

less familiar that I found novel and stimulating. The broad topic area would ensure that most readers would find something new. In addition to the intrinsic interest of the systems covered, the chapters illustrate the uses and limitations of a variety of methods to examine nucleic acids and their complexes at different structural levels. Examples include quantitation of DNA distortion by gel retardation analysis, described in detail for Fos and Jun complexes, and hydroxyl radical footprinting and the missing nucleoside experiment described for TFIIIA complexes. Like many specialized scientific books, it is a little expensive but probably less so

than going to a conference in which all these topics were discussed. Indeed, the book is rather like attending a series of lectures at a good conference with the advantage of having a permanent record of the proceedings together with appropriate references.

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Books received

The Evolutionary Biology of Viruses. Stephen S. Morse (ed.) Raven Press, New York. 1993. Pp. 367. Price £59.00, hardback. ISBN 0 7817 0119 8.

Transcription: Mechanisms and Regulation [Raven Press Series on Molecular and Cellular Biology (Volume 3)]. Ronald C. Conaway and Joan W. Conaway (eds). Raven Press, New York. 1994. Pp. 592. Price £106.50, hardback. ISBN 0 7817 0126 0.

Antisense Strategies. Renato Baserga and David T. Denhardt (eds). The New York Academy of Sciences, New York. 1992. Pp. 353. Price £114.00, hardback. ISBN 0 89766 747 6.

Biodiversity and Wheat Improvement. A. B. Damania (ed.). John Wiley, Chichester. 1993. Pp. 434. Price £59.95, hardback. ISBN 0 471 94137 9.

Corrigendum

PIEPHO, H. P. (1994) Missing observations in the analysis of stability. *Heredity*, **72**, 141-145.

In my recent paper, two procedures were suggested for estimating stability from unbalanced data. For computing the variance of Grubbs-type estimates, the covariance of the variances V_{s-r}^2 and V_{s-t}^2 is needed. There is an error in the numerator of the covariance formula given in the paper. The correct formula should read

$$\text{cov}(V_{s-r}^2, V_{s-t}^2) = \frac{2n_{srt}[(n_{sr}-1)(n_{st}-1) + n_{srt} - 1]}{n_{sr}(n_{sr}-1)n_{st}(n_{st}-1)} \sigma_s^4,$$

where n_{srt} is the number of environments in which genotypes s , r , and t were grown together.

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