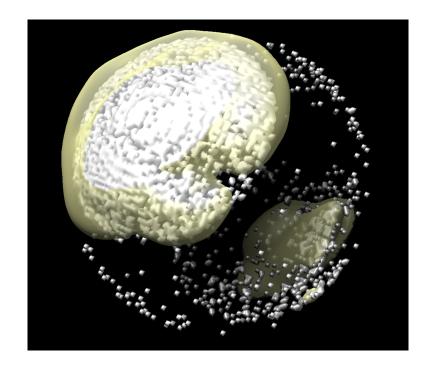




It's very clear that our 3D mrc needs smoothness. A very easy way is to lowpass. I recommend to use proc3d from EMAN package.

`proc3d test.bild.mrc test.bild\_lp.mrc apix=0.5 lp=5`

The apix is not to be used later. It only marks that the map is low-pass to 1/5 of the Nyquist frequency.



After low-pass, pick a good threshold and erase the area that you don't want. Generate mask by using relion\_mask\_create.

Next step is to generate an Euler angle table to select particles. In all, all particles whose orientation stay outside of the mask will be removed.

Generate an Euler angle table.

Please use SIRM-RELION v1.1. The command is:

`relion\_image\_handler --i test\_lp\_erased\_mask.mrc --o nouse.mrc --gen\_MP\_table --MP\_table out\_anglelist.star --MP\_stepsize "angle\_step"`

The angle\_step is the stepsize between sampling point. Normally the default value is enough.

Check the info on the relion\_image\_handler

```
------ additional subtract options ----

--optimise_scale_subtract (false) : Optimise scale between maps before subtraction?
--optimise_bfactor_subtract (0.) : Search range for relative B-factor for subtraction (in A^2)
--mask_optimise_subtract () : Use only voxels in this mask to optimise scale for subtraction
--mask_optimise_subtract () : Use only voxels in this mask to optimise scale for subtraction
--SIRM parameter. Not recommended for initial refine, except for local refinement. ---
--SIRM (false) : Perform SIRM reconstruction
--sIRM (false) : Perform SIRM reconstruction
--thres_SIRM (0.3) : SIRM threshold in Fourier space
--Hist_cutoff (0.0) : cut-off of real space restrain
--thres_hist (0.0) : SIRM, histgram threshold in real space
--iter_SIRM (30) : Number of iteraion of SIRM
--SIRM_snr_weight () : SNR weight file in RFLOAT
--max_radius_SIRM (100.0) : SIRM, histgram threshold in real space
--gen_MP_table (false) : Read_MRC file and generate Mask-Picking table. Use together with --MP_table and --MP_stepsize
--MP_table () : Output name of Mask-Picking table.
```

Dropping particles using the Euler angle table.

Please use SIRM-RELION v1.1. The command is:

relion\_star\_handler --i validation\_result.star\_lessthan\_"threshold"\_change\_line.star --o maskpick\_result.star --MP\_write\_particles --MP\_table out\_anglelist.star --MP\_stepsize angle\_step"

Check the info on the relion\_star\_handler

# Summery:

- 1. After validation, convert starfile to BILD and 3D mrc.
- 2. Low-pass the mrc and erase the area that you don't want to use.
- 3. Generate angle table and select particles. Note: Use relion\_star\_handler to handle starfile. Use relion\_image\_handler to handler mrcfile.

It should be noted that the SNR weight was automatically generated during auto-refine. However, there is no such procedure during reconstruction. So we have to generate a FSC weighting file.

Perform relion\_postprocess, then use the script convert\_star\_2\_SIRM\_weight.py.

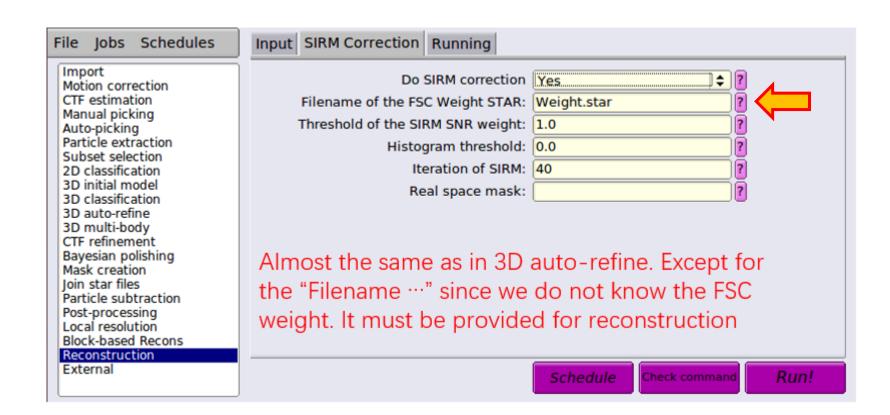
`python convert\_star\_2\_SIRM\_weight.py postprocess.star weight.star`

to generate the FSC weight.

Then use SIRM-RELION GUI.

File Jobs Schedules	Input SIRM Correction Running
Import Motion correction	Input particles:     Prowse
CTF estimation Manual picking	Symmetry of particles: C1
Auto-picking Particle extraction Subset selection	Maxres in Angstrom: -1
2D classification 3D initial model	Padding factor: 2
3D classification 3D auto-refine	Random subset: -1
3D multi-body CTF refinement Bayesian polishing	Do CTF correction Yes 💠 ?
Mask creation Join star files Particle subtraction Post-processing Local resolution Block-based Recons Reconstruction	Reconstruction dialog. Maxres limits the Fourier's distance, -1 means using full space.
External	Schedule Check command Run!

From our experience, Separately perform SIRM to the odd/even half could potentially leading to FSC raising problem beyond resolution. As a result, we alternatively to choose reconstructing all the particles, and applying FSC weight, b-factor sharpening and low-pass filter manually.



After the reconstruction, use the relion\_image\_handler from SIRM-RELION to apply the filters.

```
------- Post-process like b-factor and FSC weighting. Should be used together with --angpix ------
--postprocess (false): Do postprocess for single map.
--post_fsc (): FSC to be applied.
---lp (-1): Low-passed frequency
---bf (0.): B-factor to be applied
```

#### The command is:

`relion\_image\_handler --i reconstrct\_SIRM\_full.mrc -o reconstrct\_SIRM\_full\_lp3p6\_bfM60.mrc --angpix 1.42 --postprocess --post\_fsc weight.star --lp 3.6 --bf -60`

The post\_fsc is the exact FSC from the "convert\_star\_2\_SIRM\_weight.py".