STRUCTURE OF SOLIDS AND LIQUIDS: CRYSTALLOGRAPHY

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Summary

Crystallography is the study of structures at the atomic scale. Using radiation probes such as X-rays and neutrons, its armory of techniques enables us to determine not only the average structures of ideal single crystals, but also to obtain structural information on the various defects in crystals that are usually central to the operation of functional crystals. The rationale for determining structures is to try to understand the way a molecular-level system operates. With structural information to hand, we can often improve the efficiency or effectiveness of a process or function by appropriate modifications. It is thus an extremely powerful technique in trying to understand the way in which appropriate life support systems work at the molecular level, and hence in devising new and improved systems to increase the sustainability of our interactions on the environment.

Crystallographic techniques are not limited to application to crystals: we can also solve structures of glasses and liquids. The detail at which such disordered structures can be solved used to be relatively limited. However, with advances in radiation sources (in particular of neutrons), instrumentation, computer power, and the scientist's imagination, we are now able to determine structures of even quite complex liquids and solutions. We now know the structure of that liquid on which all our lives depend – water – and knowing that, we can begin to look at the way other molecular systems work, from important small molecules to very large ones such as proteins and viruses. We might even begin to understand the precise involvement of water in life processes as well as the mechanisms that nature uses to protect living systems from stress (for example from excess salt or drought).
Crystallography is an interdisciplinary science, used by physicists, chemists, biologists, geological scientists, materials scientists, environmental scientists and engineers. Understanding structure is a prerequisite of understanding function, whether of superconductors, high performance magnets, rechargeable batteries, solar power generation, aerospace alloys, specialist glasses, protein folding, virus infectivity, or the chemistry of green liquids. It is central to understanding the operational components of most life support systems.

1. Introduction

"If you want to understand function, study structure." So said Francis Crick of DNA double helix fame. Not only did he apply this maxim with respect to the functioning of biological molecules in his early days as a molecular biologist; he also believed in the neurobiological work he was doing right up to his death that structures were central to understanding even such a far more complex system as the functioning of the brain.

We exploit the properties of materials in almost everything we do. Computers depend on semiconductors which function in the way they do because of their structures. New materials are developed to enable us to build more efficient vehicles which use fewer resources. The properties of these materials that we exploit depend on their structures. An enzyme, be it one operating in our bodies, or one developed to process raw materials into useful products or to transform waste into reusable material, catalyses a reaction in a way which depends on its structure.

Methods to enable us to determine atomic level structures have been developed since the early nineteenth century. These were made possible by the discovery of X-rays by Röntgen in 1896, the realization by von Laue and Ewald, together with the experimental observations by Friedrich and Knipping in 1912, that crystals placed in the path of X-rays gave rise to patterns that could be related to the underlying arrangement of the atoms in the crystals. So began the now ubiquitous field of crystallography, which is able to tell us the structures of not only simple crystals containing only a handful of atoms. With developments over the years of sources of X-rays and neutrons, sophisticated instrumentation and fast computers, we can now determine the atomic structures of very large and complex biological molecules such as proteins and viruses that may contain hundreds of thousands of atoms. Even more impressively, we can take the data required to solve these structures in such a short time – fractions of a second – that we can in some cases follow changes in structure of a protein in real time as it

actually is doing its job. Such an ability is indeed opening up the way to understand the details of how these complex biological molecules work, offering a route to modifying them to efficiently work for us in other contexts.

Although the initial development of crystallography was, for clearly understandable technical reasons, focused on looking at materials in the crystalline form, the basic physical process that the technique exploits – the scattering of radiation with wavelengths of the same order of magnitude as the dimensions of atoms – operates on condensed matter in all its manifestations. These include glasses and liquids, as well as liquid crystals, polymer fibers, thin films, and nanometer-sized assemblies of atoms or molecules. Again thanks to advances in radiation sources, instrumentation, and computing power, not to forget a certain amount of imaginative thinking, we are now able to obtain high quality structural information on these more disordered systems. Such techniques can, for example, help us to develop glasses that are tailor made to perform a range of structural and electronic functions, as well as to improve the efficacy of chemical processes in liquid media. They can help us design new electrolytes for lighter and more efficient rechargeable batteries. One particularly interesting, relatively recent development is of ionic liquids that are thought to possibly provide the basis of a new 'green chemistry', enabling us to develop efficient chemical processing in much more benign solvents than was previously the case when we were limited to using relatively toxic organic media.

Our still-developing abilities to determine structures is enabling us to probe ever more deeply into the structures and functioning of the increasingly complex crystalline and non-crystalline materials that are increasingly needed to improve the sustainability of our existence. This article explains the basic physical process that is exploited in structure determination, and summarizes the state of development of what J. D. Bernal over 50 years ago called 'generalized crystallography' – the science of structures in crystalline and non-crystalline systems alike.

2. The Basic Principle of Atomic Structure Determination

2.1. The Scope of Crystallography

Even as applied only to determining the average structures of ordered crystals, crystallography is a highly exploited field. It is also a strongly interdisciplinary one: attend any major crystallographic conference such as the triennial congress of the International Union of Crystallography and you will likely find physicists, biologists, chemists, materials scientists, geologists, environmental scientists, chemical and electronic engineers all present and interacting with one another. The techniques used are so powerful, and so fundamental to structural science, that they are essential tools in a range of scientific subject areas. Extend the consideration to non-crystalline systems such as liquids and glasses and the field encompasses an even wider range of scientists and technologists – in fact, all who need to understand structures of any kind at the atomic level. In recent decades the techniques have been further extended to look at structures of two dimensional systems such as thin films and surfaces, while recent years have seen a further extension to nanoscale systems. Understanding the atomic level structures of all these systems and others offer the possibility of technical

advances that can be used positively in enhancing the sustainability of our existence.

2.2. The Crystallographic Ruler

What then is the physical basis of the crystallographic technique?

As for every structural measurement, we need a 'ruler' to measure distances between different elements of our system of interest – in our case primarily atoms but also electrons (see section 3.5). On a trivial level, if we want to determine the structure of a macroscopic object such as a piece of furniture, we would use some sort of measuring device like a graduated tape measure to determine the distances between different parts of the structure. Using our knowledge of simple geometry, and perhaps trigonometry, we could then reconstruct a model of the chair or table from this set of measurements. We might also then be able to see how we might, with a few small modifications, improve the functionality of the object, for example make the chair more comfortable for our bad back, extending its function by developing a rocking chair, or a fold-up one to carry about with us. Crystallography in its simplest essence is just the extension of this process to structures at the atomic scale.

First, then, we need an appropriate ruler.

The most frequent 'rulers' used are X-ray and neutrons. These can both be considered to be wavelike disturbances that have a characteristic wavelength. As we want to measure distances of the order of atomic distances, we need this ruler to be graduated in units that are compatible with the size of the structures being examined. In effect, the graduations on our ruler that in the macroscopic case would be centimeters are now the wavelength of our X-rays or neutrons which are of the order of magnitude of the interatomic distances we want to measure. We generally use neutrons or X-rays of wavelengths of typically around an Ångström unit or two ($1\text{Å} = 10^{-8}\text{cm}$).

Now we have an appropriate ruler, how do we use it to measure these small distances in our crystal or liquid?

To understand this, it is useful to go back over two centuries to the classical experiment of Thomas Young, who in 1803 published a paper that was to demonstrate conclusively the wave nature of light. In Young's Experiment we place narrow slit in front of a source of light to produce a narrow beam of light. Between this 'source slit' and a screen, we place an opaque sheet in which have been cut two slits aligned parallel to the source slit. This setup is shown in Figure 1(a). What we now observe on the screen is a set of 'fringes' – alternately dark and light regions as shown in Figure 1(b). We can now easily show that the separation of these fringes is related to the separation of the pair of slits in a simple way: if the separation of the slits is s, the distance between these slits and the screen is d, and the wavelength of the light used is λ, then the fringe separation D is given simply by $\lambda d/s$. If we now change the subject of this equation, we find that the separation between the slits is given by the expression

$$s = \lambda d/D \qquad (1).$$

Knowing the scale of our ruler (λ), this simple experiment thus enables us to use it to measure the distance *s* between our two slits.

We now extend this to the atomic level situation. Replacing our slits by a pair of atoms and our light source by a source of neutrons, measuring the separation between the fringes produced on a detector (the equivalent of the screen in the optical two-slit Young's experiment) by the two atoms will enable us to calculate how far our atoms are apart. We will have used our neutron ruler to obtain the distance between our two atoms.

This very simple concept is the basis of the whole of X-ray, neutron, and electron crystallography. This is the case whether we are looking at crystals of simple or complex molecules, solutions of polymers, or complicated glasses. The details of the application of the technique may be more complex and can be found in the relevant texts (see bibliography), but the above discussion contains most of the physics of the process. In effect, all else is detail.

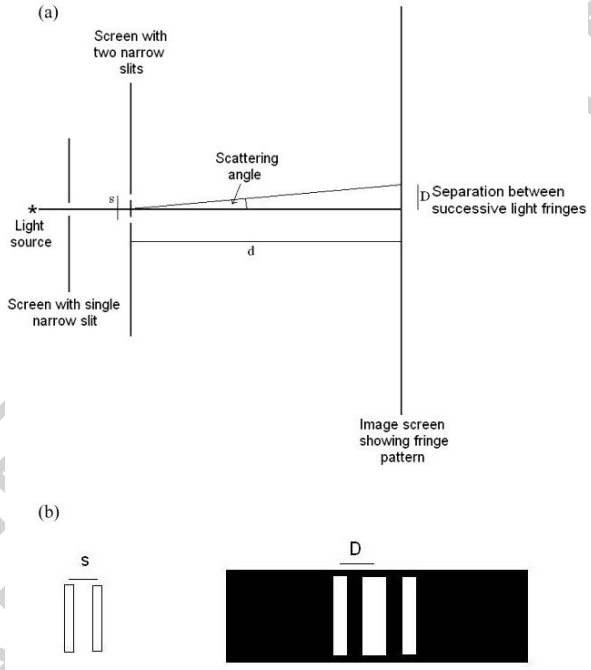

Figure 1. (a). The Young's slit experimental setup. (b). A schematic of the fringes seen on the screen (right) for the pair of slits shown on the left. The fringe separation *D* relates to the slit separation through the simple equation (1) given in the text. Because of the inverse relationship between *s* and *D*, as we reduce *s*, the position of the first fringe moves along the screen away from its centre and the scattering angle increases. Higher scattering angles therefore probe shorter distances in the sample.

3. Crystallography of Crystals

3.1. Diffraction from 'Ideal' Single Crystals

As argued above, the results of a diffraction experiment, for example of neutrons, on an

array of scattering centers, for example the nuclei of an assembly of atoms, will depend on all the distances between all pairs of nuclei in the assembly. We then need to look at this diffraction pattern to extract the information we want on the structure of the assembly – for example the coordinates of all the atoms in it. Although this information on pair distances is contained in the observed pattern of diffracted neutrons, the nature of this diffraction pattern can take on different characters depending on the nature of the atomic or molecular assembly that we are investigating. As it is the simplest kind of system from which to extract this structural information, we examine first crystalline arrangements of molecules, for which it is possible to make major simplifications.

First of all, we need to appreciate that in an ideal crystal, the molecules are arranged on a regular, repeating lattice. Although the formal definition of a lattice is that the surroundings of each lattice point are identical, the simplest way to picture the main structural consequence of this definition is that the lattice points are arranged in a regular, repeating way, for example as in the two dimensional analogue in Figure 2(a). We can immediately see that it is possible to describe this array of lattice points in terms of a small part of it – called the unit cell – that is defined by the two repeat distances shown (the lattice parameters *a* and *b*) and the angle α between them. The complete lattice can then be generated by translating the unit cell in the two coordinate directions. We can clearly extend this description to three dimensions, for which in general we need three unit cell parameters *a*, *b*, and *c*, and three interaxial angles α, β, and γ. For specific cases, there will be additional symmetry in the lattice, for example one or more of the angles might be 90°, or two or more of the unit cell parameters might be equal. This will reduce the number of lattice parameters we need to describe the structure. There are also different kinds of lattices that need to be considered when we look at real systems.

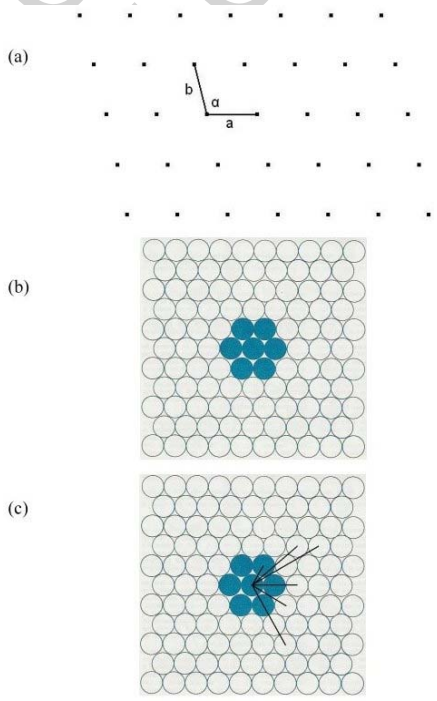

Figure 2. (a). A simple two dimensional lattice, showing the definition of a unit cell. (b).

A two dimensional hexagonal structure of disc-shaped atoms, each of which 'decorates' a lattice point of the underlying lattice. Crystals of more complex molecules are built up in the same way, with one or more of the molecules in the crystal decorating each lattice point. (c). The first few interatomic pair distances found in the structure of (b).

To obtain the crystal of actual atoms or molecules, we now need to decorate this lattice with the atoms or molecules. The simplest kind of decoration is shown in the two dimensional hexagonally symmetric analogue of Figure 2(b) in which a circular atom is placed on each lattice point. The decoration however need not be so simple: for example, each lattice point might be decorated by a relatively complex motif such as shown in figure 3. The decorating motif could be a simple molecule in a given orientation, or even one or more much more complex protein or virus molecules.

No matter how complicated the molecules that are contained in the crystal, placing them in a crystalline environment simplifies the diffraction pattern in a particularly useful way: because of the periodic regularity of a crystalline arrangement, the number of pair distances that our diffraction experiment reports back to us is limited to a number that can be handled. For example, taking the simple example of a single kind of atom in a crystal based on the two dimensional hexagonal lattice of Figure 2(b), the first few pair distances that are observed are (in order of increasing length) a, 1.73a, 2a, 2,65a, 3a, 3.46a, …, where a is the shortest distance between two atoms (Figure 2(c)). Clearly, as we go to longer distances, there are more and more pairs to consider, but as the basic structure needs only a few of these for its structure to be defined, we need only a few of these from our experiment. And these will be reported back by the diffraction experiment as discussed above. Moreover, as these basic distances are found very many times in the crystal, they will be reported by the diffraction experiment many times. Each of these reporting signals will be reported to us in the diffraction pattern many times, so the corresponding features in the diffraction pattern that we measure will be very strong.

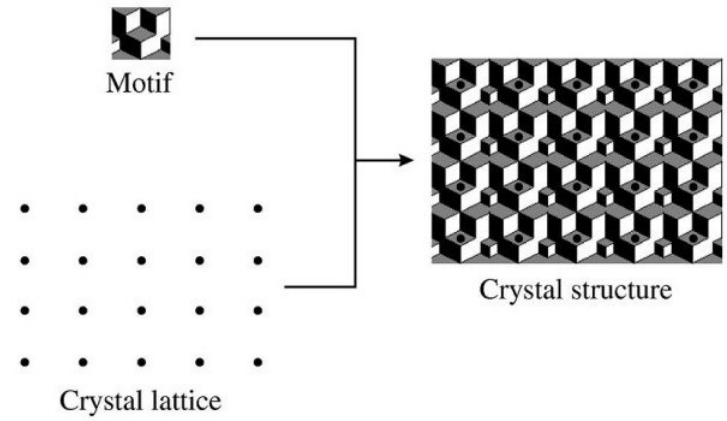

Figure 3. Generating a relatively complex crystal by decorating each lattice point by the motif shown. In real crystals, this motif might be one or several small molecules, or much larger biomolecules.

But what in this case are the features that we measure in our diffraction pattern? To understand this, let's extend the Young's slit experiment we discussed earlier. Rather

than having just the two slits which represented our two scattering centers, we now take a line of slits as in the top half of Figure 4 and look at what happens. The result is shown on the screen represented in the lower half of Figure 4 which can be compared with the two-slit result in Figure 1(b). Rather than just the few broad fringes we observed there, we now see a larger number of sharper fringes, or lines. In fact, the more slits we have, the sharper the lines become, an observation that we will come back later in the context of crystallite size. The separation between the diffraction lines is however unchanged from the two slit case – as this fringe separation relates to the slit separation (our model of the pair distance in the atom case) as described by the simple equation (1) in the previous section.

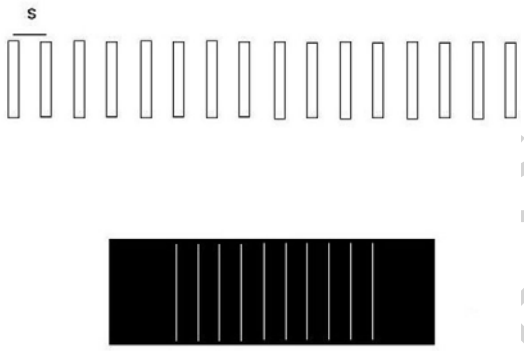

Figure 4. The effect on fringe sharpness of increasing the number of slits in the Young's slit experiment.

Let's now make the final set of generalizations from this simple multiple slit system to move us towards a model crystal. First, crystals are made up of atoms, not slits in masks. If we replace the slits in the above experiment with small holes to represent atoms, then we will still get similar diffraction effects, though the diffraction lines will be transformed into planes of intensity. So diffraction from a one dimensional 'crystal' of holes gives a set of bright planes, for example as shown in Figure 5(a). If we turn this into a two dimensional crystal by making a mask along the lines of, for example, Figure 2(a), the set of holes along one direction, say the *x* direction, will give rise to a set of planes normal to the *x* direction (Figure 5(a)), and similarly for the set of holes along the *y* direction (Figure 5(b)). If we now make the final jump into three dimensions by stacking up a set of two dimensional masks along the *z* direction to represent the full three dimensional crystal, our diffraction pattern will also include a set of planes of intensity normal to this third *z* direction, as shown in Figure 5(c). What we will observe in practice however will not be intensity in all these planes, but only their intersection. This will be just a set of bright spots in three dimensions, as indicated in Figure 5(d). And as we know that the separations of the original planes will depend on the basic distances between the atoms that gave rise to them – in this simple illustration the lattice parameters – the arrangement of these spots can themselves be used to obtain information on the basic distances in the crystal, and hence its structure.

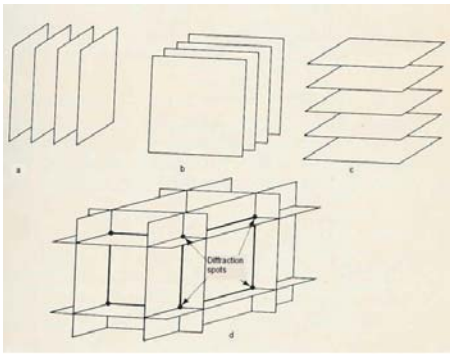

Figure 5. The generation of the diffraction pattern from a three dimensional crystal from three one dimensional sets of atoms (after Henry S. Lipson).

Of course, most crystals are much more complex than consisting of just single atoms in a unit cell, so interpreting a real diffraction pattern is in practice more complex, and a number of special techniques have been developed to do this. However, the basic physics mechanism that is operating is little more than that described above. Summarizing the results of following the development of the argument for an arbitrary crystal, we find that the geometry of the arrangements of the observed spots tells us the structure of the basic lattice on which the actual crystal is built. Each spot however will not be of the same intensity, and this intensity variation will depend on both the kinds of atoms in the crystal and their locations within each unit cell. So by measuring the positions and intensities of the diffraction spots, we can in principle obtain the position of the atoms in the crystal – the crystal structure.

Formally, the diffraction pattern is a relatively simple mathematical function – the Fourier transform – of the crystal structure. One property of the Fourier transform is that if B is the Fourier transform of A, then A is the Fourier transform of B. Thus if A represents our crystal structure, then B denotes its diffraction pattern, we should be able to Fourier invert the measured data to obtain the original structure. However, although this is in principle possible, because we are able to measure only intensities of diffraction spots rather than amplitudes (intensity is essentially the square of the amplitude), our diffraction pattern does not contain all the information we need to do this. We are missing what is called phase information for each spot; this relates to actual positions of the atoms with respect to the underlying lattice, and is a quantity that is apparently lost in the measured intensity. Much of the early effort in the development of crystallography was to find ways around this problem. Many techniques now exist for obtaining this essential information (or 'solving the phase problem') so that solving crystal structures from single crystal data is now generally a straightforward procedure.

An example of a diffraction pattern from a single crystal of a relatively complex molecule, a protein, is given in Figure 6. What is shown here is one of the planes of diffraction spots, of which many will be collected in solving the structure. The regular periodicity of the pattern reflects the regular periodicity of the underlying lattice, while the variation in spot intensity allows us to locate the positions of the atoms in the molecules that decorate the underlying lattice.

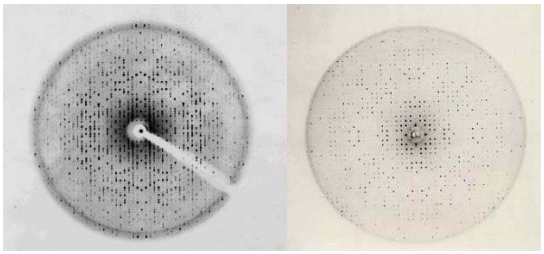

Figure 6. Two planes of the X-ray diffraction pattern measured from a single crystal of bovine γB-crystallin, a protein from the eye lens. The right hand photograph was taken along the four-fold axis of this tetragonal crystal, and clearly shows four fold symmetry in the pattern. While these patterns were measured on film, increasingly other detectors are used which allow direct readout of positions and intensities by computers. Courtesy P. F. Lindley and C. Slingsby.

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Biographical Sketch

John L. Finney, is Professor of Physics at University College London, where he set up a new research and teaching group in condensed matter and materials physics. His major research interests are in structures and interactions in liquids, with particular reference to water and aqueous solutions, the role of water in biological processes, and the structures of ice under pressure. He is a Fellow of the Institute of Physics and of the Royal Society of Chemistry, honorary Vice-President of Euroscience, Chair of the Rammal Award Panel, and Vice-Chair of the British Crystallographic Association. Obtaining a first degree in Natural Sciences at Jesus College Cambridge, he joined J. D. Bernal at Birkbeck College London as his research assistant, where he worked on structural models of simple liquids and metallic glasses. As a Lecturer there, he developed his interest in water in an environment of molecular biology and protein crystallography. He was promoted to Reader in 1977 and awarded a personal chair in 1986. From 1988 to 1993, he was Head of Neutron Science (Chief Scientist from 1990) at the UK's new pulsed spallation neutron source ISIS, where he was responsible for building up the user science program. From 1993 to 1996, he was Science Coordinator of the European Spallation Source Project, a program which subsequently led to the current construction of the US Spallation Neutron Source at Oak Ridge. He has published over 200 peer-reviewed research papers, and gave the Bragg lectures in 2004/5. He was co-chair of the 2002 Water Gordon Conference, and co-organizer of a 2003 Royal Society Discussion on 'Is Life possible without Water".