

The opening chapter has a brief historical survey of how the Indian contributions to mathematics and astronomy evolved from the Vedic times to about a millennium ago. It is a quick run through *Vedang Jyothisha*, *Siddhantas* and later astronomical traditions, coupled with accounts of the works of some major players like Aryabhata I. The next chapter describes the zodiac and the major constellations, and how they were mapped on the sky. Here the author uses modern notation, but tells us what the older contents were. The same applies to the various astronomical coordinate systems in vogue today. Thus one learns what is the difference between the sayana and nirayana systems, what are dakshinayana and uttarayana, and so on.

A major aspect of astronomical observations is linked with timekeeping over long timescales. What do the *Mahayuga*, *Manvantara*, *Kalpa*, etc. mean? How does one link the present Julian calendar to these systems? Chapter 4 deals with this aspect. The real meat of the work begins in Chapter 5 where calculations are carried out for Ahargana, that is, counting the number of days lapsed since a chosen past epoch. There are several examples worked out to illustrate the method.

The next three chapters deal with the angular motions of the Sun and the Moon across the sky, and the determination of the exact positions of these objects on specified instants. The problem would have been simple, had these objects moved on circles with uniform angular speeds. This not being the case, the Greeks had to invoke the epicyclic theory, which was also used by the Indian astronomers who refer to the calculation as Mandaphala. Here the author explains the calculation including the technical words used by the ancients, such as *Blujantara*, *Udayantara*, *Mandakendrajya*, etc.

All this is useful for determining the occurrence of eclipses which require special alignments of the Earth, the Moon and the Sun. Chapters 9 and 10 are devoted to carrying out these calculations. One needs several details and looking back one admires the attention to detail given by Aryabhata and other astronomers who followed him. The author also points out that these astronomers knew that the eclipses were shadow-plays and did not encourage the myths of Rahu and Ketu. Yet social

forces seem to have been stronger than scientific ones and the myths gained ground. What can we say today, when more than 50% of the population prefer believing in myths than in facts, judging by their responses on such eclipses?

Chapters 11 and 12 extend the calculations to the planets known in those days, viz. Mercury, Venus, Mars, Jupiter and Saturn, which had their own Indian names. Again, epicyclic corrections are needed to achieve precision.

Nevertheless, the late T. S. Kuppanna Sastry suggested improvements on the old eclipse calculations to make them more accurate. The enthusiast may follow them in Chapter 13. In Chapter 14 the author calculates corrections to the earlier planetary positions to make them more in conformity with the modern values. He points out that the earlier astronomers were aware that their computations need to be revised from time to time as the corrections (*bijas*) get larger.

As if anticipating that the modern student would be too impatient with and may lack competence with carrying out a series of tedious trigonometric calculations, the author has given computer programs in dBASE to compute most of these quantities. Around seventy pages of the book contain computer programs.

A few minor blemishes intrude from time to time. The celestial meridian is not defined where it is needed most. A uniform labelling of the celestial equator, the ecliptic, etc. would have helped in comparing different figures. A historic discussion of the epicyclic theory would have added to the understanding of why one has to do these intricate calculations. The index could have been more exhaustive.

These intrusions are, however, of a transient nature and do not in any way detract from the usefulness of this work. The author should be congratulated for undertaking it and taking it to a satisfactory level of exhaustiveness. Any student of mathematical astronomy would appreciate the effort.

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**Method for Affinity-based Separations of Enzymes and Proteins.** Gupta, M. N. (ed.). Birkhäuser Verlag, P.O. Box 133, CH-4010, Basel, Switzerland. 2002. 225 pp. Price not indicated.

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Affinity chromatography is like the queen among the various methods used for the purification of proteins and other biomacromolecules. Protein purification had generally been an arduous task until the advent of affinity chromatography. Most protein purification protocols of the earlier days involved a series of chromatographic and precipitation steps, each resulting in a diminished recovery of the active ingredient, usually with only a moderate improvement in the specific activity, ultimately yielding a small fraction of the activity in a nearly pure fraction. Papers reporting partial purification of enzymes and other proteins were not uncommon. The procedures normally took several days and often weeks. Fortunately, affinity chromatography has brought in a revolution in the approach to protein purification and made the purification of proteins a rather pleasant and rewarding task.

The book edited by Gupta gives an excellent update on the state-of-the-art separation methods that employ an 'affinity' step in the overall scheme; quite often it is the only step! For most practising biochemists affinity chromatography is a well-known technique. But the variety of improvements and modifications made to the basic affinity chromatographic technique, leading to a variety of affinity-based purification methods, which are covered in this book, is simply beyond imagination. If you have a protein purification problem, see if this book can help you solve it and most probably, it will. Even if there is a working method, it is likely that you will benefit by trying to modify the method by incorporating an affinity-based step in the protocol.

The book contains eleven well-written chapters. The introductory chapter by Gupta and Roy provides a brief historical background for affinity-based separation methods followed by an excellent overview of the variety of different separation methods that employ an 'affinity' step. The next chapter on 'Affinity Chromatography' by Labrou describes general methods for the selection of a suitable affinity ligand, its immobiliza-

tion and chromatographic separation of the desired protein. Newer developments such as expanded bed affinity chromatography, perfusion affinity chromatography, use of affinity-enabled disks for affinity-based analysis, purification and conversion of biomolecules have been covered in chapters 3, 4 and 5 authored by Lali, Farhner and Blank, and Berruex and Freitag respectively. A lucid description of the use of sugars as affinity ligands is given by Satish and Surolia in chapter 6. General, broad-based application of macroaffinity ligands such as chitosan, Eudragit and alginate in bio-separation is detailed in chapter 7 by Roy and Gupta. Use of cellulose binding domains as affinity tags is illustrated in chapter 8 by Kilburn and colleagues.

Application of two-phase affinity partitioning for the separation of animal cells is elegantly described by Kumar *et al.* in chapter 9. This technique, which employs a polymer with a covalently-linked affinity ligand as a stimuli-responsive soluble-insoluble polymer, is also useful for the purification of soluble molecules as well as subcellular organelles. Reverse phase micellar separations that employ small molecule-protein, protein-protein and antibody-protein affinity interactions form the subject of chapter 10 written by Adachi. Analysis of the kinetics of analyte-receptor interactions in biosensors by fractals is illustrated in the last chapter by Ramakrishnan and Sadana.

Each chapter begins with an appropriate 'Introduction', which provides a number of references to original literature. This is followed by a 'Materials' section that gives a list of chemicals and equipment (and, very often the sources from which they can be obtained) required for the methods described in the chapter. Specific details of the reagent conditions as well as their preparation and storage are also given in most cases. After this, a 'Methods' section gives specific 'stepwise' protocols for various procedures and explanatory notes to clarify some of the points that may not be immediately obvious. A 'Troubleshooting' section gives useful hints to circumvent or solve frequently encountered problems in the various protocols. An 'Applications' section provides specific examples where some of the methods given in the chapter are illustrated. Each chapter ends with a 'Conclusions and Remarks' section, which places the

methods described in the chapter in perspective with respect to the current practices and applications. 'Further Reading' section at the end of the chapter gives the reader additional sources where he/she can find more elaborate coverage of the topic(s) covered in the chapter. These are usually books or monographs. Each chapter also cites a good number of original references from the literature, which can be looked up for further details.

Despite the impressive appearance and many positive points in the way the book has been produced, there are a few minor errors and discrepancies, which could have been avoided/corrected by more careful editorial work. For example, the reference formatting lacks consistency and in some of the chapters, inconsistent within the same chapter. For example, *Journal of Chromatography* was abbreviated as *J of Chromatog* (p. 62, third line from bottom) and as *J Chromatog* (p. 62, last line) in the same page, while the correct abbreviation should have been *J. Chromatogr. Archives of Biochem. Biophysics* (p. 63, reference 12), *Proc. National Acad. Sci. (Biochem)* (p. 63, ref. 10), *J Chrom* (p. 81, reference 3) are some more examples. Clearly, the authors themselves are responsible for these errors, but one expects that the editors should make sure that such errors are corrected. However, notwithstanding these minor errors, this book is well brought out and hopefully, when additional copies are printed, or if another edition of the book is published in the near future, these will be corrected.

Overall, the book provides a topical collection of articles that give specific protocols describing the use of affinity-based methods not only for the separation of proteins and enzymes, but also in applications involving immobilized enzymes as bioconverters. I strongly recommend this book to all institutional libraries that are accessed by practising biochemists as well as to individual scientists who are actively engaged in protein purification.

Reading this book has been a learning experience for me, and I am sure it will be for many other readers as well.

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**Probability and Its Applications – Probability Models for DNA Sequence Evolution.** R. Durrett, Springer Verlag, Tiegartenstraße 17, D-69121 Heidelberg, Germany. 2002. 240 pp. US\$ 69.95.

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The abundance of genomic data has been a boon for a wide range of scientists, mathematicians included. This should not be a great surprise: the huge amount of sequence data that is generated is most easily subjected to a first analysis by the methods of statistics. With the sequencing of large numbers of related organisms, comparative genomics, the study of the genomes of related (or unrelated) organisms has become possible. A case in point is the recent assault on malaria, where not only was the parasite *Plasmodium falciparum* sequenced, but also *P. yoelii* which causes malaria in rodents, *Anopheles gambiae*, the mosquito which carries it, and both the human and mouse genome drafts are already available, so that two related parasites, the carrier, and their related victims were all genomically 'bared'. While the benefits of such detailed investigation of organisms at the molecular level can only be reaped slowly, and mainly by the biologist, mathematicians can hope to look at the DNA to answer a different set of questions.

What determines the variability in a bank of DNA sequences? (I was wondering what the collective noun for a set of DNA sequences should be and settled upon bank as evocative of GenBank, the megarepository of all genomic information).

Is it possible to reliably ascertain where the human race actually originated? (The 'out of Africa' hypothesis). How does DNA (the selfish genome!) itself evolve?

Such questions were asked long before there was such a surfeit of sequence data, and reflect the earliest applications of statistics and probability theory to DNA.

Durrett's monograph on Probability models for DNA sequence evolution is an accessible introduction to some of the mathematics and statistics of genome analysis, mainly that part of probability theory that deals with DNA evolution.

Stochastic methods are essential for reconstructing evolutionary history. The population that can be observed today is