for patterns that are consistent across diverse taxa. It is impressive that rather general stochastic models converge on an episodic clock, and on the Dirichlet distribution of allele frequencies. However, the actual rate of substitution, and the level of variation, both depend on a complicated mix of parameters; it is hard to see why these should be so similar across such different kinds of organism. There are other cases in biology of patterns so general that our varied and arbitrary explanations seem inadequate: for example, the scaling of metabolic rate with (body size)$^{0.75}$, or the prevalence of sexual reproduction.

Overall, Gillespie presents a convincing case that for proteins at least, both variation and evolution are dominated by selection. This selection may not be very strong – the frequencies of null alleles in natural *Drosophila* suggest selection coefficients of no more than 10^{-3} (Langley *et al.* 1981) – but will nevertheless dominate random sampling drift in all but the rarest species. One of the earliest objections to this view, and one which stimulated the development of the neutral theory, was that if the effects of different loci combine multiplicatively, then the fittest genotype would produce absurdly many offspring. Gillespie argues cogently that since such ideal genotypes do not exist, we should instead consider measurable quantities such as the genetic variance in fitness; this is consistent with moderate selection at thousands of loci. This amounts to assuming a concave relation between fitness and heterozygosity, such that the ideal genotype is not excessively fit (cf. Kondrashov, 1988); it would be interesting to know whether there is any reason why gene interactions should evolve so as to reduce the genetic load in this way. In any case, there are other constraints on the amount of variation that can be maintained by selection: the selectionist view implies substantial random perturbations due to hitch-hiking, and maintenance of variation by frequency-dependent selection requires many independently regulated resources.

The Causes of Molecular Evolution should be read by all students of the evolutionary process: it provides an admirably critical summary of our current knowledge (and lack of knowledge) about how DNA and protein sequences evolve, and as a bonus, includes an excellent introduction to the mathematics needed to understand the consequences of fluctuating selection. To me, Gillespie's view that selection acts on many thousands of linked loci is attractive, if only because it makes population genetics much more interesting than the neutral alternative. I hope that it will not be too long before we know whether he is right.

References

Hudson, R. R., Kreitman, M. & Aguadé, M. (1987). A test of neutral molecular evolution based on nucleotide data. *Genetics* **116**, 153–159.

Kimura, M. (1983). *The Neutral Theory of Molecular Evolution*. Cambridge University Press.

Kondrashov, A. (1988). Deleterious mutations and the evolution of sexual reproduction. *Nature* **336**, 435–441.

Langley, C. H., Voeolker, R. A., Leigh Brown, A. J., Ohnishi, S., Dickson, B. & Montgomery, E. (1981). Null allele frequencies at allozyme loci in natural populations of *Drosophila melanogaster*. *Genetics* **99**, 151–156.

Mackay, T. F. C. & Langley, C. H. (1990). Molecular and phenotypic variation in the achate-scute region of *Drosophila melanogaster*. *Nature* **348**, 64–66.

McDonald, J. H. & Kreitman, M. (1991). Adaptive protein evolution at the *Adh* locus in Drosophila. *Nature* **351**, 652–654.

Nevo, E., Beiles, A. & Ben-Shlomo, R. (1984). The evolutionary significance of genetic diversity: ecological, demographic and life-history correlates. In *Evolutionary Dynamics of Genetic Diversity* (ed. G. S. Mani), pp. 13–213. Berlin: Springer-Verlag.

Ohta, T. (1976). Role of very slightly deleterious mutations in molecular evolution and polymorphism. *Theor. Pop. Biol.* **10**, 254–275.

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Aging, Sex and DNA Repair. By CAROL BERNSTEIN and HARNI BERNSTEIN. Academic Press. 1991. 382 pages. Price $44. ISBN 0 12 092840 4.

Genetic Effects on Aging II. Edited by D. E. HARRISON. CRC Press. 1990. 573 pages. Price £50. ISBN 0 936923 318.

Sex and death are topics of absorbing interest beyond mere academic circles. Understanding their causes is an important challenge, and the level of research activity devoted to them is attested by a recent plethora of texts on both subjects. Part of the fascination for academics comes from the very varied scientific cultural backgrounds and goals of the participants. Death is often a consequence of ageing or senescence, which brings with it a baleful catalogue of biological malfunctions responsible for the increased likelihood of mortality with age. Gerontologists in general view the process mechanistically, and want to know what goes wrong, how it goes wrong, and how to fix it. Evolutionary biologists, on the other hand, are more interested in the ultimate reasons for the presence of ageing: is it a late life cost of processes that were beneficial in youth, or is it a reflection of the failure of the weak natural selection on the late part of the life history to eliminate from populations mutations with nasty effects then? In theory either community could continue to work in blissful ignorance of the activities of the other, because gerontologists do not need to worry about population biology and the evolution of ageing can be studied, for a time at least, without any knowledge of the mechanisms at work within individuals. However, each approach can help the other to make sense of its findings. For instance, the evolutionary findings

suggest that ageing is not an adaptation, and that it is likely to have multiple mechanisms and causes, rather than to be a unitary process under the control of one or a few genes. Similarly, the gerontologists can point to mechanisms that might tie together events early and late in the life history, or that might make the effects of mutations age-specific.

Bernstein and Bernstein explicitly try to bring the gerontological and evolutionary approaches into register, by attributing both ageing and sex to the effects of damage to DNA. Damage results in an abnormal chemical structure, unlike mutation which resulted in an altered base sequence. The importance of this distinction is that damage can be detected and repaired using either the homologous DNA strand or the homologous DNA molecule. Ageing is, they argue, a result of accumulation of unrepaired damage to DNA in somatic cells. Sex, on the other hand, has evolved as a mechanism for repairing damage to DNA in the germ line. Although both ideas are attractive, and apparently unify disparate phenomena as part of the same mechanism, the evidence presented for either point of view is less than conclusive. The problem is that critical tests of either hypothesis are not presented. For instance, one line of evidence for unrepaired damage to DNA as the primary mechanism of ageing is as follows: (a) Damage to DNA can be shown to increase with age in various mammalian tissues, especially those that are post-mitotic or have a slow rate of cell division; (b) rates of transcription and translation also decline with age; (c) cells and tissues work less well as they get older; (d) therefore ageing is caused by damage to DNA. But this is a giant *non sequitur*. The four phenomena may approximately co-occur, but this does not mean that any one necessarily causes any of the others, or indeed that any one mechanism takes precedence in causing ageing. Lots of things may be going wrong together, and the search for the zeitgeber may be quite futile. The conventional way to unravel knots of this kind is to do an experiment, manipulating the putative causal variables (rate of DNA damage or rate of repair) and observing the response in the supposedly dependent variable (ageing). Unfortunately nearly all the evidence presented is correlational: an association is sometimes found across species between lifespan and both oxidative damage to DNA and levels of DNA repair in response to damage by UV. However, neither of these studies controlled for possible third variables such as body size, which also shows a strong correlation with lifespan. The demonstration that both the general phenomenology of ageing and the level of oxidative damage to DNA are accelerated in Down's syndrome is similarly problematic, because trisomy undoubtedly has multiple effects. Few would doubt that damage to DNA is *a* cause of ageing, but that it is *the* cause is much more contentious.

The second claim of Bernstein & Bernstein is that meiosis is an adaptation to promote recombinational repair of DNA damage in the germ line. Again, there can be no argument against the association, which is very thoroughly documented by these authors, but the claim of causality needs unpacking. Sex may have originally evolved to facilitate endogenous error-correction in the germ line, although mutations as well as damage to nucleic acid may have been important. However, other functions for sex may have subsequently become more important in its maintenance. Extant germ lines are, to a first approximation, immortal, which means that some mechanism of error-correction is indeed necessary. In addition to endogenous repair mechanisms, natural selection provides an effective means of exogenous repair; if the organism does not work properly, it will leave fewer descendants. Natural selection can both remove deleterious mutations and incorporate beneficial ones more effectively with sexual than with asexual reproduction, which may well explain the prevalence of sex. Bernstein & Bernstein object to this line of argument on the basis that it invokes group selection. However, some mutational theories of sex do not invoke group selection, and even those that do are supported by the data; asexual populations are more likely than sexual ones to go extinct. The authors counter-argue that some short term advantage is necessary to explain the prevalence of sex, because of its two-fold cost. However, that argument assumes that mutations to functional asexuality are readily available in sexual species. In many groups including mammals and birds this is simply not the case, and the absence of these mutations could itself be explained by group selection in favour of lineages that do not revert to asexuality, perhaps because more than one mutational step is required.

Genetic Effects on Aging II is a compendium of reviews and specific studies, gathered with the aims of understanding and combating the ageing process in mammals. It starts with a fairly political agenda from the editor: Harrison argues that healthy lifespans are on the increase in developed countries and therefore, with the right kind of research, the way will shortly be paved to successful genetic intervention in human ageing.

The first section is on the evolutionary genetics of ageing, with excellent chapters on theory and on work with *Drosophila*. The latter has proved important, because artificial selection has been successfully used to produce lines of flies in which senescence is postponed; survival rates are higher, and fertility is maintained at a high level late in life. This has led to a lively debate on whether a similar protocol should be used to produce mice with postponed senescence, reflected in the concluding Discussion of Section 1. Mice would be a far more costly venture than *Drosophila*. Furthermore some aspects of their life history are very different, especially the long post-reproductive lifespan. Gerontologists working on mice are used to genetically homogeneous, and usually

inbred, strains. The products of artificial selection would be segregating at many loci, which could mean that larger sample sizes were necessary to characterize them, and would also make it harder to pin down any effects of selection to particular gene loci. Furthermore, the only justification for using mice is that they are more similar than *Drosophila* to humans. However, are they similar enough to justify the labour and expense of producing selected lines? There are clearly some imponderables involved here. However, the huge advantage of selected lines is that they show less ageing than the original wild type strain from which they were derived. The trouble with most of the mutants supposedly affecting ageing is that they either cause a drop in survival, or increase only longevity. This is true, for instance, of the catalase-deficient mice in Section 4 which show decreased lifespan and the *Caenorhabditis elegans* mutants described in Section 2, whose increased longevity may simply reflect the fact that they are virtually sterile, and therefore make little reproductive effort. There are lots of ways of making organisms go wrong; this does not mean that these mechanisms are involved in normal ageing. To understand the mechanisms of ageing it is necessary to postpone it by increasing longevity and late-life fertility: then one can be sure that any mechanism underlying the effect must have been involved in producing the earlier onset of ageing in the base stock.

In keeping with the focus on mammalian ageing, much of the volume is given over to accounts of ageing in specific tissues in mice and rats. There is also a section on human progeroid syndromes and Altzheimers, which make very interesting, if sad, reading. This is a valuable collection for those actively involved in research on ageing, although the frequent typos are an irritant. At £50 the volume is too expensive for the general reader to buy, but some of the chapters would make it worth borrowing from the library for a browse.

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The Comparative Method in Evolutionary Biology. By PAUL H. HARVEY and MARK D. PAGEL. Oxford University Press. 1991. 239 pages. Price £12.50. ISBN 0 19 854640 8.

Evolutionary biology is not an experimental subject. That statement would probably appear to be self-evident to the vast majority of the audience for this book, although it is not entirely true. In consequence of the inability to experiment, knowledge has to be gained by the use of extreme rigour in inference. Darwin's writings are permeated throughout with the awareness of this need, as have been those of the other great contributors to the study of adaptation. There is an extreme contrast with a prokaryotic molecular biologist who can have the most way-out ideas, but has to test them by tightly controlled experiments. So the establishment of an accepted approach which is quantitative and based on appropriate statistical techniques, which is the Comparative Method, has been an important development of the last decade or so and one with which Harvey has been closely associated. In particular, he has pointed out the importance of taking out the effect of phylogeny when making such comparisons, and in this book gives a comprehensive description of a rigorous approach to evolutionary inference based on these principles. This book is undoubtedly an important contribution and will serve to consolidate the recent developments in the area by making them more widely disseminated.

The book introduces the problem posed by relationships between taxa in the analysis of adaptation and takes the reader through the reconstruction of phylogenies, emphasizing the cladistic method but also discussing to what extent this is appropriate for phylogenies based on purely molecular data. The problems involved in comparative analysis in the content of a known phylogeny are then discussed, first with discrete data and then with continuous characters. The statistical frameworks within which knowledge of the phylogeny can be taken into account are then presented with numerous examples. After reading it I should feel confident that any competent behavioural ecologist would be able to put their investigations of the adaptive significance of a particular trait on a sound basis. The main direct criticism I have of the book is a tendency to make references to some studies in an almost cryptic manner; for example on page 25 'Sandell's (1989) optimality model... is a fine example'. A fine example it may be but the reader is not told why, and this detracts from our understanding of the point which follows, which is about the requirement for 'suitable data'. Likewise, the subsequent presentation of Martin's analysis of the relationship between brain mass and body size in birds and reptiles: '(he) had both pre-empted Armstrong's explanation and cast doubt upon it...' is not made clearly. The extent of the difference in metabolic rate between these two groups, which is the critical point in this discussion, is not given. Perhaps this is the 'Oxford' style?

That brings me to the main point which occurred to me on reading the book. This cannot really be levelled at this book but perhaps indicates the need for another one. Evolutionary ecology is a highly anthropocentric field, with most of the publications centring on either furred or feathered animals. Yet the biggest development in biology recently has of course been in the molecular areas and in developmental biology, and investigators in those areas are forever making 'evolutionary' comparisons and deductions. These are frequently naive because these scientists have been trained in an experimental subject, as outlined above. Yet they have every reason to want to know how to make reliable inferences from evolutionary compari-