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Tue, 12/18/2018 - 16:29 #1

whiteqiu

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Dear CisTEM community,

I collected a tilt dataset, and processed it as normal in cisTEM. At later step, I used relion 3.0 ctf refinement to get the corrected defocus value. Then I tried to import ctf values from relion ctf refinement (particles_ctf_refine.star) back into cisTEM refinement package. However, due to the different image/column order, the ctf value wasn't aligned with corresponding paricle. Is there any existed script can match image names and ctf values, and import them into cistem?

Thanks in advance!

Yu

timgrant

Hi Yu,

Hi Yu,

I don't have a script for doing this. Have you tried running CTF refienment in cisTEM?

Tim

Thu, 12/20/2018 - 10:01 #3

whiteqiu

Hi	Tim,
Hi	Tim,

I tried running CTF refinement in cisTEM without much improvement. I guess because the resolution is not as high as 4A and also the protein itself is relatively small (350KD).

Thanks,

Yu

Thu, 12/20/2018 - 14:21 #4

timgrant

Hi Yu,

Hi Yu,

I think if you run "relion_preprocess --operate_on particles.star -- operate_out mystack.mrc" it will make a stack in the same order as the .star file?

Tim

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