Stewart Scherer: A short guide to the human genome

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Among the pre-Christmas offerings at my local bookshop are *Whitaker's Almanac*, *Schott's Almanac*, *Foyle's Philately*, *Things to Know*, *Stuff you Forgot from School*—and so on, at some length. On a quick first impression, *A Short Guide to the Human Genome* looks like it might belong in this company—‘One hundred must-know facts about the human genome’ perhaps. This is because each chapter consists of around ten self-contained one- to three-page articles, each with a question as its title. Typical examples are ‘Do gene-rich chromosomes have smaller genes?’ or ‘How are human and bacterial ribosomes related?’

The headings of the nine chapters cover the ground you expect of a textbook: DNA and the chromosomes, Genes, RNA, Proteins, Translation and protein modification, Gene families, Mobile elements and rearranging genes, Polymorphism, and Comparative genomics. However, the content, those short articles each based on a question, makes clear that this is not a standard textbook. The question is then, does each chapter form a coherent whole, or is it more of a set of random, albeit interesting, jottings, like the books mentioned above? In cultured households, such compilations of random facts are destined for the smallest room, as flexible aids to contemplation. You can dip into them for a minute or an hour, depending on need.

To distinguish this book from those random compilations, one looks for a central concept. Scherer sets himself a challenge by aiming his Short Guide at people who already understand the basics. He is not out to explain what DNA or chromosomes are, at a level where a dozen questions could cover the ground. His audience is researchers and

teachers, not students. So he asks ‘Which amino acids are commonly located in the amino-terminal region of a protein?’ and ‘How does codon usage differ in the Eukaryotes?’ At this level, each chapter has hundreds of possible questions. Why did he choose those particular questions to address, out of all the possibilities?

In terms of content, I would have to say it is not obvious that there is any unifying principle. I kept it on my desk while working on the fourth edition of Strachan & Read's *Human Molecular Genetics* (be patient, dear reader—it will appear one day soon, honestly!). Sometimes it answered a question I had, quite often it did not. There is not really a unifying core of fact. However, there is a unifying core of method. Each little article ends with a section on *Data sources, Methods and References*. These sections show how almost every question was answered by reference to Build 36.2 of the NCBI Reference Sequence, and sometimes also the RefSeq collection.

I am not sure whether Stewart Scherer would agree with this, but I think what he has done is write a primer on bioinformatics. He picks a semi-random set of questions, and demonstrates how to answer each one by using the resources of the NCBI. The questions are interesting enough in themselves, but they function better as examples than as a coherent guide to the human genome at this level. The real value of the book is as a demonstration of how to answer questions like these.

If you are confident about using all the innumerable Internet resources for analysing the human genome, you probably would put this book in the smallest room. It will serve the purpose well: the examples are interesting and diverting. However, for the rest of us, the place for it is beside the mouse, for all those times the information you want is not in this engaging little book, but somewhere on Web, if only you could work out how to get at it.

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