From: Axel Brunger
To: CCP4BB@JISCMAIL.AC.UK
Subject: Re: [ccp4bb] FW: [ccp4bb] Resolution and distance accuracies
Date: Sunday, December 26, 2010 4:26:19 PM

We defined "super-resolution" in our DEN paper as achieving coordinate accuracy better than the resolution limit d_min of the diffraction data. We proposed this definition in analogy to its use wide-spread use in optical microscopy: "super-resolution" methods such as STORM, PALM, and STED achieve accuracy of positions of fluorescent labels significantly better than the diffraction limit (in some cases, sub-nanometer accuracy - Pertsinidis, Zhang, Chu, Nature 466, 647-651, 2010).

We found DEN to be useful to move some atoms into correct positions in cases where electron density maps are difficult or impossible to interpret at low resolution. By default, DEN is active during the first torsion angle molecular dynamics stages, but then turned off during the last two stages. In addition, the DEN network is deformable. Thus, DEN is very different from "secondary structure" restraints or point restraints to reference models which are "on" all the time. Rather, DEN steers or guides the torsion angle conformational search process during refinement.

Cheers,
Axel

On Dec 24, 2010, at 2:14 PM, Bernhard Rupp (Hofkristallrat a.D.) wrote:

> > I find the "super-resolution" claims in this paper a bit of a conjuring
>
> trick.
>
> I think it is understood that information cannot come from nothing. You cannot cheat in basic physics. Interestingly, I had the same discussion with
> bioinformatics colleagues a short time ago. The problem is the same and seems of a semantic nature. They are using prior information of some sort
> (undisclosed) to successfully improve maps and they suggested to call this
> 'resolution increase'. I had the same objection and said that in crystallography resolution is a relatively hard term defined by the degree to which experimental observations are available, and as crystallographers
> we won't like that claim at all.
>
> On the other side it is uncontested that as long as the model fits

(crossvalidation-) data better when prior information is used, something useful has been achieved - again with all the caveats of weights and bias etc admitted.

However, how to entice non-experts to actually use new methods is another
thing, and here the semantics come in. In essence, if at the end it results in better structures, how much of the unfortunately but undeniably necessary
salesmanship is just right or acceptable? Within contemporary social constraints (aka Zeitgeist) that remains pretty much an infinitely debatable
matter..

Merry Christmas, BR

Dear Bernhard,

I must say that I find the "super-resolution" claims in this paper a bit of a conjuring trick. If the final refined model has greater accuracy than one would expect from the resolution of the data it has been refined against, it is because that extra accuracy has been lifted from the higher resolution data that were used to refine the structure on the basis of which
the elastic network restraints were created.

Should we then say that we achieve super-resolution whenever we refine
a macromolecular structure using Engh & Huber restraints, because these enable us to achieve distance accuracies comparable with those in the small
molecules structures in the Cambridge Structural Database?

Perhaps I have missed an essential point of this paper.

With best wishes,

Gerard.

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