17. X–1 THEORETICAL DIRECT METHODS. By C. Giacovazzo, Istituto di Mineralogia e Petrografia, Università, 70121 Bari, Italy.

The phenomenal development of direct methods in recent years is due both to theoretical progress and to more effective computing algorithms. There are two main themes of development. The multisolution approach develops many possible sets of phases among which the correct solution is found. The other approach uses relationships among phases of a more complicated nature in order to analyse a small number of possible set of phases.
Direct methods will play an important role also in macromolecular crystallography. The combination of the methods with the anomalous dispersion and isomorphous replacement techniques will probably be a powerful tool for the solution of the crystal structures of proteins.
The current status of the area will be described.

17. X–2 PRACTICAL DIRECT METHODS. By Isabella L. Karle, Laboratory for the Structure of Matter, Naval Research Laboratory, Washington, D. C. 20375, U.S.A.

Thousands of crystal structures are being solved routinely by a variety of computer programs that have been based on the theoretical developments concerning phase determination and their practical implementation. In many instances, however, a chasm may arise between theory and experiment. The theoretical formulas are often adversely affected by limited data, imperfections in crystals and non-random distributions of atoms in unit cells; nevertheless, practical procedures have been developed that are largely successful for small and medium-sized molecules. Problems in phase determination still remain, particularly in larger, equal-atom structures. These problems manifest themselves as ambiguous or incorrect phase indications for strong reflections and by the difficulty of expanding some known fragment to a complete structure. Two of the reasons for such problems are a scarcity of experimental data as compared to the number of independent atoms and, perhaps the greater difficulty, a large amount of pseudo-symmetry. Pseudo-symmetry as encountered in peptide backbones, for example, often leads to ambiguities in the placement of the known fragment of a molecule with respect to the origin, with many positions having almost equal probability. In cases of difficult structures, all possible remedies are used, such as translation functions, relaxation to a space group of lower symmetry, restraints on initial phase values during phase extension, auxiliary phase formulas, and procedures such as the use of random phases if sufficient computer time is available. Information from vector maps computed with $(|E|^2-1)$ values as coefficients can be valuable, such as the position of a Mg^{++} ion leading directly to the derivation of a 100 atom structure. Examples of difficulties and the manner in which they were overcome will be shown for structures of various sizes, ranging up to 215 independent, almost equal atoms.

17. X–3 RADIATION SOURCES AND DETECTORS FOR MEASUREMENT OF ACCURATE INTENSITIES. By U. W. Arndt, MRC, Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH.

The experimental methods which have been used in the past for the accurate measurement of the intensities of structure factors have necessarily been a compromise between the desirable and the available. Accurate measurements have been time-consuming and the very duration of the experiment has introduced systematic errors due to such causes as instabilities or drift of the source, the detector and the sample. In recent years high-brilliance sources have been developed, both in the laboratory and at storage rings. For most purposes the experimenter now has at his disposal as high an X-ray flux as he can hope to utilize, over a wide range of X-ray wavelengths. At the same time area detector diffractometers are becoming available which allow the simultaneous measurement of a large number of reflexions; some of these detectors have high efficiencies over the same wide wavelength range. Consequently, it has now become worthwhile to examine afresh optimum X-ray wavelengths, and optimum collimation conditions and also strategies which will minimise systematic errors due to absorption and radiation damage.

17. X–4 A ROBUST/RESISTANT ALTERNATIVE TO STANDARD LEAST SQUARES. By E. Prince, National Bureau of Standards, Washington, DC 20234, U. S. A., and W. L. Nicholson, Pacific Northwest Laboratory, P. O. Box 999, Richland, WA 99352, U. S. A.
A data fitting technique is said to be robust if it performs well for a wide variety of distributions of error in the data, and resistant if it is not sensitive to variations in small subsets of the data. Least squares is the optimum fitting technique if the error distribution is Gaussian, and the variance of the error distribution for each data point is known, but it is neither robust nor resistant. It performs poorly if the data contain large deviations with frequencies substantially exceeding those predicted by a Gaussian distribution. A robust/resistant procedure should behave like least squares when the deviations are small, but it should downweight, or even totally ignore, large deviations. The region between large and small should be filled in reasonably smoothly. A least squares program can be modified to make it robust/resistant by modifying the weights in each cycle so that $w' = w(1 - x^2)^2$ for $|x| < 1$, and $w' = 0$ for $|x| \geq 1$. Here $x = (|F_o| - |F_c|)/ms$, where σ is the standard deviation of F_o, s is a resistant measure of the width of the error distribution, calculated in a previous cycle, and m is a constant chosen so that extreme deviations do not influence the solution. [Nicholson et al. Crystallographic Statistics, Ramaseshan et al., eds. Bangalore: Ind. Acad. Sci. (1982), pp 229-263] Experience with this modified procedure has shown that it produces results substantially identical to least squares with good data sets. If a data set contains a small proportion of outliers, the program provides an efficient and objective means for identifying them. In synthetic data sets with higher proportions of large deviations than in a Gaussian distribution, the robust/resistant procedure shows a better ability to reproduce the correct structure.