historian, for not understanding the role of influential individuals in historical bifurcations, and so on. Further, are these instances of historical ‘collapse’ relevant to today’s societies? Are we not now better informed about the natural world and its limits; do we not have reader information flow and democratic decision-making; are we not better equipped technologically to find solutions to problems? Yes, says Diamond, but contemporary societies are, in many ways, even more vulnerable by dint of population size, immovability, and dependence on extremely high levels of resource consumption.

Manifestly, the story of environmental mishandling continues today. Societies are often slow to recognize the enormity of the problems bearing down on them. Think of the recent doubts and denial in relation to climate change. Besides, societies are reluctant to incur costs today for the sake of the future. China, Haiti (compared with its island-sharing neighbour Dominican Republic), and Australia, Diamond argues, all point in that direction. In Australia’s case, European and other settlers have rapidly degraded much of the natural environment in just two centuries—river systems, aquifers, forest and woodland cover, soil fertility, stocks of biodiversity, and, now, the Great Barrier Reef (bleaching from warming and polluted coastal water-runoff) and the Kakadu wetlands (including the invasion by cane toads, foolishly introduced from Hawaii in the 1930s).

What does this book mean for epidemiologists? Well, first, as citizens of the world, we can learn from history something about the prerequisites for sustainable management of the natural resource base and of cohesive societies. Second, the unprecedented scale of the changes to Earth’s natural systems, now occurring in response to the weight of human demand, poses widespread risks to population health. We face diverse environmental, demographic, and social changes on a scale beyond human experience. Yet we know that erosion of the basic supports for population health—food yields, freshwater supplies, climatic stability, constraints on microbial activity, the recycling of nutrients, and the aesthetic and spiritual values that flow from nature—will jeopardize health.

Epidemiologists, during the expansive ‘modern’ era of their discipline, have spent the past half-century mostly studying determinants of within-population disease risks. Hopefully, we will now extend our efforts to assisting society understand the spectrum, and significance, of emerging large-scale risks to health. Behind the contemporary concern to achieve a sustainable way of managing the natural world lurks the fear that the alternative may entail ‘collapse’. If so, for at least some populations, the DALYs count would then dwarf the illustrative figures in our textbooks.

A J MCMICHAEL
E-mail: tony.mcmichael@anu.edu.au

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argument for a closer approximation to truth. This needs urgently to be done, and is by no means a simple task. One reason the ‘reformers’ have had it so easy has been the generally authoritarian and undemocratic nature of public health care systems preceding these ‘reforms’. If people find themselves pushed about, patronized or despised as citizens, they may not find it too difficult to imagine they will fare better as consumers. The human and scientific material already exists everywhere from which beginnings for gift economies and cultures of participative democracy could be developed, but this must be done concretely, through real experience in real places with real people, not just in university departments and libraries.

JULIAN TUDOR HART
E-mail: julian@tudorhart.freeserve.co.uk

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With data from the human genome becoming widely available to both geneticists and clinicians alike, the field of genetic epidemiology is evolving rapidly. Such is the ubiquity of publicly available data on human genetic variation that one may perform a predictive association study in a phenotypically characterized population cohort without collecting any novel genetic data, having a full understanding of the implications of genetic variation, or realizing the techniques involved in its attainment. While the relative ease with which genetic data can be harvested is undoubtedly contributing to the inconsistencies present in current literature, it is evident that the problems associated with such research are being identified. As such, it is evident that there are important aspects of genetic epidemiology that must be understood before entering this burgeoning sphere of research. Just as observational epidemiology presents potential pitfalls, genetic analysis presents hidden devils.

Duncan Thomas, along with a valuable introductory contribution from Sue Ingles, delivers a necessary addition to the epidemiologist’s collection of handbooks in his text ‘Statistical Methods in Genetic Epidemiology’ (OUP, 2004). With respect to this, there are a number of features that are important in review. First, the coverage of methods and approaches to the study of genetic variation and its application to the understanding of the aetiology of human disorders is both accurate and logically ordered. Following a comprehensive introduction to the field, including both the biological and statistical principles of genetic analysis, the reader is guided through the observation and relevance of familial aggregation and segregation. Importantly, through these descriptive sections, there is regular reference to the application of such aspects to real analyses. For the practising epidemiologist, such reflections on how real studies may be initiated and oriented to facilitate genetic analysis, prove useful additions.

While this theme of fundamental demonstration followed by pragmatic grounding runs through subsequent sections, the smooth transition from conceptual understanding to real epidemiology and analysis is more tenuous in later chapters. By far the most challenging sections of this book are those brought forward in Chapters 7 and 8. Here, the reader is introduced to the principles of linkage analysis and then to population genetics. Although extensively covered in descriptions of length and detail, the fundamental differences between essentially family-based analyses (linkage) and population-based analyses (association) can be lost. This is not to criticize the clarity and progression of these sections, more to highlight the statistical tendencies (as expected) and technical concentration that can obscure the relevance of less tangible and more conceptual features of these topics (e.g. linkage disequilibrium).

Further criticism aside, other less transparent aspects mentioned in the main sections are generously demonstrated in the concluding chapters, Chapters 11 and 12. Chapter 11 brings forward further issues for consideration when applying the more theoretical areas of genetic analysis to real cohorts; Chapter 12 presents a real historical example. From biology, through genetic analysis and to clinical implications, colorectal cancer is well examined. Although rare, as complete stories are in the field of genetics, this is an important and binding addition to the latter stages of the text.

Finally, it is worth noting that the pre-emptive considerations made in the final section assigned to the ‘future’ of genetic epidemiology, are largely being realized. Furthermore, applied uses of genomic variation are now being increasingly used as epidemiological tools for the re-assessment of conventional observational analyses. However, while it would be easy to criticize such a section, it is more valuable and certainly more exciting, to request a regular update. This is a clear and succinct tour of the analytical side of genetic epidemiology. There is a suitable balance of biology and statistical details and the text is well pitched for its target audience of graduate epidemiologists, biostatisticians, and human geneticists.

NIC TIMPSON
E-mail: N.J.Timpson@bristol.ac.uk

Reference