gives an overall description of neutrino propagation in dense astrophysical systems, their transport and hydrodynamics, starting from various initial conditions. It also discusses the many-body interaction of neutrinos with matter. The results presented in the article are, however, indicative, not definitive, because of the complexity of the problem and the uncertainty in the input quantities ('Neutrino propagation in dense astrophysical systems' by M. Prakash et al.).

Many compelling questions in nature are addressed in nuclear astrophysics. They relate to nucleosynthesis at different astrophysical sites, stellar evolution, total density of matter in the universe, etc. Since at the stage of evolution of the universe the nuclear interaction time was considerably shorter than the lifetime of nuclei, critical quantities which enter in the astrophysical models of these environments are the rate and energy release of several nuclear reactions involving unstable (radioactive) nuclei. Rapid developments in accelerator technology and nuclear instrumentation have initiated a new era in nuclear physics where beams of radioactive nuclei with sufficient intensity, purity, and quality are being made available for experiments. This book carries an excellent review article on this subject. It identifies specific nuclear reactions entering in stellar dynamics, describes different techniques for producing radioactive ion beams (RIB) and summarizes different existing and upcoming RIB facilities worldwide. The RIB, in addition to being of fundamental importance in astrophysics, is also of much interest in nuclear physics currently. It opens up new horizons in nuclear physics for the study of structure of nuclei away from the stability line in general ('Nuclear astrophysics measurements with radioactive beams', Michael S. Smith and K. Ernst Rehm).

In traditional nuclear physics, the most challenging task had been the understanding of nuclear properties starting from the realistic nuclear forces. This requires the knowledge of nuclear forces and the availability of techniques to solve the many-body problems. We do have by now a tremendous amount of experimental data on nucleon–nucleon scattering that can be accurately described in terms of two-body potentials. These potentials, of course, are complicated, depending on the relative positions, spins, isospins and momenta of the nucleons. This makes

finding accurate quantum mechanical solutions of the bound and scattering states of the nucleus a demanding task. In addition, such calculations, when carried out for three- and four-nucleon systems, reveal the existence of three nucleon forces, which makes the task even more difficult. Till recently, exact quantum mechanical calculations with the realistic potentials had been possible up to mass-4 systems only. In the shell-model framework 'no core' calculations have been done recently for p-shell nuclei using effective interaction derived from the realistic potential using the G-matrix method. One article in the volume goes beyond this. It focuses on recent developments in quantum Monte Carlo methods, which make it possible to access the p-shell nuclei at the level of accuracy close to that obtained in exact calculations for the s-shell ($A = 4$). The article presents the technical details of the calculations, which include the variational Monte Carlo and Green's function Monte Carlo techniques. Results for more than 30 states in $A < 9$ have been obtained with an excellent reproduction of the experimental energy spectrum. This is a landmark achievement. It encourages us to believe that the nuclear system can be understood quantum mechanically starting from a known two- and three-body force, provided we have techniques to solve the many-body systems accurately ('Quantum Monte Carlo calculations of light nuclei' by Steven C. Pieper and R. B. Wiringa).

Another many-body system which has been seen to have tremendous similarity in their properties with nuclear systems, are atomic clusters. They are the confined aggregates of atoms or molecules varying in numbers from a few to several tens of thousands. Thus they provide the paradigm for understanding how matter builds from its elementary constituents to the bulk matter. Clusters, like nuclei, lie between these two limits. Their properties show novel structures and thermodynamic properties not present in bulk matter. Like nuclei, these clusters show shell structure and associated magic number behaviour. Two systems show similar shape, dipole vibration mode and thermodynamic decay behaviour in excited states. One article in this volume discusses in detail the metal clusters. These clusters are composed of delocalized electrons from the metal atom and the resulting ions. The presence of ions, which are absent in nuclei, introduces difference in

some properties like fission and particle decays. While many theoretical nuclear physicists have contributed to the atomic cluster studies, experimental nuclear physicists have not been forthcoming to the same extent. The article invites this community to join in the endeavour. ('Atomic clusters as a branch of nuclear physics' by S. G. Frauendorf and Claude Guet).

Gerald E. Brown has made several pioneering research contributions in many areas of theoretical physics. He has worked with many scientists like Gregory Breit, Rudolph Peierls and Hans Bethe, and had been associated with many international centers of pioneering physics research. The volume contains a brief autobiographical write-up by Brown, which starts with his observation about how his training in many areas of physics derived impetus from 'flying with eagles'. It is a revealing and an interesting article ('Fly with eagles' by G. E. Brown).

All in all, this volume of *Annual Review of Nuclear and Particle Science* gives an overview of several research areas of this subject, which are of current interest. It is good to have such a volume in one's library.

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Molecular Systematics and Evolution: Theory and Practice. R. DeSalle, G. Giribet and W. Wheeler (eds). Birkhauser Verlag, P. O. Box 133, CH-4010 Basel, Switzerland. 2002. 309 pp. Price not mentioned.

This is an interesting book, dealing with molecular techniques in systematics and evolutionary biology. It is a compilation of 18 papers by eminent scientists in their respective fields. The book is divided into three sections and contains an extensive list of references. The editors have done a great job in putting together recent advances in the areas of molecular systematics and evolution. It covers both computational and experimental developments.

The first section has six chapters. It deals with the importance of morphological data in evolutionary and systematics analysis. There have been many concepts in defining a species. The phylogenetic concept is more important from the standpoint of empirical testing. In order to understand phylogenetic relationship, systematic studies at the taxonomic level may be necessary. The addition of taxa may minimize the probability of getting 'incorrect phylogenies'. The phylogenetic information, not adequately present in the avian anatomy, may be obtained from molecular genetics. It may be necessary to include both molecular and morphological data for the same taxa in a single phylogenetic analysis, so that the conflict between these two can be directly addressed. It may so happen that the functional properties of simple nucleotide characters cannot be well understood. However, the evolutionary history of certain morphological characters can be followed by palaeontological methods to infer the functional significance. Some biologists prefer to depend more on sequence data by considering the fact that morphological characters are more prone to selective convergence. One set of data can be preferred over another depending on the evolutionary problem one is interested in. Some topics in this list are the rate of evolution, susceptibility to convergent selection pressures, rates of insertions and deletions of nucleotides, mode of inheritance and complexity of characters. One faces difficulty in estimating higher-level phylogeny through the alignment of sequence data from divergent groups. The alignment becomes tedious, especially for non-protein coding regions. The alignment ambiguity can be related to taxon sampling and more closely related taxa which have less alignment ambiguity. This ambiguity may be resolved in some alignment regions by adding more taxa to a study because the new taxa may have intermediate states that can shed light about homology statements across alignments. The combination of taxon sampling and analyses of molecular data can provide greater insights into the evolution of most diverse groups of organisms. The ribosomal gene 18S rRNA data set is the one currently available for understanding the full diversity of metazoan taxa. The patterns reflected in the evolution of 18S rRNA loci are highly congruent with morphological data.

The second section has seven chapters that discuss the problems of multiple sequence alignment, the popular methods of constructing phylogenetic trees, designating species through molecular data and evolution-development (evo-devo) studies in systematics. Multiple sequence alignment is a method to convert sequences of unequal length into equal-length character strings by inserting gaps. A gap implies that an insertion or deletion of a residue has occurred when the sequences diverged from a common ancestor. As a result, homologous residues are absent in the gapped regions. The different alignments can be the product of alternative ways of parametrization resulting in the complexity of phylogenetic analyses. Although the genomic and other biological data are being accumulated at a faster rate, our attempt to synthesize the data into the evolutionary picture is still incomplete. Phylogenetic tree analysis is a promising approach in this direction, although it generates certain computational problems. The number of evolutionary trees expands as more organisms need to be examined. The challenge of evolutionary computation can be tackled by creating efficient heuristic tree-search algorithms and developing parallel algorithms. The two most popular methods of constructing phylogenetic trees from genetic sequence data are 'maximum parsimony' and 'maximum likelihood'. There are some relationships between them. Parsimony can be regarded as a type of maximum likelihood estimator in the absence of a common mechanism between sites. Some statistical properties of the parsimony criterion are presented. One can choose different methods to analyse sequence data, which is called 'pluralism'. It is suggested that one should use a method on the basis of philosophical rationale and that there is no justification for pluralism in phylogenetic systematics. An important problem in evolutionary biology has been the search for a species concept as a unit in the hierarchy of life. The general interpretation of cladograms as proper representations of phylogeny is viewed as inconsistent. Certain philosophical ideas about this are examined. As we gather more molecular sequence data, we feel the diminished importance of morphological data, especially when they enter into conflict with sequence data. The authors emphasize the importance of the interactions of taxa and data. Morphological data have clear

advantages as they provide fossil taxa, cost-effectiveness and character data not containing molecular biases. The purpose of evo-devo is to incorporate the molecular developmental data into evolutionary analysis. The importance of evo-devo studies in systematics has consequently been highlighted.

The third section covers comparative methods in both molecular and bacterial evolution. Due to the process of gene duplication and divergence in the course of evolution, majority of the proteins are organized hierarchically into families. Molecular phylogenetics constructs evolutionary relationship among genes and provides a framework for comparative evolutionary analyses of proteins and their functions. Some comparative analyses are the construction of diversification of gene families, evolutionary changes in protein functions and prediction of structure–function relationships. On asking the question as to why traits evolved, comparative biology attempts to investigate the process of evolution. The homology approach focuses on a single inferred evolutionary event and draws conclusions from the sequence of correlated character changes. The various homoplasy methods arrive at inferences by considering repeated origination of correlated traits. The symbiotic association between eukaryotic hosts and their microbial partners provides a model to study the evolution and speciation of mutualistic partnerships. By measuring the degree of infectivity between closely related pairs and unifying the morphological and molecular data, one can study the patterns of co-speciation. The reconstruction of evolutionary history in microbial organisms depends on the nature of genetic information that is passed vertically from parent to daughter, or horizontally among distant relatives. The genomic data of microorganisms should examine both types of inheritance.

The book is meant for students and researchers in evolutionary biology, molecular systematics and ecology. Both theoreticians and experimentalists will benefit immensely.

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