

## Moving quantum crystallography from sub-atomic XRD to near-atomic 3D ED

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One of the kinds of information gained from high resolution (sub-atomic) structures is the observation that electron density parameters are transferable between atoms having similar chemical topology. This stimulated creation of databases of multipolar pseudoatoms (Invariom [1], ELMAM2 [2], MATTS – successor of UBDB [3], etc.) and their applications in (a) structure refinements on standard (atomic) resolution data for small-molecule crystals, and (b) electrostatic properties and non-covalent bonding characterisations for macromolecules.

Transferable Aspherical Atom Model (TAAM) of scattering built from a pseudoatom database proved to be advantageous in refining the structure on X-ray diffraction (XRD) data compared to the Independent Atom model (IAM) [4], leading to better fit of the model to the data and improved localization of hydrogen atoms. We have recently showed [5] that also for small-molecule 3D electron diffraction (3D ED) data, a better model-to-data fit and more accurate structures should be expected from TAAM.

To improve its usability, we further extended the MATTS bank to cover 98% of atoms found in all the structures deposited in the Cambridge Structural Database [6] composed of chemical elements like C, H, N, O, P, S, F, Cl and/or Br. It is planned that the remaining 1% will be covered by the more general atom types resulting from multidimensional cluster analysis.

Some benefits of TAAM over IAM refinements were also reported for macromolecular XRD data of 0.9 Å resolution and better [7]. As most macromolecular crystals diffract to lower resolutions, we recently moved our investigation towards near-atomic resolutions. We quantified the differences between the macromolecular electron density Fourier maps obtained with TAAM and IAM, calculated with a resolution of 1.8 Å. We did the same for electrostatic potential maps, a key property in the context of 3D ED.

TAAM refinements affect not only the positions of the atoms, but also the atomic displacement parameters (ADPs) [8]. ADPs appears to be less resolution dependent with TAAM than with IAM. With IAM, ADPs increased for XRD and decreased for 3D ED by about 30%, when the resolution was reduced from 0.6 Å to 0.8 Å [5]. From modified Wilson plots we recently predicted, and then verified by TAAM refinements on macromolecular XRD or 3D ED data, what will happen with ADPs (B-factors) with a further resolution worsening, up to 1.8 Å.

All the above helps to understand if there will be any benefits of TAAM refinements on lower than atomic resolutions.

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