
Preface

Rapid advances in computer science, biology, chemistry, and other disciplines are enabling powerful new computational tools and models for toxicology and pharmacology. These computational tools hold tremendous promise for advancing applied and basic science, from streamlining drug efficacy and safety testing to increasing the efficiency and effectiveness of risk assessment for environmental chemicals. These approaches also offer the potential to improve experimental design, reduce the overall number of experimental trials needed, and decrease the number of animals used in experimentation.

Computational approaches are ideally suited to organize, process, and analyze the vast libraries and databases of scientific information and to simulate complex biological phenomena. For instance, they allow researchers to (1) investigate toxicological and pharmacological phenomena across a wide range of scales of biological organization (molecular \leftrightarrow cellular \leftrightarrow organism), (2) incorporate and analyze multiple biochemical and biological interactions, (3) simulate biological processes and generate hypotheses based on model predictions, which can be tested via targeted experimentation *in vitro* or *in vivo*, (4) explore the consequences of inter- and intra-species differences and population variability on the toxicology and pharmacology, and (5) extrapolate biological responses across individuals, species, and a range of dose levels.

Despite the exceptional promise of computational approaches, there are presently very few resources that focus on providing guidance on the development and practice of these tools to solve problems and perform analyses in this area. This volume was conceived as part of the *Methods in Molecular Biology* series to meet this need and to provide both biomedical and quantitative scientists with essential background, context, examples, useful tips, and an overview of current developments in the field. To this end, we present a collection of practical techniques and software in computational toxicology, illustrated with relevant examples drawn principally from the fields of environmental and pharmaceutical sciences. These computational techniques can be used to analyze and simulate a myriad of multi-scale biochemical and biological phenomena occurring in humans and other animals following exposure to environmental toxicants or dosing with drugs.

This book (the first in a two-volume set) is organized into four parts each covering a methodology or topic, subdivided into chapters that provide background, theory, and illustrative examples. Each part is generally self-contained, allowing the reader to start with any part, although some knowledge of concepts from other parts may be assumed. Part I introduces the field of computational toxicology and its current or potential applications. Part II outlines the principal elements of mathematical and computational modeling, and accepted best practices and useful guidelines. Part III discusses the use of computational techniques and databases to predict chemical properties and toxicity, as well as the use of molecular dynamics. Part IV delineates the elements and approaches to pharmacokinetic and pharmacodynamic modeling, including non-compartmental and compartmental modeling, modeling of absorption, prediction of pharmacokinetic parameters, physiologically based pharmacokinetic modeling, and mechanism-based pharmacodynamic modeling; chemical mixture and population effects, as well as interspecies extrapolation, are also described and illustrated.

Although a complete picture of toxicological risk often involves an analysis of environmental transport, we believe that this expansive topic is beyond the scope of this volume, and it will not be covered here; overviews of computational techniques in this area are contained in a variety of excellent references [1–4].

Computational techniques are increasingly allowing scientists to gain new insights into toxicological phenomena, integrate (and interpret) the results from a wide variety of experiments, and develop more rigorous and quantitative means of assessing chemical safety and toxicity. Moreover, these techniques can provide valuable insights before initiating expensive laboratory experiments and into phenomena not easily amenable to experimental analysis, e.g., detection of highly reactive, transient, or trace-level species in biological milieu. We believe that the unique collection of explanatory material, software, and illustrative examples in *Computational Toxicology* will allow motivated readers to participate in this exciting field and undertake a diversity of realistic problems of interest.

We would like to express our sincere thanks to our authors whose enthusiasm and diverse contributions have made this project possible.

Colorado, USA

*Brad Reisfeld
Arthur N. Mayeno*

References

1. Clark, M.M., *Transport modeling for environmental engineers and scientists*. 2nd ed. 2009, Hoboken, N.J.: Wiley.
2. Hemond, H.F. and E.J. Fechner-Levy, *Chemical fate and transport in the environment*. 2nd ed. 2000, San Diego: Academic Press. xi, 433 p.
3. Logan, B.E., *Environmental transport processes*. 1999, New York: Wiley. xiii, 654 p.
4. Nirmalakhandan, N., *Modeling tools for environmental engineers and scientists*. 2002, Boca Raton, Fla.: CRC Press. xi, 312 p.



<http://www.springer.com/978-1-62703-049-6>

Computational Toxicology

Volume I

Reisfeld, B.; Mayeno, A.N. (Eds.)

2013, XII, 612 p., Hardcover

ISBN: 978-1-62703-049-6

A product of Humana Press