

Computational Biology and Bioinformatics: Gene Regulation. Edited by Ka-Chun Wong. Boca Raton, Florida: CRC Press; 2016. US \$169.95 (Hardcover). 425 p. ISBN: 978-1498724975

In *Computational Biology and Bioinformatics: Gene Regulation*, the editor successfully took on the herculean task of clearly and succinctly summarizing the current state of a fast-changing field. Despite the title, the scope of this book extends far beyond gene regulation. The initial sections are organized to follow the flow of information as a gene is expressed: from DNA to RNA to protein. The text begins by discussing important areas of bioinformatics research related to gene expression, then moving to visualization of the RNA interaction network and finally understanding protein function. After these three sections are a section on epigenetics, a case study using a variety of bioinformatic techniques, and several advanced topics that do not fit well into any previous section.

Each chapter is written by a different set of experts. This allows each chapter to be written by experts within the field, but also leads to large variations in the structure and tone of each chapter. For example, Chapter 6 is a high-level discussion of various computational methods to uncover the function of hypothetical proteins, while Chapter 2 focuses on one particular software package for identifying gene expression that differs across studies, CorMotif, and compares it to other algorithms available. In contrast, Chapter 4 does not discuss computational tools at all; rather, it is a summary of biological research on gene regulation and a discussion of sequencing methods for RNA. Finally, Chapter 10 discussed a case study where several different computational methods are applied to the problem of understanding drug resistance in non-small-cell lung cancer.

According to the cover text, the intended audience for this work is "...senior undergraduate and junior graduate students..." in fields related to computer science, biology, and bioinformatics. Enough background information is given that large sections of the work, though possibly not all chapters, will be accessible to those who have trained only in biology or computer science. However, it will likely be most beneficial for those who work at the overlap of the two fields. Computer scientists interested in extending these tools outside of biological problems will be disappointed that the tools are often presented as black boxes, with little to no discussion of the underlying algorithm, while biologists with no background in coding may find the tools described difficult to implement due to the lack of information on how to run the programs.

In sum, *Computational Biology and Bioinformatics: Gene Regulation* provides a summary of tools available for a variety of problems in cell biology, not just

gene regulation, making it a good reference text for computational biologists. Clear chapter titles and an index make it easy for a reader to search for a particular topic of interest. Unfortunately, occasional grammar errors can distract from the text, and large variations in content between chapters may make it less useful as a textbook.

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Making Sense of Genes. By Kostas Kampourakis. Cambridge, UK: Cambridge University Press; 2017. US \$32.00 (Paperback). 307 p. ISBN: 978-1107567498.

In *Making Sense of Genes*, Kostas Kampourakis conceptualizes the field of genetics through the lens of biology's evolving understanding of heritability and genes. Accessible but layered with nuanced detail, *Making Sense of Genes* not only breaks down the basic biochemistry behind complexities such as genetic mutation but also discusses the societal implications of genetic discoveries. By using detailed, clear schematics alongside illustrative analogies, Kampourakis elucidates the intricate molecular interactions and conceptual frameworks necessary to learn genetics out of the classroom.

Alongside the detailed biology, Kampourakis provides a historical backdrop, grounding the research at each stage of genetic comprehension in the current understanding of the time. By walking the reader through genetics as it was perceived, Kampourakis offers context for fundamental discoveries, providing an often-overlooked perspective on the people responsible for basic biological research and the role of science in answering "economic and technological [questions]" rather than satisfying "human curiosity alone" (p. 26).

Along with a historical context, Kampourakis addresses familiar fallacies that have become commonplace, even among textbooks. From Mendel to Watson, Crick and Franklin, *Making Sense of Genes* makes the reader rethink the stories they have been told about genetic discoveries.

At the same time, *Making Sense of Genes* pinpoints common misconceptions associated with genetics in society and the way they affect culture. Throughout the book, Kampourakis points out the disconnect between the popular conception of what genes are and how they work, and how genes actually function in both good health and disease. Kampourakis dedicates a large portion of *Making Sense of Genes* to explaining the development of this misconception. In addressing the varied concepts of genes presented in genetics courses and books,

Kampourakis spells out how these misconceptions arose and presents a model for teaching genetics in a way that breaks down the barrier in communicating about genes.

Overall, *Making Sense of Genes* presents familiar material in an unfamiliar light, keeping non-expert readers engaged without oversimplifying or relying on textbook narratives to explain genetic principles.

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Genomes 4. Fourth edition. By Terence A. (T.A.) Brown. New York, NY: Garland Science; 2017. US \$120.00 (Paperback). 524 p. ISBN: 978-0815345084

With high-throughput sequencing, transcriptomics, and proteomics no longer in their “infancy” as described in the preface by author T.A. Brown, *Genomes 4* offers an expansive review on a broad spectrum of topics in genetics ranging from the central dogma of genes coding for proteins, to the fine technical details of genome mapping. This edition retains the four-part organization from the previous edition: studying genomes, genome anatomies, how genomes are expressed, and how genomes replicate and evolve.

Similar to the 3rd edition, the updated text contains both short answer questions and in-depth problems to assess understanding of the chapter material. While the questions are well-written and generally encompass the chapter material, the answers to the questions seem to be solely an instructor resource, which may make learning the material outside of a course setting difficult. All chapters contain bolded key words that are defined in the glossary section of the textbook, as well as a bulleted summary of the material at the end of each chapter. Although these learning aids may largely serve undergraduate students in exam-based courses, the further reading section also found at the end of each chapter offers advanced students additional articles and research papers that are helpful in pursuing chapter topics in greater detail. The suggested resources from this section are organized and annotated with respect to the major concepts detailed in the chapter, making it easy to pinpoint articles and papers students may find helpful in their studies.

Aesthetically, the figures in the book are colorful, well-designed, and easy to follow. The figures that detail the basic order of relevant biological processes and protocols are cleanly designed in a way that avoids superfluous details and contributes to a better understanding of the material. Images from the book can be downloaded from the publisher’s website (www.garlandscience.com) in

either PowerPoint or JPEG formats.

One of the major strengths of *Genomes 4* is how it utilizes the figures to explain what techniques typical labs or researchers use in their studies. Before jumping into the technical details, however, the book also takes great care in laying out the concepts behind them so as to convey a complete and whole understanding of the techniques and their advantages and disadvantages. Further considerations are given to how different methods compare in terms of their accuracy, resolution, and application context. On top of describing the techniques in detail, the text also gives real-world examples of efforts in science that have used these technologies in order to solve unanswered questions.

With this in mind, *Genomes 4* is a great resource for students wanting to understand genomes and the tremendous advancements in the field that have been made over the past decade since the previous edition.

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Developmental Biology. Eleventh Edition. By Scott F. Gilbert and Michael J. F. Barresi. Sunderland, MA: Sinauer Associates, Inc; 2016. US \$155.95 (Hardcover). 810 p. ISBN: 978-1605354705

The task of educators to impart a comprehensive understanding of organisms and their creation can seem daunting. This is especially the case in the era of advanced technology, with the challenge of capturing the attention of students who are accustomed to entertainment and social media at their disposal. The authors of *Developmental Biology, Eleventh Edition* have proven to adapt to this reality, by combining thorough text with online learning to allow for an in-depth exploration of its material.

Developmental Biology is divided into seven parts, within which there are a total of 26 chapters to further expand on the given topics. These include: “Part I: Patterns of Processing of Becoming;” “Part II: Gametogenesis and Fertilization;” “Part III: Early Development;” “Part IV: Building with Ectoderm;” “Part V: Building with Mesoderm and Endoderm;” “Part VI: Postembryonic Development;” and “Part VII: Development in Wider Contexts.” Part I offers a framework for understanding animal development, which leads the reader to Part II’s exploration of the circle of sex, in terms of sex determination and the beginning of creating new organisms. Part III discusses cleavage, gastrulation, and axis formation, while Part IV elaborates on the vertebrate nervous system and epidermis. Part V focuses on organogenesis, with sections devoted to limb