Computational Biology

Computational biology, which includes many aspects of bioinformatics, is the science of using biological data to develop algorithms or models in order to understand biological systems and relationships. Until recently, biologists did not have access to very large amounts of data. This data has now become commonplace, particularly in molecular biology and genomics. Researchers were able to develop analytical methods for interpreting biological information, but were unable to share them quickly among colleagues.

• Book: Computational Biology - Genomes, Networks, and Evolution (Kellis et al.)

This text covers the algorithmic and machine learning foundations of computational biology combining theory with practice. We cover both foundational topics in computational biology, and current research frontiers. We study fundamental techniques, recent advances in the field, and work directly with current large-scale biological datasets.

  ◦ Front Matter
  ◦ 1: Introduction to the Course
  ◦ 2: Sequence Alignment and Dynamic Programming
  ◦ 3: Rapid Sequence Alignment and Database Search
• Book: A Primer for Computational Biology (O’Neil)

A Primer for Computational Biology aims to provide life scientists and students the skills necessary for research in a data-rich world. The text covers accessing and using remote servers via the command-line, writing programs and pipelines for data analysis, and provides useful vocabulary for interdisciplinary work.

- Front Matter
- 1: Introduction to Unix/Linux
- 2: Programming in Python
- 3: Programming in R
- Back Matter

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