catalytic activities, are even less well studied for their *in vivo* effects.

RON TRENT

The Yeast Two-Hybrid System. Editors Paul L. Bartel, Stanley Fields. New York: Oxford University Press. 1997. ISBN 0-19-510938-4.

It is now difficult to open a life science journal without reading at least one paper with the sentence "a yeast two hybrid screen was performed..." so the arrival of this attractively produced book caused a stir in my laboratory. It is written by the people who developed the system. Late one afternoon in 1987, Stanley Fields (then a new assistant professor at SUNY in a small laboratory working on an obscure aspect of yeast pheromone responses) suddenly realised that he could use two different hybrid proteins, one containing a DNA binding domain and the other a transcription activation domain, to detect protein-protein interactions. He immediately recognised that it might be feasible to use the system to search cDNA libraries to find novel protein partners. It is ironic that a seed grant proposal written later that same year was rated by the review panel as "having no possibilities for commercial development" and the research was eventually supported by Procter and Gamble. Eleven years later Fields and his colleagues must feel entitled to a quiet glow of vindication as they survey the honour roll of proteins pulled out of yeast two hybrid screens. For example, in working out cell cycle checkpoint control during the early 1990s, the CDK inhibitors p16, p18, p19, p21, and p27 were all discovered by different groups using the system.

Many people will buy the book for the three early chapters which describe the nuts and bolts of manipulating yeast and performing a basic library screen. Each of these chapters is devoted to one of three different systems that have been developed by different groups over the years. The protocols are clear and sufficiently detailed to allow someone who has never worked with yeast to perform a two hybrid screen (chapter 3 is an improved and more detailed version of a much photocopied protocol which our laboratory has used successfully over the past three years). We have found that the scientists who developed the system are generous with their time and reagents and this impression is reinforced by the list of laboratory web pages, e-mail addresses, telephone and fax numbers at the end of chapter 4. These first four chapters justify the price of the book. I also enjoyed the clear description of the ingenious reverse two hybrid system for mapping critical residues in protein-protein interactions and will use the protocols presented here, which seem straightforward. A chapter on constructing activation domain-fusion libraries did not provide much more information than can be obtained from Maniatis. Other chapters are more descriptive or speculative; there are reviews of ligand-receptor interactions, cell cycle and signal transduction pathways which, although well written, cannot provide more than an overview in the space assigned to them, and I was disappointed that the one hybrid system which holds great promise for detecting DNA binding proteins was only given a brief space. The possibility of using the yeast two hybrid system to generate massive whole genome protein interaction connectivity networks in

the "post-genomic future of the 21st century" is discussed in a very readable chapter; it sounds like science fiction, but given the achievements of the yeast community in the last decade, I wouldn't be surprised if they pull it off.

LUKE HUGHES-DAVIES

Genetics. A Molecular Approach. 3rd edition. T. A. Brown. (£27.50.) London: Chapman and Hall. 1998. ISBN 412 798700.

The field of molecular genetics is vast and complex with its own extensive vocabulary and it is hard for a novice to approach it without feeling daunted. However, an understanding of genetics is now essential for most undergraduate and postgraduate science and medical students. This well written book will be welcomed by both newcomers and experienced geneticists as well as those who teach the subject to undergraduates.

Starting with DNA rather than Mendel, the author tells the story of genetics in three parts. In part 1, he explains the structure of DNA and the chemical nature of the gene with chapters describing control of gene expression and DNA replication, mutation, repair, and recombination. In part 2, genes are put into the context of genomes, both prokaryotic and eukaryotic, with an excellent chapter describing the structure of the human genome including gene families and pseudogenes, extragenic DNA, and polymorphisms. Part 3 describes patterns of inheritance with sections on Mendel's experiments and their subsequent molecular explanations, genetic linkage, the human genome mapping project, and an overview of the techniques currently used in the molecular biology laboratory. An historical context is maintained throughout the book with descriptions of landmark experiments such as those used by Hershey and Chase in the 1950s to show that genetic material is DNA and not protein.

The text is clear, succinct, and liberally illustrated and no new term is introduced without being defined and listed in the extensive glossary. The author is clearly an experienced teacher of his subject and has written a book which is both readable and informative. I would have no hesitation in recommending this book to anyone needing a thorough grounding in molecular genetics.

JULIA RANKIN

The Calculation of Genetic Risks: Worked Examples in DNA Diagnostics. 2nd edition. Peter J. Bridge. (£34.50.) Baltimore: The Johns Hopkins University Press. 1998. ISBN 0-8018-5744-9.

Apart from a few exceptional people, I think that geneticists, whether clinical or in the molecular diagnostic laboratory, are not particularly mathematically inclined. Indeed, I am fairly certain that there are many, including me, who develop a curious form of mental fugue when faced with the more complex risk calculations that we sometimes come across in clinical genetic practice. Peter Bridge's book is written for us. The main aim of the book is to provide the reader with the skills required to formulate sensible risk calculations, and it takes a very practical approach, building from problems which use only pedigree information to increasingly

complex problems incorporating biochemical and molecular genetic information. The problems are not abstract; service geneticists could expect to meet very similar ones on a regular basis. The particular beauty of this book lies in its comprehensibility. Rather than inflicting difficult equations on us, the author instead uses clarity of ideas and expression, and emphasises general principles. My one criticism is the lack of "self-test" problem sections at the end of each chapter, which would allow readers to really test their new understanding. However, I would unhesitatingly recommend this book to clinical geneticists, molecular geneticists in diagnostic laboratories, and to anyone who wants to have a good grounding in the principles of risk calculation for genetic disease.

EVAN REID

NOTICES

British Human Genetics Conference

The British Human Genetics Conference will be held on 28-30 September 1998 at the University of York, England. There will be special sessions on: Practical approaches to methylation and imprinting; FISH: present and future; Predictive testing protocols - who benefits; The genetics of human behaviour; Human evolution; Joint symposium on multiple endocrine neoplasia with the Cancer Family Study Group, as well as plenary sessions. The Carter Lecture will be given by Professor Ken Kidd on "Evolution of modern humans". Further information from Professor Peter Farndon, British Society for Human Genetics, Clinical Genetics Unit, Birmingham Women's Hospital, Edgbaston, Birmingham B15 2TG, UK. Tel/fax: 0121 627 2634, e-mail: bshg@bham.ac.uk <http://www.bham.ac.uk/bshg>

The National Registry for Ichthyosis and Related Disorders

The purpose of this NIH supported registry is to improve methods of diagnosis, promote the search for basic defects, and develop more effective methods of treatment/prevention of the inherited scaling skin disorders. Affected people are asked to enrol through their local dermatologists. All contact information is kept confidential. Persons with ichthyoses (except ichthyosis vulgaris), erythrokeratodermas, Darier disease, Hailey-Hailey disease, palmar-plantar keratoderms, pachyonychia congenita, extensive epidermal naevi, and related disorders are eligible for enrolment. The Registry offers a means of "empowerment" for affected people and family members. It enables skin biologists, pharmacologists, and other investigators to share information about ongoing and future research with this well characterised group having specific diagnoses. For information please contact us at: The National Registry for Ichthyosis and Related Disorders, Box 356524, Seattle, WA 98195-6524, USA. Tel: 1-800-595-1265 or 1-206-616-3179, e-mail: ichreg@u.washington.edu or visit our web site at <http://weber.u.washington.edu/~geoff/ichthyosis.registry/> Philip Fleckman, MD, Principle Investigator Geoffrey Hamill, RN, Registry Coordinator