tion, repression, operons, riboswitches, RNA splicing, miRNA regulation, and epigenetics. Part II covers modeling and computational approaches both deterministic and stochastic, with examples of various mathematical functions that model the processes of transcriptional regulation, cell cycle, and noise. It also presents tools for modeling large-scale biochemical networks and whole-cell simulation. Part III focuses on the modularity of synthetic biology tools, discussing the role of information processing and actuation through the use of synthetic gene and RNAi circuits, electrochemical and optical biosensors, and metabolic engineering for bioproduction. The latter is covered more extensively in Part VI. Volume 2 shifts the focus to larger scale synthetic biology, with Part IV discussing synthetically engineered genomes. It goes into depth on the necessary components and processes of bacterial genomes, synthesis of mitochondrial DNA, and use of unnatural base pairs. Part V covers the use of synthetic biology in medicine, and focuses on stem cell engineering, cellular reprogramming, and vaccine development through analysis and construction of codon biases of viral genes.

Although the breadth of information makes these books indispensable for filling vital knowledge gaps, the cohesiveness of the text might sometimes suffer from the disparity and bias of some of the topics. For example, the chapter on the emergence of cells takes a stance against eukaryotes emerging from a rare archaeal-bacterial fusion event, and does not cover recent evidence on alkaline hydrothermal vents as cradles of life on Earth (N. Lane. 2015. *The Vital Question: Energy, Evolution, and the Origins of Complex Life*. New York: W. W. Norton and Company). The gene regulation primer and even the later modeling chapter could benefit from a more thorough coverage of first-principles bases in chemical kinetics, as well as basic introductions to nonlinear dynamics and stochasticity, which are indispensable for understanding natural and synthetic gene networks.

Overall, although these two volumes offer a comprehensive overview on the biological, chemical, and engineering bases of synthetic biology, they could cover more of the related topics in physics and mathematics. Luckily, alternative resources on these topics are available for interested readers (J. M. Bower and H. Bolouri. 2001. *Computational Modeling of Genetic and Biochemical Networks*. Cambridge (MA): MIT Press; Z. Szallasi et al. 2006. *System Modeling in Cellular Biology: From Concepts to Nuts and Bolts*. Cambridge (MA): MIT Press; N. G. Van Kampen. 2007. *Stochastic Processes in Physics and Chemistry*. Third Edition. Amsterdam (The Netherlands): Elsevier), and *Synthetic Biology* will be useful for any scientist looking for an introduction to synthetic biology. From the set of genes necessary to encode a minimal genome to the equations governing phosphorylation reactions, these volumes will be picked up and referenced again and again.

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Working with Stem Cells: A Quick and Easy Approach of Methodologies and Applications.

By Henning Ulrich and Priscilla Davidson Negraes. Cham (Switzerland): Springer. $159.00. xviii + 374 p.; ill.; index. ISBN: 978-3-319-30580-6 (hc); 978-3-319-30582-0 (eb). 2016.

Ion Channels: A Laboratory Manual.

Edited by Paul J. Kammermeier, Ian Duguid, and Stephan Brenowitz. Cold Spring Harbor (New York): Cold Spring Harbor Laboratory Press. $150.00 (hardcover); $90.00 (paper). viii + 197 p.; ill.; index. ISBN: 9781621821205 (hc); 9781621821212 (pb). 2017.

Ion channels are fascinating machines. They are central to membrane physiology in every tissue in the body and are implicated, when they are improperly altered, in numerous disorders: epilepsy and cardiac arrhythmias, for example. Conveying the biological and clinical importance of ion channels and pathways to study them to new generations of scientists is therefore of utmost importance. The book *Ion Channels: A Laboratory Manual*, edited by Paul J. Kammermeier et al., is an extremely useful guide for the study of ion channels. This volume is well written and describes in appropriate detail protocols to study diverse ion channel types in various contexts, from isolated entities to address the basis of their functional properties to their role in regulating the activity of networks of neurons in vitro or in vivo. The protocols, including troubleshooting guides, will be an invaluable resource for initiating techniques in a research laboratory. The manual would also be a fantastic basis for a laboratory class for advanced undergraduates or graduate students.

The book consists of 14 chapters and an appendix on General Safety and Hazardous Material Information. The first three chapters provide background. Chapter 1 starts off with a gentle introduction to the history of studying ion channels, while Chapters 2 and 3 give information on structure-function issues for voltage-gated K^+ channels (Chapter 2) and the physiology and clinical pathology of voltage-gated Na^+ channels (Chapter 3). All three of these chapters are concise and informative. From a personal bias, it might have been nice to also have a back-

ground chapter on ligand-gated ion channels, but this is a minor quibble.

Next is the meat of the volume: 11 chapters that describe protocols to investigate some aspect of membrane physiology, ranging from modulation of voltage-gated Ca^{2+} channels in heterologous expression systems to optogenetic manipulations and in vivo recordings. Each Methods chapter starts with a brief background to the chapter's main topic, which is then followed by detailed protocols. In addition to reading over the chapters myself, I had students in my laboratory read specific methods chapters related to their efforts. The consensus was unanimous. Everyone found the Methods chapters extremely informative, well written, and provided levels of detail appropriate for both inexperienced and experienced physiologists. One student noted that the chapters "were a great introduction to those just beginning and described in appropriate language and depth for newcomers and intermediate electrophysiologists alike." Many appreciated "how the chapter discussed benefits and limitations of the described protocols" and that "the troubleshooting sections were thorough and helpful."

Often it was the details that set a chapter apart. In Chapter 5 (Strategies for Investigating G-Protein Modulation of Voltage-Gated Ca^{2+} Channels), for example, Table 1 was viewed as "an exceptionally useful summary of the tools available for studying specific steps in G-protein pathways." In Chapter 7 (Single-Channel Recording of Ligand-Gated Ion Channels), there was an informative description of noise sources and how to address them. Any physiologist who has had to deal with noise will find this discussion refreshing and helpful. In Chapter 8 (Measuring the Basic Physiological Properties of Synapses), one student noted that "the distinctions between the concepts of quanta, release probability, and releasable pool were clearly made and can be understood by those who are new to the field."

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MANUAL OF MOLECULAR AND CLINICAL LABORATORY IMMUNOLOGY. *Eighth Edition.*

Edited by Barbara Detrick, John L. Schmitz, and Robert G. Hamilton. Washington (DC): ASM Press. $220.00. xxviii + 1240 p.; ill.; author and subject indexes. ISBN: 978-1-55581-871-5 (hc); 978-1-55581-872-2 (eb). 2016.

GENETICS

STATISTICAL APPROACHES TO GENE X ENVIRONMENT INTERACTIONS FOR COMPLEX PHENOTYPES.

Edited by Michael Windle. Cambridge (Massachusetts): MIT Press. $50.00. viii + 296 p.; ill.; index. ISBN: 978-0-262-03468-5. 2016.

The 11 chapters in this book are compiled from the Third Annual Symposium of the University of Georgia's Center for Contextual Genetics and Prevention Science, held in 2012. The chapters describe different ways of statistically analyzing the vast amount of data that comes out of genomic studies. The amount of data is both a blessing and a curse: on one hand, so much data can potentially reveal underlying genetic patterns but, on the other, the amount of data means that biologically significant effects have to be enormous in order to stand out from the large number of statistical tests carried out. This problem becomes even more difficult when testing for genotype x environment (GxE) effects. Although this volume does present some interesting and potentially useful approaches, none, not unexpectedly, provide a panacea. Chapters 2–6 deal with statistical methods focused on multiple hypothesis testing and data reduction, while Chapters 7–11 examine experimental design.

All of the chapters dealing with statistical methodologies are mathematically intense and require a sophisticated understanding of statistics. Each of these chapters deals with a different approach: two-stage procedures (Chapter 2), marker-set approaches using a gene-level perspective (Chapter 3), set-based approaches (Chapter 4), gene-based using partial-least squares (Chapter 5), and use of the RELIEF algorithm (Chapter 6). Because no approach is free of problems the use of multiple approaches is desirable. The approach using RELIEF is particularly novel. As explained by Todorov, "The aim of the RELIEF algorithm . . . is to identify features (e.g., genes, environmental factors) that are *relevant* to the trait of interest (e.g., risk increasing or decreasing), starting from a set . . . that may include thousands of irrelevant features (e.g., SNP genotypes from a whole-genome chip)" (p. 95). The algorithm has been used extensively, for example, to distinguish objects, such as persons in pictures. To date it has not been used much in genetic analyses, but the author argues convincingly that it could be a powerful tool in such analyses. The most important aspect of this chapter is that it provides programs that will carry out the necessary analyses with a worked example. For this chapter alone the book is worth reading.