PS03.02.08 A TECHNIQUE TO RECOVER MISSING SCATTER INTENSITY INFORMATION AND REDUCE NOISE, REQUIRING NO *A PRIORI* KNOWLEDGE by Gary K Doherty[1] and George A. Poland[2] [1]Saacke Combustion Systems Ltd. Marshland Spur Farlington Portsmouth PO6 1RX England [2]University of Portsmouth PO1 2RY England.

A new technique is presented which recovers missing scatter intensity data, reduces the noise levels of the measured points and estimates the incoherent level when applied to experimental small angle scattering data.

The method differs from those of other authors in that only the measured data is used; no parameters need to be supplied, such as the number of splines or sinusoids to use, and no initial estimates of particle dimensions are required. The technique takes a new view of the work presented in Doherty & Poland (1996), both simplifying and extending the application of the same underlying principle.

Doherty, G. & Poland, G. A. (1996). *J. Appl. Cryst* **29**, 53-60

PS03.02.09 XTAL3.4: NEW RELEASE OF THE XTAL SYSTEM. S.R. Hall and D. du Boulay, Crystallography Centre, U. of Western Australia, Nedlands, 6009 Australia; G.S.D. King, Fisica-Chemische Geologie, KU Leuven, B-3001 Heverlee, Belgium; J.M. Stewart, Chemistry, U Maryland, Washington DC, USA; J.R. Hester, NIRIM, Namiki 1-1, Tsukuba, Ibaraki 305, Japan; and D. Grossie, Chemistry, Wright State University, Dayton OH, USA

The Xtal System is an integrated package of crystallographic programs for single crystal structure analysis. It facilitates calculations from processing raw diffraction intensities to the preparation of the publication diagrams, tables and submission files. For some calculation steps, several programs employing different algorithms are provided, enabling a choice of approaches and the ability to cross-check results. All calculations are integrated and share a common archive file.

Xtal3.4 is distributed at cost on an ISO-9660 CD-ROM and may be implemented on any computer supporting a Fortran and C compilers, and X11 graphics libraries. Executables are provided for the most unix, linux, VMS or DOS operating systems. The sources files are also supplied with implementation scripts so that Xtal3.4 may be installed on other machines, or adapted to locally available software.

User support is mainly via internet facilities. A web server provides users with the latest Xtal information. The WWW address is http://www.crystal.uwa.edu.au/xtal/. Newsletters will be airmailed as hardcopy to users but new and updated sources will be available via anonymous FTP from ftp.crystal.uwa.edu.au directory /xtal. General queries should be directed to xtal@crystal.uwa.edu.au.

PS03.02.10 DIRECT-SEARCHER SYSTEM (Ver. 3) FOR SOME ORGANIC COMPOUND ON PERSONAL COMPUTERS. K. Okada[1*)] and S. Okada[2)]. 1)Research & Development Center, Ricoh Co. Ltd., Tsuzuki-ku, Yokohama 224, Japan, 2)Faculty of Engineering, Science University of Tokyo, Shinjuku-ku, Tokyo 161, Japan.

The Direct-Searcher system version 3 (DS*System3) has been developed for automatic structure analysis of some organic compounds running on personal computers (PC). The DS*System3 running on Windows NT is the latest version developed for Cray-1 / CDC6600 (Ver.1, J.Chem.Soc.B,1969,940; Acta Cryst.1990, A46, C70) and mainframe / workstation / PC (Ver.2, Comput.Chem.1995, in press). An organic chemist as well as a crystallographer can get results very easily with his own well-known PC. This system consists of more than twenty crystallographic programs, and each program is improved and re-written in the Fortran language. The logical structure of DS*System3is simplified as three layers by using common and independent libraries for easy maintenance. The major improvements are: Loose limitation of no. of atoms, reflection and equiv.position; Color display; Plotter output; Change peak find algorithm; Adopt data base for space group and atomic scattering factor; add CIF facility; bag fixing. We found that the molecular skeleton takes usually less than 2 min with heavy-atom analysis (PSL3+Searcher3) and 15 min with direct methods (Dircter3) by a Pentium 100PC. Comparing the computational speed, the PC has a capability of 1.55 times a Cray-1, 3.93 times a HP9000/755,7.43 times a IBM3090-200E and 33.2 times a CDC6600. The crystal structure analysis of organic compounds has been carried out more than fifty with the heavy-atom analysis and more than thirty with the direct methods.

PS03.02.11 RESOLUTION ENHANCEMENT IN POWDER DIFFRACTION USING STABLE DECONVOLUTION. Derk Reefman, Philips Research, Prof. Holstlaan 4, 5656 AA Eindhoven, The Netherlands

A recently developed method will be presented for enhancing the resolution in powder diffraction to approximately 0.025 degrees 2theta, without loss of intensity. Enhancing the resolution in powder diffraction has always been a driving force for the development of sophisicated optics in the beam path of the X-Rays, like monochromators, mirrors, etc. This equipment has contributed significantly to the improvement of the resolution of todays diffractometers. Nevertheless, the everincreasing demands set by the increasingly complex materials which have to be characterized, ask for even higher resolution. For that reason, synchrotrons are extensively used nowadays.

However, the time allocation for a particular experiment on a synchrotron is limited and one would like to perform experiments with laboratory-equipment without significant loss of resolution. An approach to achieve this is to obtain the instrument function of the equipment of interest, and to correct the measured pattern for the instrumental aberrations. A classical method used to this end is the fourier approach of Stokes. This method has the drawback of becoming unstable for resolution enhancements by more then a factor of 1.5. Recently, it has been shown that application of Maximum Entropy (ME) deconvolution techniques can be used for resolution enhancements up to a factor of 3. A problem however are the computational resources needed. Nevertheless, continuing effort in this direction has now led to a method which, based on ME as well, provides robust access to a way to enhance the resolution of a complete wide range pattern within minutes.

PS03.02.12 EXPERIENCES PORTING CRYSTALLOGRAPHIC SOFTWARE TO MODERN USER INTERFACES: A WINDOWS VERSION OF THE *NRCVAX* PACKAGE. Peter S. White, Department of Chemistry, University of North Carolina, Chapel Hill, NC 27514, U.S.A. and Eric J. Gabe, Steacie Institute for Molecular Structure, National Research Council of Canada, Ottawa, Ontario K1A 0R6, Canada

NRCVAX is a complete suite of programs for the solution and refinement of crystal structures, designed to compile and run on a wide variety of computers. This has been achieved by writing the code in standard Fortran 77 and isolating any potential machine dependencies. The package relies on the operating system to provide a mechanism for starting routines which are interconnected by files containing the crystal and reflection data. The user interacts with the individual routines by means of a series of questions and answers. The system, whenever possible, suggests reasonable default answers which can be selected by pressing return.

This user interface is extremely powerful and easy to use, however, it is fast becoming an unnatural environment for new users,

who are more conversant with the windowed style user interface of modern personal computers and workstations. *NRCVAX* has therefore been redesigned to take advantage of current graphical user interfaces (GUIs). In doing so we have been forced to make a choice of operating systems to support, as GUIs tend to be linked quite intimately to the underlying operating system. We have initially chosen the Windows95 and NT systems to be followed closely by a Motif version for Unix workstations.

A common method of providing a GUI, which works well for much code, is to write a program that interacts with the user and generates a file of input instructions for the existing routine. The routine is then executed in the background and its output trapped and presented to the user. This works well for 'batch' style software but was not suited to *NRCVAX* where the questions a user is asked are often based on prior responses. So the programs have been designed with the user interaction localized to a limited number of subroutines which are called directly by the user interface. Output in most programs is returned to a scrollable window which the user may choose to save or print.

As part of this effort the existing command line version of the software has been carefully examined and modified to reduce user input and eliminate redundant questions.

Computing III
Macromolecular Map Fitting And Modification

MS03.03.01 DENSITY MODIFICATION: SUCCESSES AND LIMITATIONS. Kevin Cowtan, Protein Structure Group, Dept. of Chemistry, University of York, Helsington, York Y01 5DD, England

Phase improvement by density modification, despite a number of theoretical flaws, is now an established part of the solution of macro-molecular structures by x-ray diffraction methods. The power of the method in the best cases has been demonstrated repeatedly by the solution of structures from the weakest of phase information, for example from single derivatives or weak anomalous scattering. If there is sufficient redundancy in the data, due to high solvent content, local symmetry or multiple crystal forms, then the method can come close to ab-initio phasing.

This success arises despite a number of fundamental flaws in the underlying protocol of most density modification calculations. In particular, the density modification 'model' is usually under-determined with respect to the observed data. This leads to degrees of freedom in the model magnitudes which in turn invalidate the assumptions behind the usual phase combination methods.

Future developments must address these problems. Particular areas under study are the integration of model building and density modification into a semi-automatic process. At a more fundamental level, statistical phasing (maximum entropy) methods may lead to a new formulation with a firmer mathematical foundation.

MS03.03.02 ELECTRON DENSITY AVERAGING USING MULTIPLE CRYSTAL FORMS OR DIFFRACTION DATASETS IN STRUCTURE DETERMINATION OF PROTEIN AT MODERATE RESOLUTION. Kalyan Das, Jianping Ding, Yu Hsiou, Karen Lentz, Wanyi Zhang, and Edward Arnold Center for Advanced Biotechnology and Medicine (CABM) and Rutgers University Chemistry Department, 679 Hoes Lane, Piscataway, NJ 08854

Obtaining accurate phases and hence reliable structures using moderate resolution data remains challenging. In the presence of non-crystallographic symmetry (NCS), electron density map averaging techniques have been successfully used to improve the quality of phases. However, many proteins form crystals without useful noncrystallographic redundancy in the asymmetric unit. A multiple electron density maps averaging technique has been developed to improve the phase quality and the interpretability of electron density maps. We averaged the electron density maps computed from structures of HIV-1 reverse transcriptase (RT) crystallized in different crystal forms (i.e., with dramatically different unit cells or space groups). We also averaged the electron density maps calculated from multiple diffraction datasets collected from the same crystal form at different temperatures. For example, the unit cell parameters were slightly different for the crystal frozen at -165°C and the same crystal cooled at -10°C. In this averaging technique, the protein structures are subdivided into segments that can be superimposed well and the averaging is carried out over the masks covering the segments. The averaged electron density maps for individual subdomains are then combined to cover the whole protein. Also, to minimize the model bias, the conventional omit maps were calculated and used as the input maps for averaging.

This technique was applied to the structure determination of HIV-1 RT in complexes with various nonnucleoside inhibitors (NNRTIs) at 3.0 Å resolution, unliganded HIV-1 RT in two crystal forms at 2.7 Å and 3.5 Å resolution, respectively and in the structure refinement of the HIV-1 RT/DNA/Fab complex at 2.8 Å resolution. The omit maps and the averaging of the multiple electron density maps have significantly reduced the model bias and improved the interpretability of electron density. The improvement of the phases after map averaging are evident from comparison of electron densities for the bound inhibitors calculated at different stages of HIV-1 RT/NNRTI structure refinements. A detailed description of the algorithm and the results will be discussed. This approach will be useful in solving various other protein structures without NCS symmetry.

MS03.03.03 PARTIAL STRUCTURE REFINEMENT COMBINED WITH ELECTRON DENSITY MODIFICATIONS BY USING MAIN. Dusan Turk, dusan.turk@ijs.si, University of Ljubljana, Josef Stefan Institute, Slovenia

In the cases, that is, in most cases, when it is not possible to build almost complete macromolecular models into initial electron density maps, progress of a structure determination is hindered by limitations of a partial model refinement against a full data set and by limitations of electron density modification procedures including phase combination. A phase combination procedure starts to make sense when substantial parts of the model have been built into electron density maps.

MAIN is a program that can be applied in various electron density modification approaches, for interactive model building and structure refinement. Now, tools that allow to combine all these methods into a single task, have been added to the program. The essence of the idea is that accordingly scaled electron density map of a partial model is scaled and merged with a background map. Resulting merged map can be subjected to any electron density modification procedure. This modified map serves then to calculate structure factors and these structure factors are used to calculated derivatives, which are applied during a partial model minimization, and to generate a new background map. This should be repeated in several cycles.

The approach is not limited by the size of a model fraction, although it is evident that small model fractions will not be capable of substantial map improvements. Visual inspection has revealed that the resulting maps are sharper, include more structural details (side chains and loops) and are less model biased than a map based on a phase combination approach.

A MAIN demonstration installation is available via an anonymous FTP server at STEF.IJS.SI.