MS4-03 The Nautilus software for automated nucleic acid model building, Bergen, 7-11 August 2012.

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The strongest constraints on the unmeasured phases of the X-ray diffraction pattern come from the atomic model. As a result one important strategy in phasing is to build as much of the model as possible as early as possible in the structure solution process. To achieve this aim, tools are required to build all the components inhabiting the unit cell, even when the electron density is poor.

The 'Buccaneer' model building software [1] has already extended the range of resolutions at which a protein model may be obtained. A companion tool, 'Nautilus', has been developed to build nucleic acid components. The interpretation of nucleic acid electron density maps is hampered by the greater flexibility of the nucleic acid backbone and the resulting higher B-factors, however this problem is partly compensated by the presence of larger rigid groups.

'Nautilus' may be used to build nucleotide structures in experimentally phased and molecular replacement maps, or to add the nucleotide components to protein complexes. The calculation depends on a very fast search target which can be used to identify the 'fingerprint' of the sugar or phosphate groups in the map. This target is used to locate likely starting points for building and extend these into connected chains. A small database of RNA fragments is used to rebuild the backbone and connect nearby fragments. A second fingerprint is used to identify the different base types and score them, allowing the know sequence to be matched against the unknown fragments. One unusual feature of the method is its speed: The calculation is much faster than either protein model building, or the refinement calculation with which model building is iterated. This speed has enabled the implementation of an interactive version of the software for use in 'Coot' [2].

[1] Cowtan, K. (2008). *Acta Cryst*. D**64**, 83-89.
[2] Emsley, P., Lohkamp, B., Scott, W. G. & Cowtan, K. (2010). *Acta Cryst*. D**66**, 486-501.

Keywords: nucleic acids; automated structure solution; model building

MS4-04 A novel function for the combination of SAD phasing, density modification and model refinement.

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Traditionally, the process of macromolecular structure solution consists of separating the processes of phasing, density modification and model building with refinement. We had derived a novel multivariate function that incorporates information from a single-wavelength anomalous diffraction experiment directly into phasing, density modification and/or refinement. Thus, the function enables to synergistically consider the traditionally separate steps of macromolecular X-ray structure determination from experimental phasing into one unified process that leads to combined and significant improvements. Tests performed on many data sets show the new approach allows for many structures to be built automatically that elude current methods, especially for data at lower resolutions or with weak experimental phase information. The improvements will also be demonstrated on two datasets that originally could not be built by expert crystallographers using any existing methods, but were solved automatically with the new function.

Keywords: SAD phasing; density modification; model refinement