tory Approach" (one chapter and an appendix) that discusses the use of antibodies raised against synthetic peptide antigens in the identification and characterization of proteins for which some sequence information has been obtained.

The first two chapters discuss protein sequence data base organization, search and alignment methods, and techniques for testing the significance of sequence matches. These chapters do much to demystify the procedures of "canned" data base search programs. The conceptual basis for each method is discussed and the techniques are well illustrated with examples that can be followed step by step. The section on significance testing should be particularly useful as many programs will produce "matches" for almost any input sequence leaving the researcher to decide what these "matches" really mean. Simple rules-of-thumb for testing significance that can be easily applied are provided and illustrated. In addition, more elaborate schemes based on comparison of the test sequence with randomized or "jumbled" versions of its supposed homologue are presented. These sections provide the tools necessary for the researcher to understand when a match is truly significant and to avoid overinterpretation of search program output. Also included in these chapters is a section on data presentation. It should help researchers produce clear presentations of their sequence search and alignment results, and also should alert readers to the misleading alignments and plots that occur all too frequently in the literature.

The third chapter covers molecular clocks and evolutionary trees. While these subjects are of less general interest, this chapter provides a simple introduction to this often controversial field. Furthermore, given the number of protein families and superfamilies that are being discovered, it is becoming increasingly important for sequencers to understand the basis for evolutionary tree construction.

The fourth and final chapter of "The Computer Approach" part deals with structural and functional conclusions that may be drawn from analysis of a sequence. Topics covered include the detection of internal repeats, evaluation of amino acid composition, hydropathy plots and analysis, secondary structure prediction, and the use of consensus sequences derived from structurally or functionally characterized classes of proteins. The discussion of these topics are quite brief but leading references are given that should be consulted by anyone actually undertaking such studies. The advantages of performing each type of analysis are discussed as are the major shortcomings, with clearly stated caveats about viewing the results uncritically.

Part II of the book describes the use of anti-peptide antibodies for isolation and characterization of proteins as one example of how the knowledge of an amino acid sequence can be used to experimental advantage. This chapter provides a relatively detailed description of many aspects of this technique including:

- Recommendations of how to choose an appropriate peptide with respect to length, amino acid content, and position within the protein sequence
- A discussion of carrier proteins and how to couple the synthetic peptides to them (some recipes for coupling peptides to carriers are given in an appendix)
- A discussion of how the antipeptide antibodies are purified and characterized; and
- A brief account of how the antibodies are used to identify with particular emphasis on SDS-gel electrophoretic analysis of immunoprecipitates. The chapter concludes with an example of the use of antipeptide antibodies in the identification of human mitochondrial proteins. The references given clearly illustrate the power of these methods.

Although the book is not (and is not intended to be) a comprehensive discussion of amino acid sequence analysis but is, as the title says, a primer, I highly recommend it to anyone involved in protein or DNA sequencing or sequence analysis and, indeed, for anyone in a field influenced by these methods, which today is virtually all of biology. Quite brief (it can be read cover to cover in a couple of hours), it hits the high spots of the topics in a critical manner enabling the researcher to perform sequence analysis thoughtfully and allowing the literature reader to evaluate published results more thoroughly. The references given provide access to the literature of the field for persons interested in more detailed study. The availability of a book like *Of URFS and ORFS* makes the protein sequence data bases a more powerful resource for the molecular biological community.

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'THE FIFTY MILLICURIE BLUES'

***Invisible Frontiers: The Race to Synthesize a Human Gene*. By Stephen S. Hall. Pp. 334. ISBN 0-87113-147-1. $19.95. (Atlantic Monthly Press, New York, NY: 1987).**

Stephen S. Hall has written a rare book. It is one of the very few scientific histories that I can wholeheartedly recommend to both my scientist and poet friends. *Invisible Frontiers*, a narrative account of the bacterial cloning of the human insulin gene—and thus an account also of the origins of Genentech, Biogen, and the entire field of biotech—is perceptive, funny, and uncannily accurate to the way molecular biology is practiced today.

For someone who thinks they know the "inside story" of the UCSF-Harvard-City of Hope-Eli Lilly-Genentech assault on the insulin gene, Hall will provide a few new twists (guaranteed). For the still naive, he mixes the science and history with intelligence and an instinct for the dramatic. In the process, he does an excellent job of explaining some rather esoteric molecular biology, while never forgetting to tell a terrific adventure story. Like Gunther Stent's *Phage and the Origins of Molecular Biology*, or James Watson's *The Double Helix*, Hall's book makes a wonderful companion to an introductory text.

But Chapter 17 alone is worth the price of the book. Entitled, "A Magician and Three Acrobats," it tells the tale of Wally Gilbert, Arg Efstratiadis, Stephanie Broome, and Lydia Villa-Komaroff, and how and why they packed an entire molecular genetics laboratory in Woolworth trunks, boarded a jet, and tried to clone a human gene in England's maximum-containment biological research facility on the Salisbury plains at Porton. This surreal story is a microcosm of biotechnology's earliest days.

Harvey Bialy, Ph.D., is the research editor of *Bio/Technology*.