17.2-19 FALSE MOLECULAR IMAGES IN DIRECT AND HEAVY ATOM PHASE DETERMINATIONS. By W. Wong-Ng and S. C. Nyburg, Department of Chemistry, University of Toronto, Toronto, Ontario, Canada M5S 1A1.

We have found, in several instances, that direct methods or heavy atom methods can lead to false solutions in which two images of the true molecules overlap. In all cases some of the atoms of the two images were superimposed. Methods of unravelling the true structure will be illustrated with examples. 17.4-01 RESTRAIN: THE PRACTICAL APPLICATION OF A RESTRAINED LEAST SQUARES REFINEMENT PROGRAM IN PROTEIN CRYSTALLOGRAPHY. By D. S. Moss, Laboratory of Molecular Biology, Birkbeck College, London, U.K. and A.J. Morffew, IBM United Kingdom Ltd., Scientific Centre, Winchester, Hampshire, UK

A restrained least-squares procedure is described that has been designed for refining protein structures in conjunction with an interactive computer graphics facility. By allowing the assignment of relative weights to individual atoms in the graphics database, the user can interact with the refinement program.

The sum of residuals minimised in RESTRAIN is a function of structure amplitudes, phases and target geometry. The normal equations are solved by the Gauss-Seidel method with Δ^2 acceleration and the under-determined case is solved by the Levenberg-Marquardt method. It is the 'Marquardt factor' that has been adapted to apply the individual relative weights to the atoms.

The methods, strategy and some results of this program are described.

17.2-20 A REAL APPROACH TO DETERMINATION OF PHASES, By <u>D.F.Grant</u> and R.C.G.Killean, Physics Department, University of St.Andrews, North Haugh, St.Andrews, Fife KY16 9SS, Scotland.

It is well known that trivial solutions to phase determination in the centrosymmetric case yield a maximimum value for $\int \rho^{3} dv$ for x-ray data. A procedure has been devised for obtaining non-trivial solutions which gives maximum values of this integral for certain restricted sets of structure factors. The contribution of each structure factor to the integral is evaluated in turn and then the structure factors are arranged in order of importance. This order is used to build up sets of phases giving the maximum value of the integral. Procedures have been evolved for handling the different parity groups and for terminating the process with a limited number of sets of phases. The technique operates in real rather than reciprocal space, uses the observed structure factors, and involves no statistical arguments. The method will be illustrated by reference to a number of three-dimensional data sets in the space group P1.

17.4-02 A ROBUST/RESISTANT TECHNIQUE FOR CRYSTAL STRUCTURE REFINEMENT. W. L. Nicholson, Battelle Pacific Northwest Laboratories, Richland, WA 99352, U. S. A., <u>E. Prince</u>, National Measurement Laboratory, National Bureau of Standards, Washington, DC 20234, U. S. A., J. Buchanan and P. Tucker, Battelle Pacific Northwest Laboratories, Richland, WA 99352, U. S. A. A refinement technique is "robust" if it works well

A refinement technique is "robust" if it works well over a broad class of error distributions in the data, and "resistant" if it is not strongly influenced by any small subset of the data. Least squares possesses neither property. A more robust/resistant procedure is to minimize, instead of a simple sum of squared differences, a sum of terms of the form

The minimum equations of the form $\rho(\mathbf{x}) = (\mathbf{x}^2/2)[1 - (\mathbf{x}/a)^2 + (1/3)(\mathbf{x}/a)^4]$ for $|\mathbf{x}| \leq a$, $\rho(\mathbf{x}) = a^2/6$ for $|\mathbf{x}| > a$. Here $\mathbf{x} = \mathbf{r}_1(\theta)/s$, where $\mathbf{r}_1(\theta) = \mathbf{w}_1^{1/2}[|\mathbf{F}_{01}| - \mathbf{m}_1(\theta)]$, $\mathbf{m}_1(\theta) = |\mathbf{F}_{c1}(\theta)|$, and s is a measure of the width of the error distribution based on the results of the previous cycle. a is a constant chosen so that extreme data do not influence the solution. The function $\rho(\mathbf{x})$ behaves like the sum of squares for small x, but is constant for large x, so that the effect of large differences is deemphasized. Most least-squares refinement programs can easily be modified to be more robust/resistant. Both weighted least squares and the modification are examples of a class of estimation methods which, for crystal structure refinement, take the form, minimize the loss function, $f(\theta) = \Sigma\rho[\mathbf{r}_1(\theta)/s]$ by selecting θ so the normal equations $\nabla f = 0$ are satisfied. Let $\phi(\mathbf{x}) = (1/x)\rho'(\mathbf{x})$ and $\omega(\mathbf{x}) = \rho''(\mathbf{x})$. Linearization of the normal equations gives the iteration formula

$$\Delta \theta_{j}^{q+1} = \sum_{k=1}^{p} C^{jk} \sum_{i=1}^{N} \phi[r_{i}(\theta^{q})/s^{q}] w_{i}^{1/2} r_{i}(\theta^{q}) \frac{\partial m_{i}(\theta^{q})}{\partial \theta_{k}}$$

for updating parameter estimates. Here C^{jk} is an element of the inverse to the linearized Hessian matrix, whose typical element has the form

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