

FOREWORD

The *FEBS* Summer School on *Computing Techniques in Biochemistry* was not designed to teach advanced programming methods, but was organized in the belief that there is a large area of sophisticated computation in biochemistry in which the mathematical techniques have either not been worked out, or are not readily available to the average biochemist. For many reasons, not least economic ones, the techniques of interest have been much more intensively studied in chemical engineering, or in aerospace or nuclear energy research. At the same time, biochemical applications have their own particular problems, and it seemed desirable that biochemists with a wide range of interests and mathematical training should have the opportunity to discuss their difficulties at length with professional statisticians and numerical analysts. At the same time, it proved possible to invite several world leaders of research in this area who are nominally or actually biochemists to present their most recent results and to take part in the discussions.

Biochemical interest is at present concentrated on the simulation of single-enzyme and multi-enzyme systems (metabolic pathways), and in the estimation of rate constants from the results of isotopic tracer experiments. A particularly urgent problem here is the provision of confidence regions for the estimates, and the testing of goodness of fit of the results with the model hypothesis. An associated technical problem is the extent to which analog – and particularly hybrid analog – computers can usefully contribute to the solution of both simulation and optimization problems. Analog computation is almost inevitably undervalued in most computing centres, which are staffed almost conclusively by digital computer experts.

The foregoing summary assumes that problems of data processing or data transformation are not of sufficient interest to justify discussion at such an extended assembly. To some extent this is not at all true. Leaving aside the computation associated with X-ray

crystallography of biological structures (which in Europe, at least, is concentrated in rather few Institutes), the deduction of amino acid sequences in proteins from partial degradation data, and the related problems of computing the most stable configurations of proteins (and perhaps also of nucleic acids), are not straightforward. They certainly ought to be discussed, together with other programs which by then may exist in the field of “quantum biochemistry”, in any future meeting of this kind.

The participants in the School did indeed find the discussions, arranged on the plan outlined above, helpful, and many asked that a permanent record might be made of the main conclusions. The invited lecturers and discussion leaders agreed that any printed record should concentrate on giving practical advice and detailed directions of immediate relevance to situations which had been discussed at the School. It was agreed that this could most easily be achieved if the papers were published informally in a Journal, and I am very grateful to the Editoriat of *FEBS Letters* for making this possible.

The technical content of the contributions varies very widely, from the philosophical papers of Dr. Berman and Dr. Garfinkel, outlining their approaches to modelling problems on the basis of many years' experience, to the detailed mathematical arguments of Dr. Barnes and Dr. Cooper. This mixture of strategy and tactics is a deliberate one, and it is hoped that it will be helpful at all stages of dealing with problems of this kind. One contribution should be mentioned in somewhat more detail. Aris has already pointed out that chemical engineers might well tackle the problem of tracer movements in terms of expected residence time in each compartment, rather than by the traditional reliance on differential equations. Although there was no discussion at the School of Markov chains, Dr. Sheppard's paper on Monte Carlo methods in treating diffusion problems is a welcome reminder of the rather neglected power of probability theory in dealing with tracer kinetics.

The School would not have been a success if it had not been for the friendliness, and readiness to help in what was to them an unfamiliar field, of the applied mathematicians who acted as advisers. One would particularly like to thank Dr. A.Curtis, of A.E.R.E. Harwell, Mr. B.Girling, of The City University, Mr. E.F. Harding, of the Statistics Department in Edinburgh, Dr. W.H.Swann, of I.C.I. Ltd., and above all Prof. Sidney Michaelson, Head of the Computer Science Department in Edinburgh.

The theoretical discussions were interspersed with an ~~extensive~~ programme of practical computing, in the arrangement of which Drs. E.M.Chance and A.K. Grzybowski, of University College London, were par-

ticularly helpful. This practical work would not have been possible without a generous provision of free computing time and other services from the Edinburgh Regional Computing Centre, to the Director of which, Dr. G.E.Thomas, many thanks are due. IBM (UK) Ltd. and Electronics Associated Ltd. provided much specialist help with programs and equipment. Finally, our thanks are due to the Royal Society and the Volkswagen Stiftung for generous financial assistance, without which many participants would not have been able to attend.

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