Computational Systems Biology of Cancer (Chapman & Hall/CRC Mathematical and Computational Biology)

Emmanuel Barillot, Laurence Calzone, Philippe Hupe, Jean-Philippe Vert, Andrei Zinovyev

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The future of cancer research and the development of new therapeutic strategies rely on our ability to convert biological and clinical questions into mathematical models?integrating our knowledge of tumour progression mechanisms with the tsunami of information brought by high-throughput technologies such as microarrays and next-generation sequencing. Offering promising insights on how to defeat cancer, the emerging field of systems biology captures the complexity of biological phenomena using mathematical and computational tools.

Novel Approaches to Fighting Cancer
Drawn from the authors' decade-long work in the cancer computational systems biology laboratory at Institut Curie (Paris, France), **Computational Systems Biology of Cancer** explains how to apply computational systems biology approaches to cancer research. The authors provide proven techniques and tools for cancer bioinformatics and systems biology research.

Effectively Use Algorithmic Methods and Bioinformatics Tools in Real Biological Applications
Suitable for readers in both the computational and life sciences, this self-contained guide assumes very limited background in biology, mathematics, and computer science. It explores how computational systems biology can help fight cancer in three essential aspects:

1. Categorising tumours
2. Finding new targets
3. Designing improved and tailored therapeutic strategies

Each chapter introduces a problem, presents applicable concepts and state-of-the-art methods, describes existing tools, illustrates applications using real cases, lists publically available data and software, and includes references to further reading. Some chapters also contain exercises. Figures from the text and scripts/data for reproducing a breast cancer data analysis are available at www.cancer-systems-biology.net.

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