

Home > Split stack using select file?

## **Split stack using select file?**

Mon, 04/01/2019 - 05:53

#1

Split stack using select file?

Dear all,

I have completed refinement of a dataset with a large box and used the same particles with smaller box for classification into sub-sets.

Now I have alignment parameters at a large box and want to create a new sub-stack according to the class-results.

How would you accomplish this keeping alignment parameters?

Best, tarek Wed, 04/03/2019 - 14:18

timgrant

Hi Tarek,

Hi Tarek,

Was this done in cisTEM? In which case you can great the new refinement pakackage for the desired class. Then export the parameters from the refined class and then import a new refinement package, selecting your exported parameters, and the stack with the larger box size.

Would that work?

Cheers,

Tim

Wed, 04/03/2019 - 15:45 (Reply to #2)

Hi Tim,

Hi Tim,

thanks for your reply.

It was done with cistem but this way should not work. Particle numbers between the exported parameters file and the stack with larger box will differ.

Let's assume particle no. with large box are 200,000. Selected particles after classification with small box are 20,000.

This 20,000 are of course a fraction of 200,000 but I would have to selectively pick the parameters out of the 200k par file.

Cheers,

timgrant

Hi Tarek,

Hi Tarek,

I'm not sure i understand? When you created your new refinement package with 20,000 particles it should have carried over the parameters. You can then export the parameters of these 20k and then do what I suggest above? Will that not work?

Tim

Thu, 04/04/2019 - 14:34

Hi Tim,

Hi Tim,

the 20,000 particles were from decimated data and only refined at large pixel size.

I need to take over the alignment parameters of the large box 200k stack but only take the 20k particles which were identified using the small box.

The point is: the 20 k particles have too crude alignment parameters at small box. When just exchanging the particles with the large boxed ones, I need to re-align too liberately (interpolation errors...) what will cause even poorer alignment. It's a tricky dataset, few particles, poor signal :(

It would be great to have something similar like "original image name" in the par files that would be as in the imported the star file ;) Thu, 04/04/2019 - 23:16

timgrant

Hi Tarek,

Hi Tarek,

Aaah, I see the problem now. Yes, there is no easy way to do this. You could probably do it through a combination of database queries and scripting, but it would be somewhat complicated.

Tim

Fri, 04/05/2019 - 05:22

thanks for the chat, I will

thanks for the chat, I will have to go the hard way...

Thu, 07/04/2019 - 07:11

**Daniel Asarnow** 

Hey tarek,

Hey tarek,

You can use a few programs from my <u>github</u> (master branch) to accomplish it pretty easily, though with some extra files to track.

- 1. par2star.py Assets/Parameters/output\_N\_\*.par output\_N.star --apix 1.0 --cs 2.7 --kv 200 --ac 0.1 --stack refpkg.mrcs
- 2. star.py --augment --merge-fields=rlnClassNumber -merge-key=ucsfImageIndex --merge-source
  output\_N.star refpkg.star refpkg\_classes.star OR
  star.py output\_N.star refpkg.star
  refpkg\_classes.star --class K --copy-alignments
  output\_N.star
- 3. stack.py <star> <mrcs out> --star <star out> [-class K]

Maximum occupancy is used to assign particle parameters and class number. You can choose how to merge the information using all the options in star.py, or expand the --merge-fields example. Let me know if it does/doesn't work for you. Source URL: https://cistem.org/split-stack-using-select-file