

View Protocols SPA

- import particles
- import volumes

more

Micrographs

- xmipp3 - preprocess micrographs
- CTF estimation

Particles

2D

3D

- Initial volume
- Preprocess
- Classify
 - reion - 3D classification
 - grigoriefflab - frealign classify
- Refine
 - reion - 3D auto-refine
 - reion - particle polishing
 - xmipp3 - highres
 - xmipp3 - projection matching
 - eman2 - refine easy
 - cryosparc2 - 3D homogeneous refinement
 - cryosparc2 - 3D non-uniform refinement

more

- cryosparc2 - subtract projection
- cryosparc2 - Local refinement

Postprocess

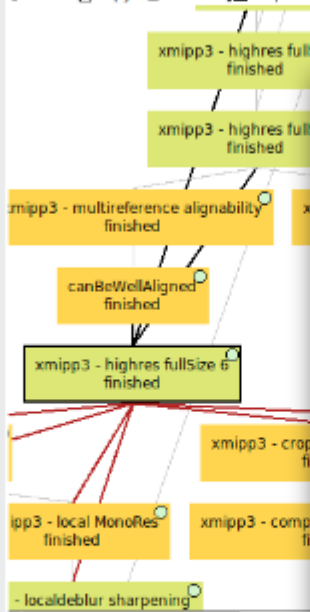
- xmipp3 - localdeblur sharpening

Analysis

Heterogeneity

- xmipp3 - solid angles
- xmipp3 - split volume
- xmipp3 - structure mapping
- xmipp3 - calculate strain
- xmipp3 - normalize strain

Edit Copy Delete Steps Browse Db Collapse Labels



Summary Methods Output Log

Input

inputParticles (from canBeWellAligned -> outputParticles [outputParticles])
 inputVolumes (from xmipp3 - highres 2 -> outputVolume [outputVolume])
 continueRun (from xmipp3 - highres fullSize 5)

Output

xmipp3 - highres fullSize 6 -> outputVolume
 xmipp3 - highres fullSize 6 -> outputParticles

Protocol Run: XmippProtReconstructHighRes



Protocol: xmipp3 - highres

finished

Cite ? Help

Run

Run name xmipp3 - highres fullSize 6 Comment
 Run mode ☒ Continue ☐ Restart Host localhost
 Parallel Threads 1 MPI 8 Use queue? ☐ Yes ☒ No
 GPU IDs ☐ Yes ☒ No 0 Wait for

Expert Level ☒ Normal ☐ Advanced

Input Next Reference Angular assignment Weights Post-processing

Input

Continue from a previous run? ☒ Yes ☐ No

Full-size Images canBeWellAligned.outputParticles

Select previous run xmipp3 - highres fullSize 5

Symmetry group 0

Close

Save

Execute

SetOfParticles (3485 items, 450 x 450, 0.49 Å/px)
 Volume (74 x 74 x 74, 1.98 Å/px)
 xmipp3 - highres fullSize 5

Volume (297 x 297 x 297, 0.75 Å/px)
 SetOfParticles (3485 items, 450 x 450, 0.49 Å/px)