

## **Book reviews**

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### **J. NICOLAS & A. GOTELLI: A primer of ecology.**

Sunderland, Sinauer Associates Publishers, 1995, 206 pp. ISBN 0-87893-270-4 (soft-cover).

The book under review is manual for U. S. university students of ecology who have specific interest in studying mathematical approaches to ecology and population genetics. Its author, NICOLAS J. GOTELLI, professor of Vermont University, sees the main task of the book in detailed elucidation of the most general mathematical models in ecology of populations and communities.

All the chapters of the book are organized according to a single scheme which includes the following: model presentation and predictions, model assumptions, model variations, empirical examples and problems.

The book consist of seven chapters which are devoted to exponential population growth, logistic population growth, age-structured population growth, metapopulation dynamism, competition, predation, island biogeography.

The advantage of this work, apart from the apt and thoroughly analysed examples, in our opinion, is in the fact that it is intended for the ecologist who have not come across mathematical model earlier. In this way the book will be very useful not only to students, but to the researchers who want to master the new methods of mathematical modelling as well.

V. KRICSFALUSY

## **Book reviews**

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### **L. WANG & A. CUMING [eds.]: Embryogenesis, the generation of a plant**

BIOS Scientific Publishers Ltd, 9 Newtec Place, Magdalen Road, Oxford OX4 1RE, U.K., 1996, ISBN 1-85996-065-0

The book brings together recent advances on plant embryogenesis by key workers in this field. The application of genetics and molecular biology to the study of embryogenesis represent major advances in the understanding of plant development.

The chapters in this book represent papers presented at the Society for Experimental Biology's meeting at St. Andrews University on April 3-5, 1995. The morphological descriptions of the development of crucifers (Chapter 1), grasses (Chapter 6) and legumens (Chapter 12) are included. Chapter 10 is devoted to endosperm development. Several chapters have been allotted to *Arabidopsis*, the model system. Major crop species (such as maize) have been considered. Comparisons with development in *Drosophila* have proved fruitful for studies on many aspects of plant development.

I can recommend the book to advanced undergraduate students, postgraduate students as well as researchers interesting in plant development.

R. BRUTOVSKÁ

## **Book reviews**

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### **PRUSINKIEWICZ P. & LINDENMAYER A.: The Algorithmic Beauty of Plants**

Springer Verlag New York Inc., 175 Fifth Avenue, New York, NY 10010, USA; first soft cover printing 1996; XII+228 pp., 150 illustrations, 48 in colour; ISBN 0-387-94676-4 (pbk).

Many people admire a beauty of plants. Somewhat less people admire a beauty of mathematics. This exclusive book is devoted to those, who understand both plants and mathematics. Among the factors, which contribute to the beauty of plants (e. g. symmetry) the book deals with developmental algorithms; rules which describe plant development in time and self-similarity, the basic principle of Mandelbrot's geometry of fractals. These factors are, however, closely linked together, because self-similarity in plants is a result of developmental processes. These are captured using the formalism of L-systems. They were introduced in 1968 by Aristid Lindenmayer as a theoretical framework for studying the development of simple multicellular organisms, and subsequently applied to investigate higher plants and plant organs. Unfortunately, seriously ill, Prof. Lindenmayer (1925-1989) co-authored and edited several chapters, but was not able to participate in the completion of this work.

The book is divided into 8 chapters: Graphical modelling using L-systems, Modelling of trees, Developmental models of herbaceous plants, Phyllotaxis, Models of plant organs, Animation of plant development, Modelling of cellular layers, Fractal properties of plants. After the epilogue the following appendices complete the book: Software environment for plant modelling and detailed description of the colour images.

Perfect pictures are one of conspicuous features of this book and represent link between science and art. Even those who do not like mathematics too much will certainly look them over with an interest. However, the study of book itself requires only general knowledge of mathematics at the junior college level. Thus the book is intended for wide circle of readers especially for those who like combining of several disciplines, interdisciplinary approach to problem solution and those who are thus inspired to non-traditional view to further problems of science.

P. MÁRTONFI

## **CRUSE H.: Neural Networks as Cybernetic Systems**

Georg Thieme Verlag, Rüdigerstraße 14, 70469 Stuttgart, Germany; 1996; VIII+167 pp., 125 illustrations; ISBN 3-13-102181-0 (G. Thieme Verlag); ISBN 0-86577-672-5 (Thieme Medical Publishers).

Excellent textbook for graduated courses in neurobiology, neuroinformatics and ethology. However, dynamic systems occur not only in these fields, but in various fields of biology and tools provided can also be applied outside of biology, e. g. psychology, economics, physics, etc.

The author combines in the book classical systems theory with its simple neural models and recent developments in the field of artificial neural networks with their large number of channels. He proceeds from basic input function (step, impulse, sine, statistical & ramp function), through Fourier analysis, the properties of the most important filters to the chapters on linear and non-linear systems, feedback systems, massively parallel systems and feedforward networks. Pattern completion and other questions of recurrent networks would certainly be interesting for botanist, or better, taxonomists. Final chapters are devoted, besides other problems, to learning, some special recurrent networks, animats and last chapter 18 deals with the question „Might machines have feelings?“ Two appendices are devoted to Laplace transformation and simulation of dynamic systems and the textbook is completed by essential references and index.

Text is well-arranged, clear and is based not on differential equations or on complex variables, but rather on illustrations.

The book can be recommended for all interested in neurobiology, ethology, ecology, metabolism and morphogenesis.

P. MÁRTONFI

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## **JOHN H. GILLESPIE [ed.]: The Causes of Molecular Evolution**

Oxford University Press, Inc., 200 Madison Avenue, New York, New York 10016, 1991; ISBN 0-87893-452-9.

The book is divided into three parts. The first consists of three chapters (Protein Evolution, DNA Evolution, and The Molecular Clock) that review the experimental observations on genetic variation. The second is made up of two chapters (Selection in a Fluctuating Environment and SSWM approximations) that give a unified treatment of the mathematical theory of selection in a fluctuating environment. The final two chapters (Neutral Allele Theories and Selection Theories) combine the earliest chapters in a treatment of the scientific status of two competing theories for the maintenance of genetic variation.

The chapter on protein evolution begins with a series of examples of microadaptations, where one or few amino acid changes in a protein are implicated in an adaptation. Part of the arguments involves a short treatment of the thermodynamics of protein folding designed to show that it is not chemically unreasonable for even conservative amino acid changes to alter kinetic properties of proteins.

The chapter on DNA evolution concentrates on silent variation within coding regions. Two general questions are examined: does mutation limit the rate of silent substitution, and does the

spectrum of silent substitutions match the mutational spectrum? Both questions are answered in the affirmative, although the available data are still too sparse to make these answers definitive. Next, the evolution of GC% and codon usage is discussed. Finally, patterns of DNA polymorphisms are reviewed.

The molecular clock is the focus of the third chapter. In it we see that rates of nucleotide substitution are anything but constant. Variation in rates may be partitioned into lineage effects, variation shared by all loci on a particular lineage, and residual effects, variation left over once lineage effects are removed. One example of a lineage effect is the generation-time effect.

In the fourth chapter we turn from data to mathematics. If we are to propose that molecular evolution is due to the action of natural selection, we need a mathematical theory to demonstrate that the dynamics of selection are compatible with the observations on molecular variation. This chapter is littered with unresolved problems that should prove interesting to those with a mathematical bent.

The next chapter demonstrates how population genetic models that involve strong selection and weak mutation may be approximated by a technique that brings even the most difficult of problems into submission. The approximating models, called SSWM Markov chains, can be used to describe the genealogy of alleles. In this chapter the author formulates a number of models that exhibit the same episodic pattern of substitutions inferred in the analysis of the protein evolution data.

The chapter on neutral allele theories, the first of two concerned with the fundamental scientific issues posed by the first three chapters, begins with an examination of the assumptions underlying the neutral theory, proceeds to examine the arguments that bear on the theory, and concludes that the theory should probably be abandoned for amino acid variation but may be valid for silent variation. Whatever neutral variation is present is likely to be far from equilibrium, reflecting historical events.

The final chapter presents the selection alternative. After summarizing the arguments supporting the role of natural selection on amino acids, a strong-selection model is described that is compatible with the episodic molecular clock. Some speculations on a unified theory of selection in a fluctuating environment are presented that should provide a springboard for further work.

I would like to recommend the book to all who is interested in field of molecular evolution.

P. KUŠNIRIKOVÁ

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### **RIDLEY M. [ed.]: Evolution**

Oxford University Press, Great Clarendon Street, Oxford OX2 6DP, UK; 1997; VIII+430 pp.; ISBN 0-19-289287-8.

Mark Ridley, Lecturer at Somerville College, a member of the Zoological Department at the University of Oxford arranged an interesting anthology of works about evolution since the period of Charles Darwin up to these days (1996). Ridley start with historical section, but only in a chronological sense, because people are still interested in ideas of Ch. Darwin, R. A. Fisher, S. Wright and others. Section B (Selection in action) brings several examples of scientific studies from various research programmes, e. g. A. C. Allison - Protection afforded by sickle-cell trait

against subtertian malarial infection (1954); famous study by H. B. D. Kettlewell - A résumé of investigations on the evolution of melanism in the Lepidoptera (1956) and J. B. S. Haldane - The theory of selection for melanism in Lepidoptera (1956) and newer studies: H. Lisle Gibbs and Peter R. Grant - Oscillating selection on Darwin's finches (1987), R. M. Nesse and G. C. Williams - Bacterial resistance to antibiotics (1996). In the 1960s the research programme became more complicated when it encountered the first ripples of molecular evidence (Section C - Neutral drift and molecular evolution - R. C. Lewontin, M. Kimura, T. Ohta, M. Kreitman). In section D (Adaptation) the papers deal with three main issues: what adaptation means; whether adaptations evolve gradually; and the importance of adaptation in living things (from authors for example R. A. Fisher, H. Allen Orr, Jerry A. Coyne, A. J. Cain, S. J. Gould, R. C. Lewontin). Section E is devoted to Biodiversity (E. Mayr, V. Grant, M. Ridley and others). Section F is titled Reconstructing the past and consist only of four works, which deal with the study of human evolution by computers (A. W. F. Edwards), homology (Gavin de Beer, W. J. Dickinson) and the question „the eyeless gene“ (R. Dawkins). Section G. Macroevolution deals with evolution on the grand scale and mainly studies in the fossil record. And section H - it is a section with case studies, of course. Among nine papers in this section let us mention at least two: classical paper on the genetic code: F. H. C. Crick - The origin of the genetic code (1968) and J. Maynard Smith - The maintenance of sex (1971). Final two sections (I and J) are devoted to Human evolution and Evolution in education, ethics, philosophy and religion. Among the authors, the following ones are mentioned: Frank B. Livingstone, Theodosius Dobzhansky, J. L. Monod, T. H. Huxley and final essay by George C. Williams (Gaia, nature worship, and biocentric fallacies) is devoted to hypothesis of superorganism and planetary homeostasis.

The book is completed by selected bibliography, biographical notes and index. To conclude, we can state nothing, but agree with Jared M. Diamond from University of California, whose opinion can be found on the cover of paperback: „Ridley gathers together dozens of the most important writings on evolution, from Darwin's own unpublished thoughts to the latest results of molecular biology. This Reader profits from Ridley's clear introductions, setting the papers into large framework ... a book that makes as interesting bedtime reading for the educated layperson as it offers an interesting and valuable resource to students and professional scientist.“

P. MÁRTONFI

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**HILLIS D. M., C. MORITZ & BARBARA K. MABLE [eds.]: Molecular Systematics. Second Edition.**

Sinauer Associates, Inc., Massachusetts, USA; 1996; XVI+655 pp., ISBN 0-87893-282-8 (paper lay - flat bdg.)

New edition of book already reviewed in *Thaiszia - Journal of Botany* (5: 196, 1995). Excellent specialists from The University of Texas and University of Queensland re-wrote the text of handbook with regard to new knowledge.

The book is divided also into three main parts (Sampling, Molecular Techniques and Analysis). Authors decided to drop the chapter on immunological techniques, which are no longer widely used in systematic studies and included a new chapter devoted to polymerase chain reaction (PCR). They also aimed at incorporation of more information on the processes of molecular evolution. In the third part besides the evaluation of questions of intraspecific differentiation

(Chapter 10) the authors devoted extensive chapter 11 (p. 407-514) Phylogenetic Inference. Types of data and optimality criteria are dealt in detail. Parsimony methods are dealt as the first and besides frequently used ones (e. g. Fitch and Wagner parsimony) the reader obtains also information about Dollo parsimony, Camin-Sokal parsimony or transversion parsimony (but not in a sense of Lake J. A., *Mol. Biol. Evol.* 4: 167-191, 1987 and other authors!). Parsimony on protein sequences and on allozyme data is dealt in detail, too. Further optimality criteria are methods based on models of evolutionary change. maximum likelihood methods, pairwise distance methods, Hadamard conjugation and Lake's method of invariants are described very well. Of course, methods of searching for optimal trees and discussion about systematic and random errors in phylogenetic studies follow afterwards. Appendix of this chapter, which lists programs and software packages available for conducting phylogenetic and population genetic analyses is useful.

For a systematist who looks into certain systematic problem and would like to solve it by means of molecular methods and have not become familiar with them so far, the table 1 can be recommended (p. 517). Tables summarizes possibilities of applications of various molecular techniques to problems in systematics. Basic techniques are defined as follows: isozymes, cytogenetics, DNA hybridization, restriction analysis, fragment analysis (includes recommendations for RAPDs, single locus mini- or microsatellites and multilocus DNA fingerprinting) and DNA/RNA sequencing. Basic problems are covered by gene evolution, population subdivision, mating systems, clonal detection, heterozygosity, paternity testing, individual relatedness, geographic variation, hybridization, species boundaries and phylogeny (divided 0-5, 5-50, 50-500, 500-3500 mya).

P. MÁRTONFI

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### **MICHAEL J. E. STERNBERG [ed.]: Protein Structure Prediction: A Practical Approach**

Oxford University Press Inc., Walton Street, Oxford OX2 6DP, U.K., 1996, ISBN 0-19-963496-3.

Prediction of the three-dimensional structure of a protein from its sequence is a problem faced by an increasing number of biological scientists as they strive to utilize genetic information. *Protein Structure Prediction: A Practical Approach* provides a timely description of current approaches and their validity. It describes in detail the various computer-based strategies for translating sequence into structure, highlighting the degree of confidence that can be attributed to different algorithms.

The increasing sizes of the sequence and structural databases, the improvements in computing power, and deeper understanding of the principles of protein structure have led to major developments in the field over the last few years. To present an integrated review of the practical approach, the book is organized along the same lines as the procedure one follows starting with a sequence. First, the book summarizes the principles underlying prediction and overviews the general procedure. Chapter 2 focus on sequence analysis to identify homologies. Chapter 3 reviews methods for the automatic identification of a given sequence motif in a sequence or set of sequences. The next chapter deals with the prediction of protein secondary structure that is a major part of the general protein folding problem and the most general method of obtaining some

structural information from any newly-determined sequence. Chapter 5 focus on the topology prediction problem: how to identify transmembrane segments and how to predict the overall orientation of the protein in the membrane. Chapter 6 describes obtaining coordinates from comparative (homology) modelling with the application of this methodology to antibody structure being reported in the following section. In Chapter 8 the authors describe progress in the methods for tertiary structure prediction, based on fold recognition from amino acid sequence. The combinatorial approach reported in Chapter 9 spans secondary and tertiary structure prediction. The application of energy calculations to protein modelling is reported in Chapter 10. A major goal of prediction is to assist in the design of novel ligands and the present methodology is then reported. Finally the results of blind trials of the success of prediction are described.

*Protein Structure Prediction: A Practical Approach* is a unique compendium of facts and advice in this increasingly important field. It will be invaluable both for non-specialists who require guidance in identifying and evaluating appropriate strategies and for experts who require up-to-date information on the latest techniques and approaches.

P. KUŠNIRIKOVÁ

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**TOLMACHEV A. I. (Russian Edition Editor), PACKER J. G. (English Edition Editor), GRIFFITHS G. C. D. (Translator): Flora of the Russian Arctic. Volume I. Polypodiaceae - Gramineae.**

The University of Alberta Press, Athabasca Hall, Edmonton, Alberta, Canada T6G 2E8; 1995; XXXVIII+330 pp., 23+85 maps; ISBN 0-88864-269-5 (Vol. I.).

**TOLMACHEV A. I. (Russian Edition Editor), PACKER J. G. (English Edition Editor), GRIFFITHS G. C. D. (Translator): Flora of the Russian Arctic. Volume II. Cyperaceae - Orchidaceae.**

The University of Alberta Press, Athabasca Hall, Edmonton, Alberta, Canada T6G 2E8; 1995; XXVIII+233 pp., 65+31 maps; ISBN 0-88864-270-9 (Vol. II.).

Dr. John G. Packer, Professor Emeritus of Botany at the University of Alberta initiated translation and publication of the 10-volume *Arkticheskaya flora SSSR* (*Flora Arctica URSS*) in 1988, when the publication of original volumes have been finished (1960-1987). *Arkticheskaya flora SSSR* was written by taxonomic specialist at the V. L. Komarov Botanical Institute, St. Petersburg, under the editorship of A. I. Tolmachev and, following his death, by B. A. Yurtsev. Original Russian edition of the flora uses the classification of Engler and treats some 360 genera, 1650 species and 220 infraspecific taxa, mostly subspecies. Included are descriptions of many new species and subspecies and numerous new combinations.

The English translation, *Flora of the Russian Arctic*, will be published in six volumes (1995-1998) and represents the first English-language flora of the arctic region from the Barents Sea to the Bering Strait. The first two reviewed volumes of translation comprise 19 families, namely Volume I (volumes I & II of original edition, Polypodiaceae, Ophioglossaceae, Equisetaceae, Lycopodiaceae, Selaginellaceae, Pinaceae, Cupressaceae, Sparganiaceae, Potamogetonaceae, Juncaginaceae, Alismataceae, Butomaceae and Gramineae) and Volume II (volumes III & IV of



original edition, Cyperaceae, Lemnaceae, Juncaceae, Liliaceae, Iridaceae and Orchidaceae). Families contain keys to genera, genera keys to species, synonymy, discussion to the species and their distribution, in many cases original distribution maps are present.

As far as linguistic aspect of translation is concerned, translator remarkably chose so-called „popular system“ of transliteration of cyrilic, that has evolved in English-language newspaper, which is the same as that used on maps produced by the National Geographic Society of the USA except for omission of the apostrophe used to represent the cyrilic hard and soft signs. In tangle of various systems of transliterations in botanical texts (e. g. Paclt J: Taxon 2: 159-166, 1953; ISO-1 standard, etc.) this approach seems to me one of the best, first at all by its simplicity.

Including of translator Preface in every volume can be considered as positive feature; besides other things the reader learns, that since this is translation, not a revised edition, new nomenclatorial proposals are presented in the same form as in the original Russian edition, indicated by „sp. nova“, „comb. nova“ etc.

In conclusion nothing remains to do but to evaluate this editorial act in accordance with the note on cover, that the comprehensive content and accomplished scholarship of this work, along with the size of the area covered, make Flora of the Russian Arctic an essential part of every botanical library.

P. MÁRTONFI