Book Reviews

Translational Control in Biology and Medicine. Eds.
M. B. Mathews, N. Sonenberg & J. W. B. Hershey.
Cold Spring Harbor Laboratory Press. 2007. 934
pages. ISBN 0 87969 767 9. Price $135. (hardback)

The popular molecular biology and genetics text
books by-and-large convey the impression that the
control of gene expression is essentially achieved
through the modulation of transcription. Except this
is not strictly true. As is amply illustrated by this ex-
cellent new edition of the Cold Spring Harbor Lab-
oratory Press monograph on Translational Control,
numerous post-transcriptional control mechanisms
have now been identified from studies on viral, uni-
cellular and multicellular model systems, many of
which act via modulation of the translational ma-
chinery.

When the first edition of Translational Control
appeared just over a decade ago, several mRNA-
specific and global translational control systems had
been identified that largely operated through mod-
ifications to the translation initiation machinery,
specifically the initiation factors eIF2 and eIF4. In
the subsequent decade, which has taken in a second
edition of this monograph in 2000, many new types
of translational control mechanism have emerged and
we can now more fully appreciate the range of cellular
and disease processes that involve and exploit such
levels of control. In this new (third) edition, the three
editors (who have remained the same through all
three editions) have revamped the focus of the
monograph to take into account many of these new
developments, especially those relating to human
health and disease. Consequently, among the 30
chapters that make up this near 900 page monograph,
we find chapters dealing with subjects ranging from
apoptosis through to signal transduction and cancer
with the final chapter describing the opportunities
translation-based targets hold for new drug discovery.

As the editors point out in their preface, this is not
a book that should necessarily be read from cover-
to-cover. There is no obvious conceptual framework
which defines the order the chapters are arranged
in; for example Chapter 5 deals with how internal
ribosome entry sites (IRES) facilitate translation of
viral mRNAs in infected cells, yet it is not until
Chapter 20 that we get an overview of translational
control during viral infection. But this is not a criticism
nor a problem for the reader as each Chapter provides
a self-contained, authoritative and impressively up-
to-date account of a specific area of translational con-
trol. The editors are to be congratulated on assembling
an outstanding collection of contributions and con-
tributors. While which chapters you choose to read
will undoubtedly reflect your specific interests, I would
encourage all to read the opening chapter written by
the editors where they provide a highly readable re-
view of the origins, mechanisms and targets of trans-
lational control and in so doing provide an important
historical context for readers new to this 'hot' topic.

Even if you already have the previous edition of
Translational Control (as I do), then that should not
inhibit you from buying this new edition; it is not
just an updated version of the previous editions. The
editors have introduced a significant number of new
topics, some of which (for example, microRNAs)
were not yet on the radar in 2000. Where topics have
been covered in the previous edition(s), they have
succeeded in their stated aim of getting chapters that
are "stimulating, edifying and authoritative" and in
several cases have used different authors to 'ring the
changes'. And if you are one of those 'students' of
molecular biology and genetics brought up on a diet
of transcriptional control, this book will provide you
with a tasty and equally satisfying second course.

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*Bioinformatics for Geneticists: A Bioinformatics
Primer for the Analysis of Genetic Data. 2nd Edn.*
Ed. M. R. Barnes. Wiley. 2007. 528 pages. ISBN
978-0-470-02620-5. Price £45. (paperback)

Put a group of bioinformaticians in a room and
the chances are that the skill base for each of
them will differ considerably, even those involved
in genetics based projects. By the nebulous definition

of bioinformatics they could be involved in IT-infrastructure, including data management and storage, or involved in data processing and analysis using any combination of the myriad of software tools available in each field of genetics. It is essential, therefore, to restrict the scope of any book that deals with bioinformatics. "*Bioinformatics for Geneticists*" does that by focusing on human disease genetics and limits the bioinformatics aspect to associated software tools and techniques. Given this (relatively) specialised viewpoint a layperson may question the need for a new edition of this book as the last was published under three years ago. However the fundamental changes to our understanding of some areas such as non-coding RNAs and the rapid expansion of key resources such as single nucleotide polymorphism data produced from the HAPMAP project, have left a void in the knowledge base covered by textbooks. To this book's credit, these topics, in conjunction with more mature areas, are covered in a way that is both understandable and interesting.

The book is split into 19 chapters with five main sections: An introduction to bioinformatics for the geneticist, Mastering genes, genomes and genetic variation data, Bioinformatics for genetic study design and analysis, Moving from associated genes to disease alleles, and Analysis at the genetic and genomic data interface. Each chapter is written by different authors but assembled such that they describe a different and often research-focused area. As the book's subtitle "*a bioinformatics primer for the analysis of genetic data*" suggests, the chapters are often useful for directing the reader to further information resources. However, the level of detail differs considerably between chapters. The HAPMAP project for example is covered at great length, and as arguably one of newer and faster growing datasets this attention is easily justifiable. Microarray analysis on the other hand is described at a more fundamental level and mentions alternative applications such as chIP-chip, going into much detail on their analysis.

A benefit of research focused chapters is that the reader gains a basis in a variety of bioinformatics tools and techniques aplicable to each subject area. One of my favourite chapters in this aspect is Chapter 9 "*Integrating genetics, genomics and epigenomics to identify disease genes*". Here a range of software tools and techniques are taught together while focusing on a particular case study. Despite this, the opportunity to summarise the relevant resources and repositories is not missed. Perhaps the main drawback to this integrated approach is that knowledge from many of the data repositories and software packages common to multiple fields (such as those at ensEMBL, SwissProt and NCBI) is learned in a piecemeal fashion to the detriment of understanding the ethos and connectivity behind these key data sources.

Other aspects of a bioinformatician's job are data management and programming. Chapter 2 "*Managing and manipulating genetic data*" alludes to covering these topics but the focus of the chapter is extremely basic. Although essential reading for complete novices, some of the Perl code examples are quite confusing to the target audience. Moreover, it does not emphasise the use of the pre-existing libraries available in BioPerl. In my opinion the premise of showing and teaching limited code examples (especially just one programming language), to a target audience of non-programmers is flawed. A more useful approach may have been to suggest the best languages to learn, based on their ease of use and the availability of existing code repositories for specific tasks, and to emphasise the best books and resources for self-learning. On the whole the absence of any mention or review of the repositories of reusable code is rather disappointing as although the R-language, Perl and BioPerl are briefly mentioned, ensEMBL Perl API, BioConductor [R-language], BioPython [Python], BioRuby [Ruby] and BioPostgres [Postgres database] are not. Lastly, as both academic and corporate labs are now generating a mountain of data, a review of specific database storage solutions would have been advantageous. Only the microarray chapter (15.5) addresses this, providing an excellent (albeit already slightly outdated) review of microarray data storage.

Although I have highlighted some drawbacks in the style and scope of the book I wish to emphasise that the content in the chapters is mostly of the highest quality. *Bioinformatics for Geneticists* is an excellent resource not just for the geneticist wishing to learn bioinformatics tools available in their field, but also for bioinformaticians wanting to learn background genetics in new or parallel areas of research. Moreover this book should ensure that any researcher's skill base is maintained, and that they are exploiting the growing and maturing bioinformatics resources freely available to the scientific community.

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Epigenetics. Eds. C. D. Allis, T. Jenuwein, D. Reinberg & M.-L. Caparros. Cold Spring Harbor Laboratory Press. 2007. 502 pages. ISBN 0 87969 724 5. Price $150. (hardback)

"Epigenetics" – the New Testament of chromatin biology

In the past fifteen years several books have attempted to provide a coherent overview of the rapid and