17.2. Molecular graphics and animation

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17.2.1. Introduction

Visualizing the unseeable world of molecules is the fundamental goal of crystallographic structure determination. Thus there is a natural synergy between the science of unravelling molecular structure and the technology of representing it. Graphics have always had a significant role in the analysis of diffraction data, the synthesis of molecular models and the communication of the information and knowledge gained in these scientific pursuits. At least since the time of René Häuy in the 18th century, crystallographers have attempted to use graphics and physical models to understand and explain the underlying nature of the solid state (Fig. 17.2.1.1). Over the years, crystallography has pushed the development of new technologies to aid in structure solution, and crystallographers have been early adaptors of new technologies. No technology has had more impact on crystallography than electronic computing. Nowhere is that impact more apparent than in what we have been able to study and how we have been able to visualize our structural results. With the pervasiveness of three-dimensional computer graphics in many aspects of everyday life, it is easy to forget the role that X-ray crystallography has played in its genesis and the role that graphics technology continues to play in the advancement of molecular structure analysis.

The human genome project and other efforts in biology and medicine have produced heightened emphasis on molecular depictions of increasing complexity. Visualization of such systems through computer-graphics technology is a key component in our understanding of these data and the models that we use to explain them. In fact, modelling and visualization techniques provide a bridge between experimental data at different scales, enabling placement of detailed atomic models of molecules from crystallography into lower-resolution data on large assemblies from electron microscopy or scanning probe imaging.

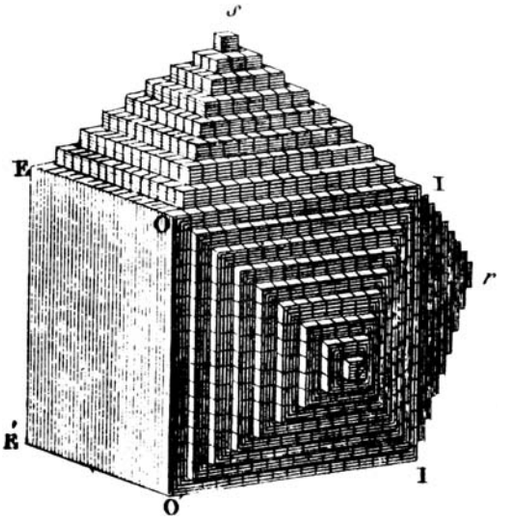

Fig. 17.2.1.1. Model of a crystal structure proposed by René Häuy in *Traite elementaire de Physique*, Vol. 1 [Paris: De L'Imprimerie de Delance et Lesueur, 1803]. This model, proposed in 1784, was the first to connect the external facets of a crystal with an underlying regular arrangement of building blocks.

17.2.2. Background – the evolution of molecular graphics hardware and software

The complexity of molecular structure and the fact that these submicroscopic objects of study are not directly visible have necessitated the use of physical or pictorial representations to aid in interpretation, manipulation and understanding. Illustrations and models made of wood, plastic or metal served these purposes from the development of the original theories of molecular structure through to the first nucleic acid and protein structures solved in the 1950s. Over the following years, computer graphics has evolved into a significant and ubiquitous technology, helping to sustain the explosive growth of macromolecular structure research. Today, computer graphics pervade the activities of much molecule-based research, from quantum chemistry to molecular biology.

Computer-based molecular graphics can be traced back to 1948 and the X-RAC project of R. Pepinsky at Pennsylvania State University (Pepinsky, 1952). Pepinsky developed an analogue computer to carry out the Fourier transformation of X-ray structure factors to produce electron-density maps. Integrated within X-RAC was an oscilloscope that could display the contours of the electron density (Fig. 17.2.2.1). These displays were, to my knowledge, the first computer-generated images of molecular structure. Crystallographers from around the world came to Pennsylvania State University to use X-RAC and to marvel at the speed and automation possible in the solution of molecular structures. While the digital revolution quickly overtook the analogue approach, X-RAC clearly set the precedent for molecular scientists as early implementors and adaptors of computational and graphics technology.

In the 1960s, two seminal projects laid the foundation for modern molecular graphics. Early in the decade, Johnson's *ORTEP* (Johnson, 1970) program became widely available, allowing crystallographers to produce illustrations of three-dimensional (3-D) molecular structures on a pen plotter. These black-and-white line drawings of ball-and-stick models were used both for working drawings during structure analysis and for creating illustrations for publication. A few years later, experiments lead by Levinthal under Project MAC (Levinthal, 1966) at MIT pioneered the interactive display and transformation of 3-D molecular structures on a computer screen. By the end of the

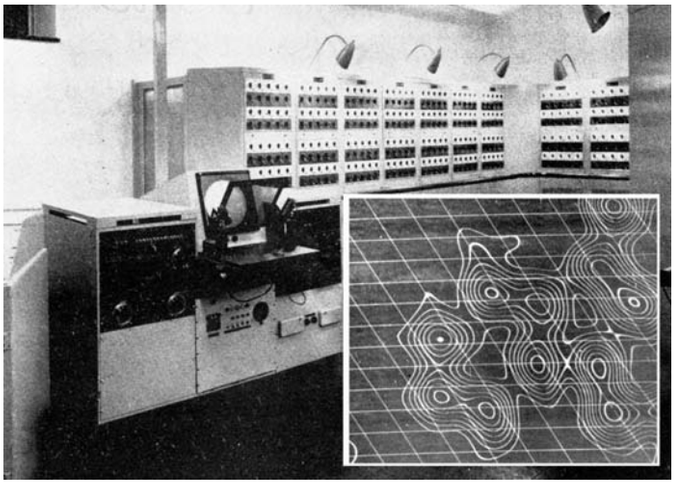

Fig. 17.2.2.1. One bay of X-RAC showing coefficient panels and the display oscilloscope. Inset: photo from the oscilloscope, showing a region of the phthalocyanine Fourier map. Reproduced from Pepinsky (1952).

references