

There was very little use of still frames which, for example, could have made a dramatic difference to the demonstration of oviduct transfer. The range of techniques demonstrated is quite wide, and it is questionable if this were desirable at the expense of a deeper and more comprehensive coverage of basic transgenic techniques. Perhaps a demonstration of tail biopsy could have been included, an essential but simple technique which could have been demonstrated quickly. There are other omissions, for example no mention of the use of retroviral infection was made; while this is not widely used, it would have been appropriate to mention retroviruses when showing the removal of the zona pellucida from 8-cell eggs. One serious criticism of the video is that there was no demonstration of production of the various pipettes used for embryo manipulation. Production of good pipettes is not trivial, and the use of poor pipettes can make the techniques much more difficult.

Production of such a video is an ambitious undertaking. The same factors which make the techniques difficult are those which make them difficult to demonstrate. The video gives an impression of what is involved in transgenic mouse work, but a visit to an established laboratory would be of far greater benefit

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Computational Molecular Biology Sources and Methods for Sequence Analysis. Edited by ARTHUR M. LESK. Oxford University Press. 1989. 254 pages. £25.00. ISBN 0 19 854218 6.

It is now impossible to do experimental molecular biology without occasional recourse to computers and in many cases, for example a shotgun sequencing project, operating the computer has become a major component of the process.

As most molecular biologists still do not have any formal training in computing there is a real need for books on computation molecular biology. This one, prepared under the auspices of the CODATA Task Group on Protein Sequence Databases and edited by Arthur Lesk, draws together contributions from many

of those who are active in the provision of computing resources for molecular biologists.

The book is organized around the four questions: (1) What data are available? (2) What calculations can be done? (3) How does one gain access to the necessary data and to the necessary programs? and (4) How can the results of the calculations be intelligently and cautiously interpreted? The book consists of twenty relatively self-contained contributions in the style of scientific papers from about forty authors; something that is probably essential to cover adequately such a wide-ranging subject. The suitability of the editor as a person to organize such disparate material is attested to by his own contributions, the subjects of which range from computer networks to molecular evolution.

All of the contributions are from workers in the forefront of their fields and many, particularly those at the beginning of the book intended to answer questions (1) and (3), are extremely detailed indeed. For this reason the book will prove of especial value to someone charged with setting up computing resources for any group that has previously been without them.

The later chapters on methods of analysis, perhaps wisely, do not descend to the same level of detail, concentrating instead on how the user should interpret the output of the programs. The reader who is actually interested in details of algorithms and implementations will, however, be well served by the extensive bibliography, complete, I am happy to say, with titles. For a newcomer to the field this alone will be worth the price of the book.

Although this book is expensive for its size, it can be recommended for the very large amount of useful information fitted into so small a space. For my own part I was pleased to see the clearly articulated warnings included in the descriptions of the more speculative types of analysis. Those included in the chapters on assessment of significance of sequence similarities and on protein secondary structure prediction should be put on the syllabus of all undergraduate biochemistry courses.

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