**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,