

ML.12-1 CRYSTALLOGRAPHY IN THE LIFE SCIENCES.
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The main focus of this address will be to review recent developments in macromolecular crystallography. However, because this lecture commemorates the Braggs it is appropriate to briefly review their Australian roots.

W.H. Bragg, at age 23, was appointed to the University of Adelaide as Elder Professor of Mathematics and Experimental Physics. At age 40 he began a series of experiments on radioactivity and soon became an acknowledged expert. W.L. Bragg, the son, was born in Australia and completed an Honours degree in Mathematics at the University of Adelaide before returning to England with his family in 1908.

As is well known, W.L. Bragg was an enthusiastic advocate of macromolecular crystallography. Following the first successful protein structure determinations by Kendrew, Perutz, Phillips and others the growth in the field has been explosive. The ability to determine the three-dimensional structures of increasingly complex macromolecules is an ongoing testimony to the power of the crystallographic technique. At the same time, the impact that the results have had in the life sciences has become all-pervasive.

Major achievements during recent years include the determination of the structure of the photosynthetic reaction center by Drenth, Michel and Huber, and the determinations of the structures of the common cold and polio viruses by the groups of Michael Rossmann and James Hogle. These and many other accomplishments have been facilitated in part by improved methods of data collection but especially by enhanced computing power and computer-graphics capabilities.

The potential benefits of protein crystallography have prompted many pharmaceutical firms and genetic engineering companies to establish crystallographic groups. Progress is being made in areas such as rational drug design.

Several years ago the structures of the first known DNA-binding proteins were determined. These studies suggested how such proteins recognize their specific binding sites on the DNA. More recently, the understanding of DNA-protein recognition has been substantially expanded by structure determinations of DNA-protein complexes.

The "protein folding problem" is another area of longstanding interest. By using techniques of genetic engineering it is possible to manipulate macromolecules in ways that were not feasible a few years ago. This had made it possible to systematically explore the factors that determine protein stability. Progress is being made in finding ways to increase the stability of proteins.

In summary, the future of macromolecular crystallography has never been brighter. The results already in hand dramatically demonstrate the power of the technique. However, the results to be anticipated from the combination of crystallography with allied techniques including chemistry, genetics, protein engineering and computer graphics are even more exciting.

ML.13-1 STRUCTURE SOLUTION AND REFINEMENT FROM NEUTRON AND SYNCHROTRON POWDER DIFFRACTION DATA.
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Users of powder diffraction are often not crystallographers, but chemists and materials scientists who want a technique for looking at the structure of real materials often not available as single crystals. In the years 1967-1987 the use of high resolution neutron and X-ray powder diffractometers and Rietveld methods of profile analysis, has grown rapidly: from a handful of papers in 1973, over 1000 were published in the following 10 years. These papers cover a wide range of solid state science, from catalysts to zeolites, and from battery electrodes to pre-stressed superconducting wires and welded oil pipelines.

W. H. Bragg in 1921 already saw that a powder diffraction pattern was a unique "fingerprint" of the crystal structure. Once fast computers became available, it was natural that this "fingerprint" or profile be analysed to obtain information about the structure directly, without first extracting the Bragg components. New powder diffractometers were then designed to increase the information content of the profile.

Neutron powder diffraction has been particularly successful because the absence of a form factor extends this information to small d-spacings, and systematic errors in powder averaging are smaller simply because the sample is larger. Good results have been obtained on even medium flux reactors, such as the Australian HIFAR.

With X-rays the very much higher flux available, especially with synchrotron radiation, means that very high resolution can be obtained with very small samples, though systematic errors are at present larger. Direct solution of structures is also easier with X-rays (heavy atom methods, anomalous dispersion)

I will describe some of the materials that have been recently studied, and the new machines that will extend these methods to much of inorganic chemistry. The precision of the results is such as to give chemically significant information about changes of structure with temperature, intercalation, chemical composition and applied pressure or stress in experimental times which permit detailed exploration of the effect of these parameters. The idea of measuring "the" crystal structure at standard temperature and pressure is a concept of the past.

In Grenoble we are particularly fortunate in having on the same site the high flux reactor (Institut Laue-Langevin) and the future European synchrotron source (Maxwell Institute).

Recent Reviews:

ADVANCES IN POWDER DIFFRACTION CRYSTALL. (1986)
 Guinier-Hagg Memorial Lectures, R.Swed.Acad.Sci.
 Chemica Scripta, Vol 26A, ed. Arne Magneli

HIGH RESOLUTION POWDER DIFFRACTION (1986) Proc.
 Meeting on Neutron & Synchrotron Methods,
 Materials Science Forum, Vol 9 ed. C.R.A. Catlow