

View Protocols SPA

Protocols SPA

Imports

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

more

Movies

- xmipp3 - correlation alignment
- xmipp3 - optical alignment
- xmipp3 - movie maxshift
- xmipp3 - movie average
- xmipp3 - movie gain

Micrographs

- xmipp3 - preprocess micrographs
- CTF estimation

Particles

- Picking
- Extract
- Preprocess
  - relicion - preprocess particles
  - xmipp3 - crop/resize particles
  - xmipp3 - ctf\_correct\_wiener2d
  - xmipp3 - preprocess particles

Filter

Mask

2D

- Align
- Classify

3D

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

### Protocol Run: XmippProtMovieCorr

**Protocol: xmipp3 - correlation alignment**
finished
Cite
Help

#### Run

**Run name** xmipp3 - correlation alignment edit
**Comment** edit

**Run mode** ☒ Continue ☐ Restart ?
**Host** localhost

**Parallel** ☒ Threads ☐ MPI  ?
**Use queue?** ☐ Yes ☒ No ?

**GPU IDs** ☒ Yes ☐ No  ?
**Wait for**  ?

**Expert Level** ☒ Normal ☐ Advanced

#### Input

**Input Movies** xmipp3 - movie gain rawGain.outputMovies search trash eye ?

**Alignment**

**Frames to ALIGN** from  to  ?

**Use ALIGN frames range to SUM?** ☒ Yes ☐ No ?

**Binning factor**  ?

**Crop offsets (px)** X  Y  ?

**Crop dimensions (px)** X  Y  ?

**Filter at (A)**  ?

**Compute PSD (before/after)?** ☒ Yes ☐ No ?

**Local alignment**

**Compute local alignment?** ☒ Yes ☐ No ?

Close

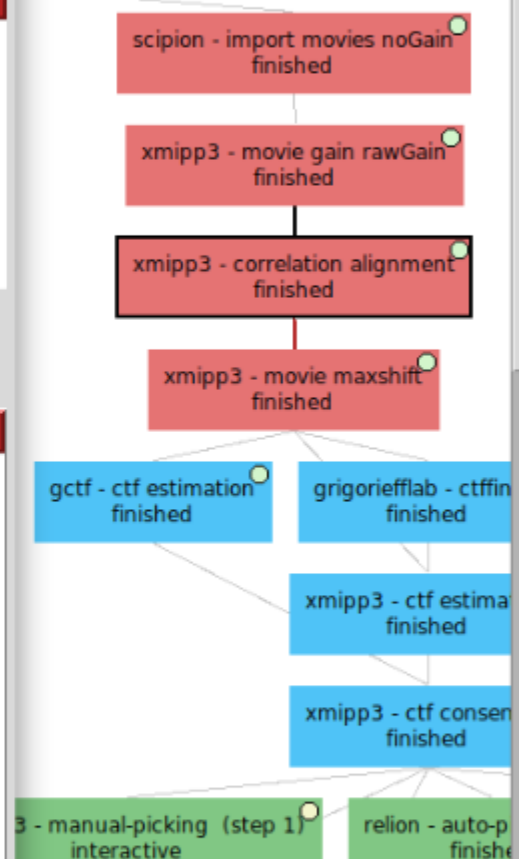
Save

Execute

Output

- xmipp3 - correlation alignment -> outputMovies
- xmipp3 - correlation alignment -> outputMicrographs

View: Tree help refresh



Analyze Results

items, 3710 x 3838 x 50 [1-50], 0.49 Å/px)

SetOfMovies (48 items, 3710 x 3838 x 50 [1-50], 0.49 Å/px)

SetOfMicrographs (48 items, 3710 x 3838, 0.49 Å/px)