

View Protocols SPA

Protocols SPA

Imports

- import movies
- import micrographs
- import particles
- import volumes

more

Movies

Micrographs

- xmipp3 - preprocess micrographs
- CTF estimation

Particles

- Picking
- Extract
- Preprocess
- Filter
- Mask

2D

- Align
- Classify

- relion - 2D classification
- xmipp3 - cl2d
- eman2 - refine 2D
- eman2 - refine 2D bispec
- cryosparc2 - 2d classification**
- grigoriefflab - frealign classify

more

3D

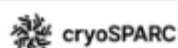
- Initial volume
- Preprocess
- Classify
- Refine
- Postprocess
- Analysis
- Reconstruct

Resolution

Tools

Exports

Model Building



Protocol: cryosparc2 - 2d classification

finished

Cite

Help

Run

Run name cryosparc2 - Cryosparc2D

Comment

Run mode

☒ Continue ☐ Restart

Host localhost

Parallel

Threads

1

MPI

2

Use queue?

☐ Yes

☒ No

Wait for

Input

2D Classification

Compute settings

2D Classification

Number of classes:

16

Maximum resolution (Å)

6

Initial classification uncertainty factor

2.0

Use circular mask on 2D classes?

☒ Yes

☐ No

Re-center 2D classes

☒ Yes

☐ No

Re-center mask threshold

0.2

Re-center mask binary

☐ Yes

☒ No

Force Max over poses/shifts

☒ Yes

☐ No

CTF flip phases only

☐ Yes

☒ No

Number of final full iterations

1

Number of online-EM iterations

20

Batchsize per class

100

2D initial scale

1

2D zeropad factor

2

Use FRC based regularizer

☒ Yes

☐ No

Use full FRC

☒ Yes

☐ No

Iteration to start annealing sigma

2

Number of iteration to anneal sigma

15

Use white noise model

☐ Yes

☒ No

View: Tree

Refresh

xmipp3 - deep micrograph clean finished

xmipp3 - extract particles sma finished

xmipp3 - screen particles finished

subset_Z_SSNR_Var finished

cryosparc2 - Cryosparc2D finished

cryosparc2 - initial model finished

xmipp3 - crop/resize volumes finished

Analyze Results

ms, 74 x 74, 1.98 Å/px)

6 items)

Close

Save

Execute