called the structure invariants.

For fixed enantiomorph, the observed magnitudes \( |E| \) determine, in general, unique values for all the structure invariants. The latter, in turn, are certain well-defined linear combinations of the phases, lead unambiguously to unique values for the individual phases. Thus the structure invariants serve to link the known magnitudes \( |E| \) with the desired phases \( \phi \) (the fundamental principle of direct methods). By the term "direct methods" is meant that class of methods which exploits relationships among the structure factors in order to go directly from the observed magnitudes \( |E| \) to the needed phases \( \phi \).

For fixed enantiomorph, the value of any structure invariant \( T \) is primarily determined, in favorable cases, by the values of one or more small sets of observed magnitudes \( |E| \), the neighborhoods of \( T \), and is relatively insensitive to the values of the great bulk of remaining magnitudes (the neighborhood principle). The conditional probability distribution of \( T \), given the magnitudes in any of its neighborhoods, yields an estimate for \( T \) that is particularly good in the favorable case that the variance of the distribution happens to be small.

Most "small" crystal structures are rather routinely solvable nowadays by traditional direct methods. For the solution of macromolecular structures, on the other hand, the method of isomorphous replacement is universally used, and anomalous dispersion often plays an important supplementary role. One naturally anticipates therefore that integrating the traditional techniques of direct methods with isomorphous replacement and anomalous dispersion will strengthen our ability to solve complex structures. This goal has recently been achieved, and the initial applications suggest that the expected improvement is in fact realized.

17.16 MAXIMUM ENTROPY AND THE FOUNDATIONS OF DIRECT METHODS. By Gérard Briecogne, L.U.R.E., Batiment 290, 91400 Orsay, France

This contribution will review and extend the author's previous work on a new approach to direct phase determination, presented in [1].

The Maximum Entropy (ME) method provides a practical yet optimal computational procedure for constructing conditional probability distributions of large numbers of structure factors, given assumed phases for a collection of large moduli. Its optimality follows from the equivalence of the ME method with the "ridgepoint approximation" (SPA) method of calculating asymptotic expansions of joint distributions in the presence of "large deviations," the latter being accommodated by constantly updating the prior distribution of the atoms in cell.

This ME formalism has now been extended to the case of families of related structures made from several types of atoms, with arbitrary (complex) structure factors. The number of atoms of each type can be different in each structure of the family. The joint probability distribution of any "cylindrical" set of structure factors (comprising a given set of reflections considered simultaneously across all members of the family of structures) can then be obtained, extending the recent results of Hoppsman and of Kiel on the incorporation into direct methods of isomorphous replacement and anomalous scattering. Other situations not hitherto considered, such as the availability of a contrast variation series, can be dealt with by this method. The equivalence between ME and SPA continues to hold in this generalised context. This derivation of statistical phase relations for arbitrary complex-valued scattering factors shows clearly that the source of such relations is the positivity of the prior probability distribution of the atoms, not the positivity of the electron density.

The ME formalism has also been extended into a statistical formulation of the molecular replacement method, by deriving joint distributions of structure factors in the presence of known structural fragments, of solvent regions, of non-crystallographic symmetries, and even in the case of multiple crystal forms. These extensions are readily merged with those concerning the treatment of families of related structures, and should provide a powerful tool for macromolecular crystallography.

Finally, the optimal Gaussian approximations of the conditional distributions given by the ME/SPA method have been used systematically to construct statistical likelihood functions from the observed data (including the error estimates). These likelihood functions afford a quantitative evaluation of the adequacy of the statistical model used to derive the conditional distribution in the first place. Their numerical optimisation affords a way of improving the statistical model, and in particular of refining the phase values associated to large moduli to make up the constraints: this refutes the commonly held view that "the ME method cannot refine phases". Furthermore, the likelihood functions have been obtained in a sufficiently general form to be able to consult not only single crystal data, but also fibre diffraction and powder diffraction data; one can thus serve to extend the use of direct methods to these data.

This is the author's firm belief that this extended ME/SPA formalism and the associated likelihood functions constitute a powerful universal framework within which all sources of phase information can be first detected, then optimally combined, through a single basic computational mechanism in which - perhaps surprisingly - phase invariants never appear explicitly.