

View Protocols SPA

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Summary Methods Output Log

Input

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

Output

xmipp3 - multireference alignability -> outputParticles
xmipp3 - multireference alignability -> outputVolumes

Protocol Run: XmippProtMultiRefAlignability

mipp Protocol: xmipp3 - multireference alignability finished Cite ? Help

Run

Run name xmipp3 - multireference alignability Comment

Run mode ☒ Continue ☐ Restart ? Host localhost

Parallel Threads 1 MPI 16 ? Use queue? ☐ Yes ☒ No ?

Wait for

Expert Level ☒ Normal ☐ Advanced

Input Preprocess

Input

Input volume xmipp3 - highres fullSize 5.outputVolume ? ? ?

Input particles xmipp3 - highres fullSize 5.outputParticles ? ? ?

Symmetry group a ?

Close Save Execute

- cryosparc2 - Local refinement
- Postprocess
- xmipp3 - localdeblur sharpening
- Analysis
- Heterogeneity
 - xmipp3 - solid angles
 - xmipp3 - split volume
 - xmipp3 - structure mapping
 - xmipp3 - calculate strain
 - xmipp3 - normalize strain
 - xmipp3 - nma alignment
 - xmipp3 - nma dimred
 - xmipp3 - cltomo
- Validation
 - xmipp3 - compare reprojections
 - xmipp3 - create gallery
 - xmipp3 - validate_nontilt
 - xmipp3 - multireference alignability**
 - xmipp3 - validate overfitting
 - eman2 - tilt validate
- Resolution
 - xmipp3 - local MonoRes
 - xmipp3 - local deepRes
 - xmipp3 - resolution 3D
 - xmipp3 - multiple fscs
 - xmipp3 - local MonoTomo
 - xmipp3 - directional resolution Mono
 - bsoft - bfilter
 - resmap - local resolution
 - atsas - convert PDB to SAXS curve
- more
 - xmipp3 - subtract projection
 - xmipp3 - convert to pseudoatoms
 - atsas - convert PDB to SAXS curve

Volume (297 x 297 x 297, 0.75 Å/px)
SetOfParticles (4505 items, 450 x 450, 0.49 Å/px)
SetOfParticles (4505 items, 450 x 450, 0.49 Å/px)
SetOfVolumes (1 items, 297 x 297 x 297, 0.75 Å/px)