第1步. 使用 relion 估算 micrographs 的 CTF 参数, 生成 micrograph ctf.star

**Step 1.** Estimate CTF parameters for micrographs by RELION and generate *micrograph ctf.star*.

- 第2步. 将 star 文件转换为 GisSPA 可读的 lst 文件
- **Step 2.** Convert .star files to GisSPA-readable .lst files

relion2lst\_dont\_write\_mics.py CtfFind/job005/micrographs\_ctf.star --lst micrographs\_ctf.lst

第3步. 为了节约计算时间,可以先对图进行压缩,根据像素大小可以选择 bin2

或者 bin4

**Step 3.** To improve computation efficiency, you can first compress the micrograph, and depending on the pixel size you can choose bin2 or bin4

```
cd MotionCorr/job003/micrographs/
```

# mkdir ms2

```
foreach file(*.mrc)
e2proc2d.py $file ms2/$file --meanshrink=2
end
```

or

```
foreach file (*.mrc)
relion_image_handler -- i $file -- o ms2/$file -- angpix 1.36 -- rescale_angpix 2.72
end
```

替换 micrograph ctf.lst 的内容:

Replace the path of micrograph:

# sed -i 's/micrographs/ms2Vmicrographs/g' micrographs\_ctf.lst

第4步. 将三维模型 rescale 成与 micrograph ctf.lst 相同的像素大小

**Step 4.** Rescale the 3D template to the same pixel size to the binned pixel size

relion\_image\_handler --i 3D\_template.mrc --o 3D\_template\_rescaled.mrc --angpix ?? --rescale\_angpix 2.72

## 第5步. 生成二维投影

Step 5. Generate 2D projections.

### project3d 3D\_template\_rescaled.mrc out=2D\_projections.hdf list=euler\_C1\_step5.lst

project3d 是 EMAN 软件包的一个用于创建二维投影的程序,下载 EMAN 即可使用 (<a href="https://blake.bcm.edu/emanwiki/EMAN1">https://blake.bcm.edu/emanwiki/EMAN1</a>)。用于投影的欧拉角文件可在测试数据中下载。

*project3d* is a program for creating 2D projections from the EMAN package, EMAN software package can be downloaded from <a href="https://blake.bcm.edu/emanwiki/EMAN1">https://blake.bcm.edu/emanwiki/EMAN1</a>. The Euler file can be downloaded from the test Data dir.

**第6步.** 写 config 文件。config 文件可在测试数据中下载,里面包含一些固定参数和可调参数

**Step 6.** Write config file, including some optional parameters.

```
= micrographs_ctf.lst
input
template
                 = 2D projections.hdf
                 = euler C1 step5.lst
eulerfile
                 = 2.72
angpix
phistep
                 = 3
                 = 3
kk
                   300
energy
                   2.7
CS
Highres
                 = 400
Lowres
diameter
                 = 160
norm_type
                 = 1
invert
                 = 1
threshold
                 = 6.2
output
                 = Output/test.lst
first
                 = 0
last
window_size
                 = 512
GPU ID
                 = 0
phase_flip
                    1
overlap
                 = 160
```

input = input micrograph lstfile with ctf information template = input 2D projections templates in .hdf format eulerfile = euler file with euler values angpix = input pixel size in angstroms phistep = inplane rotation sampling

kk = overlapping density parameter, default is 3.

energy = accerlerating voltage in kV.

cs = spherical aberration in um.

Highres = high resolution cut

Lowres = low resolution cut

diameter = target diameter in pixels Optional Parameters.

norm\_type = CCG norm optional parameter, 1 for global normalization, 0 for perwindow normalization

invert = whether to invert contrast in micrograph, 1 for yes, 0 for no.

threshold = cc threshold value, only output score beyond this value

output = output lstfile filename

first = the first image id to process.

last = the last image id to process.

window\_size = the window size which is splitted from raw IMG, which must satisfy window size % 32 == 0.

GPU\_ID = ID of GPU device, only support single ID.

phase\_flip = Whether do filtering on images, operation(1) or not(0), in case of input being filtered already).

overlap = size of overlap between different windows.

# 第7步. 运行程序进行颗粒探测

Step 7. Run program and do target detection.

# ~/GisSPA-main/main config

### 第8步. 合并重复探测的颗粒

**Step 8.** Merge duplicated particles

# remove\_repeat\_particles\_from\_list.py Output/test.lst 1 4 8 Output/test\_merge.lst

remove repeat particles from list.py

<input1> <number of images> <center> <euler thres> <output>

<input1> 1st filename generated from target detection

< number of images > the number of micrographs used for detection in this input lst file

<center> the threshold of coordinate (x,y) range used to merge detected targets

<euler thres> the threshold of Euler angle (x,y) range used to merge detected targets

### 第9步. 将合并后的颗粒文件格式转换为 relion 可读的 star 文件

**Step 9.** Convert the merged lst file to the RELION-readable star file

convert my-lst to relion mic.py

<input lstfile> <scale factor> <pixel size> <out star file> <micrographs dir>

<input lstfile> merged lst file

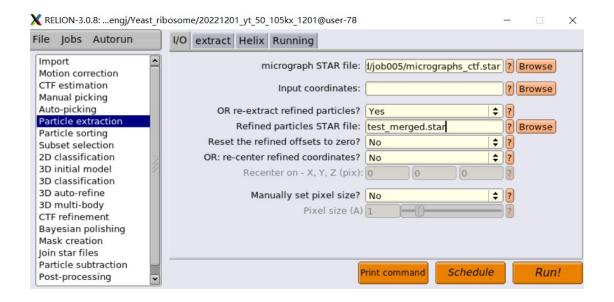
<scale factor> binning factor when target detection, 2 for bin2

<pixel size> the un-binned pixel size of original micrograph

<out star file> filename of output star file

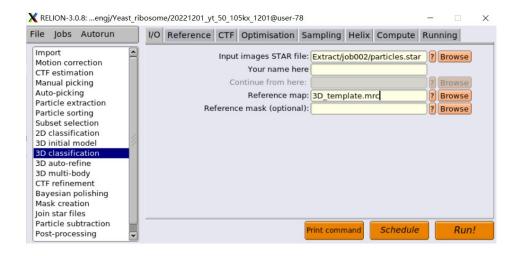
<micrographs dir> the directory of original micrographs.

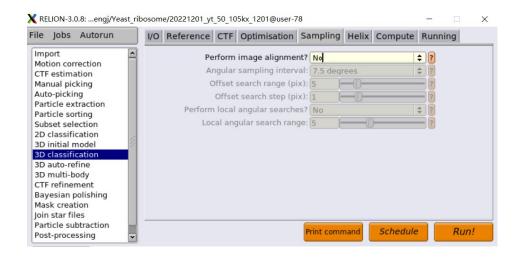
**第 10 步.** 提取颗粒。使用 relion 的 re-extract 功能从 micrograph 中提取颗粒 **Step 10.** Particle extraction by RELION.

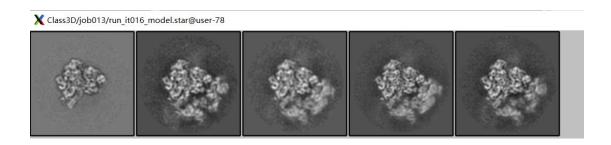


### 第 11 步. 三维分类

Step 11. 3D classification







后续的操作和分析都与单颗粒的优化类似,但是必须是 local refinement,一定不能跑全局 refinement !!!

The subsequent operations and analysis are similar to the single particle analysis, but only local refinement is allowed, never try global refinement !!!

如果需要消除模型偏差,可使用 jalign 计算颗粒与重构之间的相位残差,计算的频率范围为: 低频为 8 埃,高频由重构的分辨率决定。jalign 是 JSPR 软件包的一个程序, JSPR 下载链接为: <a href="https://jiang.bio.purdue.edu/jspr/">https://jiang.bio.purdue.edu/jspr/</a>

In case of model bias, the phase residuals between the particles and the reconstruction can be calculated using jalign for a frequency range of 8Å for low frequency cut and high frequency cut is determined by the resolution of the reconstruction. *jalign* is a program from the JSPR package, the JSPR can be downloaded at: <a href="https://jiang.bio.purdue.edu/jspr/">https://jiang.bio.purdue.edu/jspr/</a>

- (1) 首先将 run\_data.star 转换为 lst 格式的文件, 注意需要将 subset 1 和 subset 2 分开
- (1) First convert run\_data.star to a file in lst format, note that subset 1 and subset 2 need to be separated

```
relion_star_handler --i run_data.star --o run_data_subset1_star --select rlnRandomSubset --minval 0.9 --maxval 1.1
relion_star_handler --i run_data.star --o run_data_subset2.star --select rlnRandomSubset --minval 1.9 --maxval 2.1
relion_2lst_dont_write_particles.py run_data_subset1.star --lst run_data_subset1.lst --boxsize ???
relion_2lst_dont_write_particles.py run_data_subset2.star --lst run_data_subset2.lst --boxsize ???
```

- (2) 计算相位残差
- (2) calculate phase residuals

```
$PATH/jalign run_data_subset2.lst run_class001.mrc out.lst --first $firstparticleID --last $lastparticleID
--apix $pixelsize --aligner refineMicrographDefocus:batchsize=1:defocusrange=0.001:maskradius=$targetradius
:masksoft=-4:precision=0.001:stepdefocus=0.001:useOrigDefocus=1:verbose=1 --cmp phaseResRange:
ampweight=0:ctfampweight=1:lowRes=8:highRes=$resolution:abs=0 --batchsize -1 --force 1
```

- (3) 选择合适的阈值, 保留相关颗粒后重新转回 relion 格式
- (3) Select particles with score above one threshold and re-convert it to star format

delete\_bad\_score.py \$jspr\_scored\_lstfile \$score\_threshold \$output\_filename
jspr\_refine\_2\_relion\_class3d.py \$selected\_particles\_lst \$box\_size \$pixel\_size \$output\_star\_file 0/1 0/1/2