MS33 O1

Phenix refine developments Ralf W. Grosse-Kunstleve[a], Pavel V. Afonine[a], Peter H. Zwart[a], Thomas C. Terwilliger[b], Nigel W. Moriarty[a], Alexander Urzhumtsev[c], Paul D. Adams[a], [a]*Lawrence Berkeley National Laboratory, One Cyclotron Road, BLDG 64R0121, Berkeley, CA 94720 USA,* [b]*Los Alamos National Laboratory, Mailstop M888, Los Alamos, NM 87545, USA,* [c]*IGBMC, 1 rue L. Fries, 67404 Illkirch - IBMC, 15 rue Descartes, 67084 Strasbourg.*
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Keywords: refinement, macromolecules, automation

The PHENIX project [1] is an international effort to automate macromolecular crystal structure determination by developing new and improved algorithms, and by taking full advantage of current hardware and software development technology. The structure refinement module of PHENIX is the phenix.refine program. After about four years of intense development, phenix.refine includes most state-of-the-art procedures, including TLS, simulated annealing, NCS, twin refinement, maximum likelihood targets, etc. phenix.refine is embedded in the higher-level PHENIX wizards integrating model building and refinement. Under active development are alternative model parameterizations to reduce the number of refinable parameters (e.g. in torsion angle space). This is expected to stabilize refinement at lower resolutions and to increase the radius of convergence. We will present the latest results of this ongoing work.

[1] Adams P.D., Gopal K., Grosse-Kunstleve R.W., Hung L.-W., Ioerger T.R., McCoy A.J., Moriarty N.W., Pai R.K., Read R.J., Romo T.D., Sacchettini J.C., Sauter N.K., Storoni L.C., Terwilliger T.C. *J. Synchrotron Rad.*, 2004, 11, 53.

MS33 O2

Automated model building at lower resolutions
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Keywords: model building, phase improvement, automation

A number of successful automated model building techniques have been developed over the last few years, significantly accelerating one of the more time consuming stages of the structure solution process, however their success has been limited at lower resolutions. The 'Buccaneer' statistical model building software has been shown to provide a powerful tool for tracing protein chains, even at limited resolutions in the range 3-4 Angstroms [1]. More recent developments have extended the functionality of this software to allow sequencing and partial completion of the atomic model. In particular, a 'lateral growing' technique allows preferential location of new chains passing at likely distances from fragments built in earlier cycles.
Further statistical techniques are being investigated to encourage the construction of extended secondary structure features, which should provide additional stability at low resolutions. Recycling of the program with refinement of the preliminary model in 'refmac' has been demonstrated, and work is underway to incorporate phase improvement into this cycle, using the 'Pirate' statistical phase improvement software to allow the preliminary model to contribute to the phase improvement process.

[1] Cowtan, K., *Acta Cryst*. 2006, D62, 1002-1011.

MS33 O3

Improved Fa estimates from SAD data for substructure detection. Navraj S. Pannu, *Biophysical Structural Chemistry, Leiden University, The Netherlands.*
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Keywords: substructure detection, multivariate likelihood, SAD

To determine a substructure from single (SAD) or multi-wavelength (MAD) anomalous diffraction data using Patterson or direct methods, the substructure factor amplitude (Fa) must first be estimated. Currently, the absolute value of the Bijvoet difference is widely used as the estimate of Fa for SAD data. A new equation that takes into account the correlation between the observed positive (F+) and negative (F-) Friedel pairs and Fa along with the errors in measurements of F+ and F- has been derived. Preliminary results show that the new equation, derived from multivariate statistics, has a higher correlation to final substructure amplitudes (calculated from refined substructures) and can improve the robustness of direct methods substructure detection programs.

MS33 O4

MrBUMP: a smooth operator for structure determination by molecular replacement Martyn Winn, Ronan Keegan, *Computational Science and Engineering Department, STFC Daresbury Laboratory, UK.*
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Keywords: molecular replacement, search models, automation

MrBUMP is a pipeline which wraps established molecular replacement (MR) programs to automate macromolecular structure solution by this method. The aim of MrBUMP is to start from native structure factors and a target sequence, and deliver one or more positioned and partly refined models. There is a special emphasis on the discovery and preparation of a large number of search models, all of which can be passed to the core MR programs. For routine problems, the value of the MrBUMP system is simply one of convenience. For more difficult cases, the pipeline aims to discover the particular template structure and model edits required to produce a viable search model, and may succeed in finding an efficacious combination that would be missed otherwise.
MrBUMP has been publically available for over a year, and its use in straightforward cases is well-established. Recently, we have extended the functionality in a number of directions. There have been improvements to existing steps, such as changes to the multiple alignment step, and the ability to search over spacegroup candidates. There is improved visualisation of the results, through the use of the new CCP4 dbviewer. At the end of the pipeline, we are employing methods for improving the MR phases, such as the use of Acorn and Pirate, and linking to subsequent model-rebuilding. We are also looking at extending the