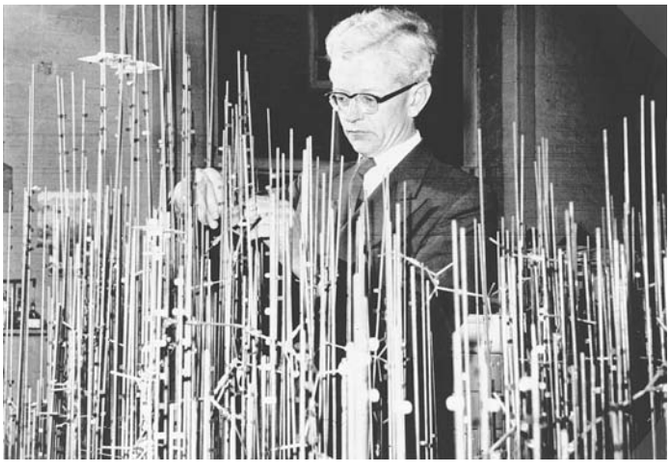

Figure 1.2.6.1
The 2 Å-resolution map of sperm-whale myoglobin was represented by coloured Meccano-set clips on a forest of vertical rods. Each clip was at a grid point. The colour of the clip indicated the height of the electron density. The density was interpreted in terms of 'Corey–Pauling' models on a scale of 5 cm = 1 Å. Pictured is John Kendrew. (This figure was provided by M. F. Perutz.)

complex equations. However, real advances came with applying the conditions of noncrystallographic symmetry in real space, which was the key to the solution of glyceraldehyde-3-phosphate dehydrogenase (Buehner *et al.*, 1974), tobacco mosaic virus disk protein (Bloomer *et al.*, 1978) and other structures, aided by Gerard Bricogne's program for electron-density averaging (Bricogne, 1976), which became a standard of excellence.

No account of the early history of protein crystallography is complete without a mention of ways of representing electron density. The 2 Å map of myoglobin was interpreted by building a model (on a scale of 5 cm to 1 Å with parts designed by Corey and Pauling at the California Institute of Technology) into a forest of vertical rods decorated with coloured clips at each grid point, representing the height of the electron density (Fig. 1.2.6.1). Later structures, such as those of lysozyme and carboxypeptidase, were built with 'Kendrew' models (2 cm to 1 Å) based on electron-density maps displayed as stacks of large Plexiglas sheets. A major advance came with Fred Richards' invention of the optical comparator (a 'Richards box' or 'Fred's folly') in which the model was optically superimposed onto the electron density by reflection of the model in a half-silvered mirror (Richards, 1968). This allowed for convenient fitting of model parts and accurate placement of atoms within the electron density. The Richards box was the forerunner of today's computer graphics, originally referred to as an 'electronic Richards box'. The development of computer graphics for model building was initially met with reservation, but fortunately those involved in these developments persevered. Various programs became available for model building in a computer, but the undoubted champion of this technology was *FRODO*, written by Alwyn Jones (Jones, 1978).

1.2.7. Meetings

The birth of protein crystallography in the 1950s coincided with the start of the jet age, making attendance at international meetings far easier. Indeed, the number and variety of meetings have proliferated as much as the number and variety of structures determined. A critical first for protein crystallography was a meeting held at the Hirschegg ski resort in Austria in 1966. This was organized by Max Perutz (Cambridge) and Walter Hoppe (München). About 40 scientists from around the world attended, as well as a strong representation of students (including Robert Huber) from the Münich laboratory. The first Hirschegg meeting occurred just after the structure determination of lysozyme, which helped lift the cloud of pessimism after the long wait for a new structure since the structures of the globins had been solved in the 1950s. The meeting was very much a family affair where most attendees stayed an extra few days for additional skiing. The times were more relaxed in comparison with those of today's jet-setting scientists flying directly from synchrotron to international meeting, making ever more numerous important discoveries. A second Hirschegg meeting occurred two years later, but this time the number of participants had doubled. By 1970, the meeting had to be transferred to the village of Alpbach, which had more accommodation; however, most of the participants still knew each other.

Another set of international meetings (or schools, as the Italians preferred to call them) was initiated by the Italian crystallographers in 1976 at Erice, a medieval hilltop town in Sicily. These meetings have since been repeated every six years. The local organizer was Lodovico Riva di Sanseverino, whose vivacious sensitivity instilled a feeling of international fellowship into the rapidly growing number of structural biologists. The first meeting lasted two whole weeks, a length of time that would no longer be acceptable in today's hectic, competitive atmosphere.

It took time for the staid organizers of the IUCr triennial congress to recognize the significance of macromolecular structure. Thus, for many years, the IUCr meetings were poorly attended by structural biologists. However, recent meetings have changed, with biological topics representing about half of all activities. Nevertheless, the size of these meetings and their lack of focus have led to numerous large and small specialized meetings, from small Gordon Conferences and East and West Coast crystallography meetings in the USA to huge international congresses in virology, biochemistry and other sciences.

The publication of this volume by the International Union of Crystallography, the first volume of *International Tables* devoted to macromolecular crystallography, strongly attests to the increasing importance of this vital area of science.

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