extreme hereditarians and their unwitting allies among "scientific radicals", of equating genetic variance with irrevocable, unswerving genetic determinism.

Ruse is rather good atⁱ dealing with such people. In America there are some genuinely good scientists who have severely criticised sociobiology, and we have to listen to them. Ruse does so, understands them, agrees with them in places, but finally remains largely unimpressed. He also gives some reassuring pats to the ruffled feathers of social scientists who fear imminent takeover by a rapacious biological imperialism.

I have concentrated on places where the book could have been improved, but there is good in it and I hope it will

be read by those who have managed to retain an interest in this rather over-publicised controversy. Ruse's sense of balance and agreeable style are well shown in his closing sentences: ". . . I am far from convinced that human socio-biologists have yet made their case. What I do plead is that their sins are not as grave as their critics argue. Human socio-biology should be given the chance to prove its worth. If it cannot deliver on its promises, it will collapse soon enough; but if it does prove viable, then its success could pay scientific dividends of the highest order". Who will disagree?   □

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Protein synthesis inhibitors

Inhibitors of Protein Biosynthesis. By David Vazquez. Pp. 312. (Springer: Berlin, Heidelberg and New York, 1979.) $32.50.

No matter how hard you try to keep up with the literature in this field, you usually find it slipping away from you. Well, here's a good chance to catch up with all of it. In this comprehensive survey David Vazquez cites 1017 references (I think), of which a mere 100 originated from his laboratory, and pulls so many rabbits out of the hat that one feels he could have directed *Watership Down*.

The book is bulging with information including the structures, empirical formulae, molecular weights (many thanks) and synonyms of antibiotics together with the names of the producing organisms. The subject of synonyms is particularly intractable and this reviewer is now glad to know that multhiomycin and nosiheptide are the same thing, to say nothing of anthelmycin and hikizimycin. All your old favourites are here and, when you turn to the appropriate Figure, you'll probably find they have a few cousins you didn't know about. It's inevitable (isn't it?) that something should have been omitted, but I'll have to check carefully before I complain that pulvomycin should have been included with the rest of the kirromycin group in Fig. 42. (You never know, it ˙ could be an alias for efrotomycin!)

All the alkaloids are in here too and when botanists have finished talking about them as being herbivore-repellents, or nitrogen excretion products, or whatever, they should note just how many of them are ribosome-inhibitors. The same is true for various other plant products known more generally as lectins and agglutinins.

Of course the main aim of this book is to deal with the action of inhibitors of protein synthesis. So, if you want to know what others think they know about the mode of action of any antibiotic or drug, David Vazquez will tell you. For this reason the book does not read like an essay; with so many facts and figures (61 of the latter) it is meant to be used as a reference book. As such it should find a place in research laboratories and in reference collections, although it cannot be recommended for students. However, no-one working in the fields of antibiotic action, protein synthesis or ribosome structure-function analysis should be without it. I warmly recommend it.

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Interpreting visual motion

The Interpretation of Visual Motion. By Shimon Ullman. Pp. 229. (MIT Press: Cambridge, Massachusetts, and London, UK, 1979.) $17.50; £11.40.

THIS book is a slight revision and extension of Ullman's doctoral thesis researched at the Artificial Intelligence Laboratory of MIT. Various parts of it have also been published independently (in somewhat different form) in various journals (*Perception, Perception and Psychophysics, Proc. R. Soc. London*). Nevertheless, the book is worth prossessing in its own right if you are an experimental psychologist or an artificial intelligence researcher interested in vision, especially in motion perception, primarily because of its special methodological qualities.

Ullman investigates the phenomenon of apparent (or phi) motion, the illusion enabling us to watch television or movie pictures despite their discrete presentation. The phenomenon is conceptualised as a computational problem and is divided into two parts, each of which is studied independently. Solving a computational problem includes specifying the goal of the computation, and then investigating possible (and plausible) methods for attaining the goal. A theory of what is being computed is thus an integral part of the understanding of the information processing system being studied, in this case the human visual system. The phi phenomenon is seen to establish the correspondences between the elements in two successive "snap-shots" of a scene, and then interpreting the resulting displacements as motions of the objects.

Ullman shows that the correspondence computation amounts to computing the so-called minimal mapping, the match that minimises costs over the covers of the graph of possible (probability weighted) pairings. He shows that the initial candidates for a set of possible pairings for a given element in one snapshot can be

restricted to elements (in the second snapshot) lying within some limited distance radius of this element. This means that the correspondence process can be effected by a simple network of locally competing processors of uniform structure. Furthermore, Ullman shows that the domain of the computation is a "token space" (D. Marr's "primal sketch": *Phil. Trans. R. Soc.* **B275**, 483-524: 1976), a symbolic representation consisting of blobs, line segments, edge fragments and the like, which is the result of pre-processing the raw image intensity distributions.

The next stage consists of interpreting the displacements obtained. Ullman develops the notion of a "rigidity test", operating locally on a nucleus of elements and leading to decisions about whether the displacements associated with the nucleus can possibly represent (and result from) a rigid object in motion. The analysis is based on his "structure-from-motion" theorem which states that the structure (relative position) of four non-planar points is uniquely recoverable from three orthographic projections. Such an interpretation does not assume any recognition of, or familiarity with the objects in question.

Finally, Ullman discusses "motion-from-structure" situations in which motion is established as a "filling-in" process linking two objects recognised as being an instance of the same object in the two successive static snapshots. He compares the two motion-analysing mechanisms and argues that various interpreting processes (analysis of static "snapshots", "motion-from-structure", "structure-from-motion", and so on) all contribute to one common representation and that they must compete or co-operate to produce the final result, the percept.

This monograph is clearly written. Within the limits he has set for himself, Ullman has achieved a great deal. This is an excellent and important piece of work.

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