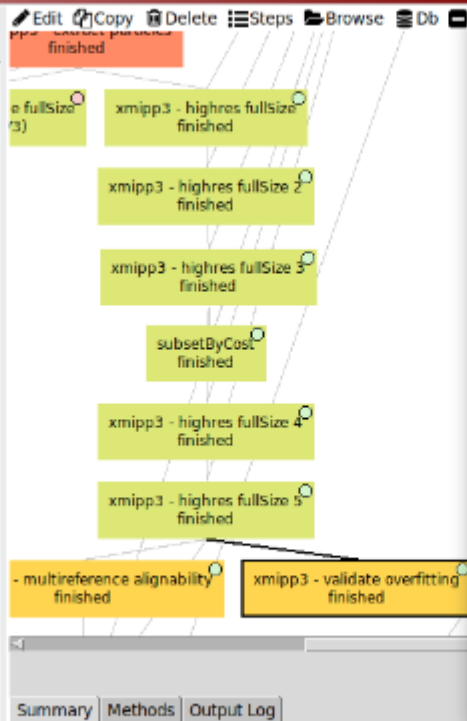


View Protocols SPA

- 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 - cftomo
  - 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



Protocol Run: XmippProtValidateOverfitting

Protocol: xmipp3 - validate overfitting finished Cite Help

Run

Run name xmipp3 - validate overfitting Comment

Run mode ☒ Continue ☐ Restart ? Host localhost

Parallel Threads 1 MPI 32 ? Use queue? ☐ Yes ☒ No ?

GPU IDs ☐ Yes ☒ No 0 ? Wait for

Expert Level ☒ Normal ☐ Advanced

Input

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

Resize input particles and volume? ☒ Yes ☐ No ?

New size (px) 297.0 ?

Calculate the noise bound for resolution? ☒ Yes ☐ No ?

Initial 3D reference volume xmipp3 - highres fullSize 5.outputVolume ? ? ?

Symmetry group 0 ?

Close Save Execute

Input

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

input3DReference (from xmipp3 - highres fullSize 5 -> outputVolume [outputVolume])

SetOfParticles (4505 items, 450 x 450, 0.49 Å/px)

Volume (297 x 297 x 297, 0.75 Å/px)