focus all our attention on these problems, or whether these are just some issues and there are others that are equally important. For example, no chapters confront in detail the evolution of interspecific interactions or the process of coevolution. The interaction biodiversity of the earth is as much a product of evolution as is species biodiversity and genetic diversity. Processes such as gene-for-gene coevolution and coevolutionary alternation mold the genetic diversity of interacting taxa.

There are so many issues to address in biodiversity that the problem is in getting our priorities straight. One of the points that emerges from these chapters, and is highlighted in one of the section overviews by Sean Nee and a group of co-authors, is the continuing real need for better integration of evolutionary perspectives with many ecological and conservation issues in biodiversity. These chapters help to show some of the places where the integration is best and worst. That, in itself, is a useful contribution, because it points to aspects of biodiversity where some of most important work needs still to be done.

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Genetic Data Analysis II. Bruce S. Weir. Sinauer Associates, Inc. Publishers, Sunderland, Massachusetts. 1996. Pp. 445. Price £24.95, paperback. ISBN 0 87893 902 4.

Do not be misled by the title of this book: it is not the second volume of Weir's *Genetic Data Analysis* (1990), but a second edition. Indeed, the publishers should take note that the Library of Congress catalogue entry refuses to record the 'II' and just lists it as the second edition. Other librarians should do likewise.

The first edition was an immediate success, filling a large gap in the literature. In the new edition the original Chapter 6 'Analyses between generations' has been expanded into three chapters, 'Individual identification', 'Linkage', and 'Outcrossing and selection'. Computer programs are no longer included, but an insert advises that they may be obtained from the author's Web site. All the typographical and other errors which I noticed in the first edition seem to have been corrected.

The field which the book covers is now so large, and growing so fast, that in many parts the treatment is necessarily introductory, especially in the cases of 'Linkage' (Chapter 7) and 'Phylogeny reconstruction' (Chapter 10), but up-to-date references to the specialist literature are given. The author has, however, missed an important book on the latter topic, perhaps because it is not in English. *Reconstruction phylogénétique* by P. Darlu and P. Tassy (Masson, Paris, 1993).

It cannot be often that a reviewer finds that a table from one of his own papers has become the cover illustration for the book under review, but my rendering of Mendel's original data is used as a kind of backdrop to the cover of the new *Genetic Data Analysis* (from *Biological Reviews*, **61**, 295, 1986, source acknowledged). In Weir's typesetting, however, the Greek χ of the χ^2 test has been replaced by a Roman X and X^2 for Pearson's chi-squared criterion is used throughout the book as it was in the first edition. This is presumably an attempt to apply the convention that random variables are lower-case while their realized values are upper-case. Introduced for χ^2 by W. G. Cochran (*Biometrics*, **10**, 417) in 1954 it is doubly to be regretted, first because although Greek χ and Roman x differ in lower case, they are both X in upper case and x is an overworked letter in statistics, and secondly because Pearson's criterion is not exactly distributed as χ^2 anyway, even when the null hypothesis is true (which it never is). It is reminiscent of the attempt to call the *ABO* blood-group genes I^A, I^B and I^O, which died a natural death. In notation, too much logic is not a good thing.

This new edition of a well-established text is greatly to be welcomed, and selects itself automatically as the preferred text for a course on the subject. There are many worked examples as well as exercises in abundances. The printing and the paper have both been improved. I hope the author will be able to keep up with the field and present us with a third edition in due course.

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Genomes of Plants and Animals (21st Stadler Genetics Symposium). J. Perry Gustafson and R. B. Flavell (eds). Plenum Press, New York. 1996. Pp. 319. Price $85.00 (USA), hardback. ISBN 0 306 45372 X.

There has been considerable controversy over the value of big budget genome projects. What of value will come from them? If most DNA is non-coding, how will the coding DNA be distinguished from the non-coding DNA and what is the point of spending any time on the non-coding sequences? *Genomes of Plants and Animals* provides some convincing answers to these questions. The book is the result of the 21st Stadler Genetics Symposium and consists of a collection of papers ranging across the field of genome biology.

Unlike many books of this nature, the papers are well presented and the figures are reproduced clearly. Papers describe advances in genome analysis technology, progress on the major genome projects, the application of current technology to breeding and conservation programmes, and the use of the technology and data generated thus far to answer a range of biologically interesting questions.

Genome projects are clearly providing a rich source of data for evolutionary biologists and several papers cover current advances in this area. Furthermore the book includes interesting papers on transgene stability, and the influence of genome structure on gene expression and on recombination frequency.

For those not directly involved in large-scale genome research this book provides a snap shot of the state of the art in 1995. The book brings together work from prokaryotes and eukaryotes, and from plants and animals, demonstrating the broad range of possible applications. It will clearly become out-dated quickly, but none-the-less includes much information and theory which are more durable. This sort of information is hard to come by without tracking down individual research papers in the area, which are scattered over diverse journals.

The impact of the technical and theoretical consequences of genome analysis projects are being felt right across biology. Whether or not you think that the money could have been better spent, there are few biologists who have not benefited directly or indirectly from their output. There are still some who seem to think that genome projects generate nothing but a string of As, Gs, Cs and Ts, to them this book will be a much needed wake up call. There are many more who think that the most important results of genome analysis are ethical dilemmas which we would rather not have to face. Dick Flavell's concluding paper addresses these issues too. He stresses the need for openness and for better education for all sectors of society, so that we can benefit from the enormous opportunities offered by the responsible use of the new data and new technologies.

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Genetics of Sex Determination (Advances in Genome Biology, 4). Ram S. Verma (ed.). JAI Press Ltd., London. 1996. Pp. 368. Price £69.50 ($109.50), hardback. ISBN 1 55938 836 6.

The mammalian testis-determining gene *SRY* was isolated over six years ago, but still we remain ignorant of which genes are regulated by its protein product and whether this likely transcription factor activates downstream genes, represses them, or both. Fortunately, this collection of articles does not dwell on our ignorance, but reviews the wealth of data which exists concerning the genetics of sex determination and other related topics.

The book begins with an historical overview of the genetics of sex determination (Mittwoch) which offers some speculative hypotheses concerning the role of the Y chromosome in male development. It is Mittwoch's contention that the well-documented precocious growth of the mammalian testis is integral to its differentiation from the indifferent gonad *and* is a Y-linked genetic trait; an ovarian fate is the normal, growth-retarded gonadal alternative. Mittwoch suggests that a growth-rate/temporal threshold model helps to explain a number of problems, including that of XY^{Pos} or XYd sex reversal in the mouse. This phenomenon is discussed in detail in the excellent chapter on sex reversal in mammals by Nagamine. Briefly, when the *poschiavinus* Y chromosome is bred onto a C57Bl/6J background, males, females or hermaphrodites develop. The sex reversal, which becomes more prevalent after further backcrossing on to the C57Bl/6J background, is presumably the consequence of X-linked or autosomal modifiers of the Y^{Pos} sex-determining activity. The nature of these modifiers remains unknown and any number of processes may be affected in the hybrid genomic environment of the XYd foetus. With respect to Mittwoch's hypothesis, the fact that testicular cords form about 14 hours later in XYd foetuses does not imply that it is growth-rate which normally dictates the fate of the indifferent gonad. Two facts are relevant here: firstly, XY preimplantation embryos develop more quickly than their XX counterparts due to the accelerating properties of the Y chromosome; and secondly, XY embryos normally develop testes due to the expression of *Sry* in the developing gonad. However, there appears to be no compelling evidence that these two phenomena are related. *Sry* is not responsible for the first phenomenon, and the mechanism by which it results in Sertoli cell differentiation in the bipotential gonad, reviewed by O'Neill and Sinclair, may not be connected with growth-rate at all. Chromosomally female (XX) embryos transgenic for *Sry* can develop as males, and this would seem to relegate growth-rate as a sex-determining mechanism to a possible statistical phenomenon, perhaps tilting the balance, but not exerting a necessary or sufficient effect.

Several chapters discuss topics not strictly related to sex determination, including X-chromosome inactivation (Lyon), the pseudoautosomal regions of the human sex chromosomes (Rappold), mammalian spermatogenesis (Hale), the genetics of pseudohermaphroditism (Simpson) and sex chromosome aberrations (Anhalt and Neely). McElreavey offers a highly plausible model of mammalian sex determination based on the genetics of human sex reversal, particularly the frequency of *SRY*-negative XX males. This model describes a repressive function for *SRY*, suggesting that it acts as a negative-regulator of a negative-regulator of male-specific gene function. The consequence of this double negative is that *SRY* activity results in male differentiation. Candidates exist for the various players in this hypothetical drama; the X-linked locus *DSS* is a plausible repressor of male-specific gene activity, and the *SRY*-related gene *Sox9* is expressed in a male-specific fashion in the developing mouse gonad, suggesting it acts downstream of *SRY* activity. Interestingly, the male-specific expression pattern of *Sox9* in the gonad is conserved between mammals and chicken (a fact no doubt