CRYSTALLOGRAPHIC IMAGING USING MAXIMUM ENTROPY @ LLB

Robert J. Papoular

Laboratoire Léon Brillouin (CEA-CNRS), CEA-Saclay91191 Gif sur Yvette cedex, France

CRystallographic **I**maging using **M**aximum **E**ntropy (**CRIME**) is used to reconstruct 3D electron and scattering densities from **X-R**ay and **P**olarized / **U**npolarized **N**eutron diffraction data. It provides a very significant gain with respect to the widespread conventional Fourier Imaging. The state of the art of CRIME is illustrated hereafter via two examples pertaining to two typical neutron examples: a spin-density study and a proton density determination.

Either one is borne from experimental data obtained at our flagship hot source single-crystal diffractometers **5C1** [using **P**olarized **N**eutrons, see Fig.1] and **5C2** [using **U**npolarized **N**eutrons and discussed below in some more detail].

A most legitimate worry relates to whether the inappropriate use of Maximum Entropy would still lead to reconstructing spurious features to be mistaken for real Physics/ Chemistry phenomena. This is why the crucial part of *a priori* modelling to produce adverse non-uniform prior densities is emphasized. New features showing up in **CRIME** reconstructions are only deemed reliable if they survive the negative bias induced by the use of plausible advert non-uniform priors, and are considered untrustworthy otherwise.

There are quite a few reasons to go beyond the standard crystallographic procedure, besides reducing the well-known Fourier series truncation errors : **i)** experimental error bars should be taken into account and **ii)** all the available information should be used, such as Fourier components that are either unphasable, overlapped in the case of powder data, or incompatible with a given direction when a 2D projection of the object is sought.

For our most recent results, see:

R.J. Papoular (2002), SCI2002 Proceedings [Orlando,USA], Vol. XVII, pp.313-320.

A. Gukassov et al (2002), Phys . Rev. Lett. **89** 087202

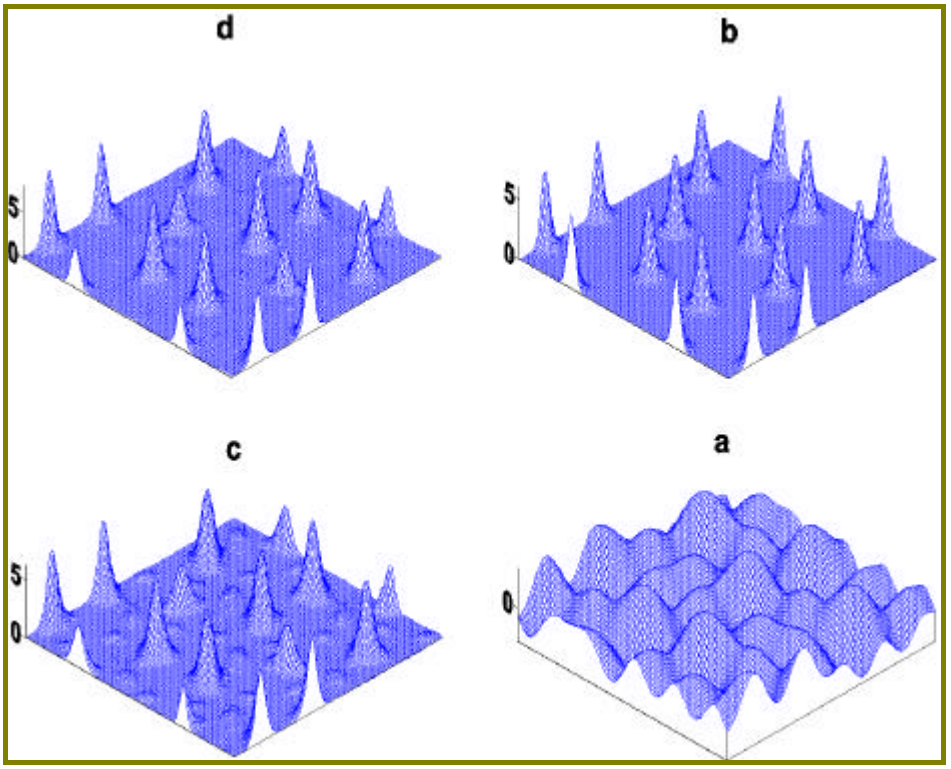

Figure 1. CRIME step by step. **a) Why** : the Standard Fourier map is unusable **b) How** : Use a non-uniform prior density biased against the expected effects [different peaks, new ones] **c) What if :** Using a uniform density prior is not good enough : new effects are now hinted at but may not be reliable **d) What** : using the non-uniform prejudice b) sets it right : there are only two different kinds of peaks. The weakest ones as found in c) are not warranted by the data.

Aspirin and Unpolarized Neutron Diffraction

As expertedly reviewed in a recent book by C.C. Wilson, entitled "*Single Crystal Neutron Diffraction from Molecular Materials*" (World Scientific, 2002), the neutron asserts itself as a unique structural probe to **i)** locate protons accurately, **ii)** quantify their thermal parameters, **iii)** investigate proton disorder. It is thus an exceptional tool to study polymorphism and hydrogen-bond networks in molecular compounds in general, and in pharmaceuticals in particular.

Perhaps surprisingly, using CRIME affects the experimental measurement process. Whereas measuring weak intensities is generally considered a waste of time and neutrons since the related Fourier components do not contribute appreciably to the conventional Fourier maps, it becomes crucial to measure them as well possible if ghosts atoms or ripples are to be avoided in an improved model-free imaging. Complete data sets (down to a certain resolution) become essential. *A first bonus* of using CRIME is the possibily to use a variety of density priors and check the stability of the reconstructed proton density against the latter. As demonstrated below in the case of aspirin, we advocate the systematic use of at least two prior densities : the bi-uniform and the non-uniform backbone one. *A second bonus* is to be able to use Fourier components than cannot be phased reliably using an appropriate model (built from the non-H atoms, and usually derived from a previous X-ray single crystal experiment). *A third bonus* is the further ability of CRIME to tackle the simultaneous reconstruction of the proton density [which is usually negative unless the sample is deuterated] and of the backbone usually positive density.

The use of this two-channel (one positive, one negative) entropy is a logical extension of our previous applications of CRIME to magnetization [Papoular & Gillon, EPL, 1990] and accurate charge densities [Papoular et al, Acta Cryst. A., 1996]

In our recent work initially aimed at studying the methyl group [Schiebel et al , PRL 1999] a single-crystal of aspirin was measured on 5C2 at the Orphée reactor at 15 K. One complete datasets comprising 1050 unique reflections was collected. Model-free imaging of the linking protons between the two molecules of the aspirin dimer [see Fig.2] resolves a controversy : do the protons jump between two possible positions, sit right in the middle of the O-H...O bonds, or preferentially belong to one of the molecules?

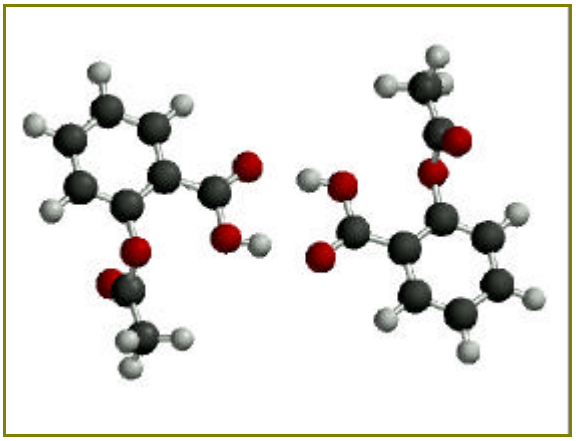

Figure 2. Schematic view of an aspirin dimer

The unambiguous result is shown in figure 3.

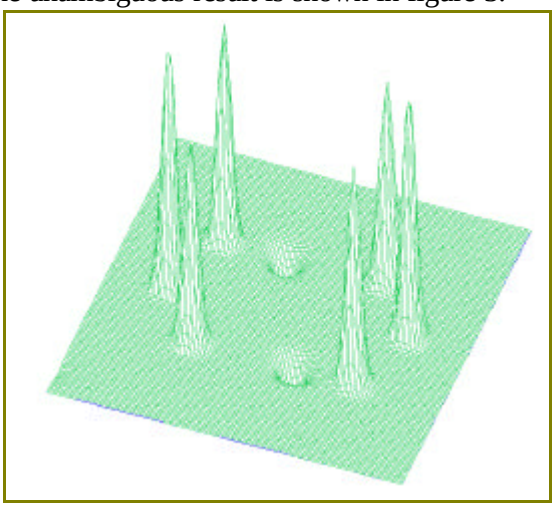

Figure 3. Model-free reconstruction of the protons involved in the carboxylic acid dimer part of aspirin at T= 15 K. The protons appear as holes because their neutron scattering length is negative