Correct FSC curves for mask effects?

Mon, 02/05/2018 - 12:26

#1

Leonid Sazanov

Correct FSC curves for mask effects?

Hi, as far as I understand, currently FSC curves in cisTEM are calculated without using high-resolution noise substitution to correct for convolution effects of the masks on the FSC curves? Would it be possible to add this option in future, to have more reliable resolution estimates?

Thanks,

Leonid

niko

cisTEM does not use tight

*cis*TEM does not use tight masks on the half-maps to calculate FSC curves. Only a spherical mask with radius specified by the user is applied. This should be chosen large enough to make sure it does not cut into the density. With such a mask, there is (virtually) no masking artifact. This is therefore different from FSC calculations that are based on tight masking, such as in **Relion**, which requires a correction for the convolution effects.

The FSC calculated from these generously masked half-maps is then converted into a so-called Part_FSC that would be expected if all the background left in the spherical mask is removed. This can be done because the volume of the particle can be estimated using its molecular mass, and the volume of the sphere is known. Please read more about FSC calculation in *cis*TEM in the related manuscript that was published on **bioRxiv** last week.

Mon, 02/05/2018 - 14:01   (Reply to #2)

Leonid Sazanov

Re:

Hi Niko,

Thanks for clarification, but I meant for manual refinement when user-supplied mask is provided, covering just part of protein, excluding disordered parts.

In that case FSC is still calculated using big circular mask?

Thanks,

Leo

niko

Yes, the masking is only used

Yes, the masking is only used during refinement, never during reconstruction.

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