# Preface

During the three years after the publication of the first edition of this book, the computational and statistical research in genomics have become increasingly more important and indispensable for understanding cellular behavior under a variety of environmental conditions and for tackling challenging clinical problems. In the first edition, the organizational structure was: *data* → *analysis* → *synthesis* → *application*. In the second edition, we have kept the same structure but have decided to eliminate chapters that primarily focused on applications.

Our decision was motivated by several factors. Firstly, the main focus of this book is computational and statistical approaches in genomics research. Thus, the main emphasis is on methods rather than on applications. Secondly, many of the chapters already include numerous examples of applications of the discussed methods to current problems in biology.

We have tried to further broaden the range of topics to which end we have included newly contributed chapters on topics such as alternative splicing, tissue microarray image and data analysis, single nucleotide polymorphisms, serial analysis of gene expression, and gene shaving. Additionally, a number of chapters have been updated or revised. We thank all the contributing authors for their contributions and hope that you enjoy reading this book.

Wei Zhang
Houston, TX

Ilya Shmulevich
Seattle, WA