

# Perl for Bioinformatics, Second Edition



Informatics in the genomic setting involves the storage, search, and manipulation of textual data such as nucleotide and protein sequences and related matter such as structural or functional annotations, authors, cross-links to other sequences or structures, and more. (See the Genbank, EMBL, and PDB databases to get a better idea.) While some of the search and manipulation needs of a user may be met by generic web interfaces, often they won't be. Some needs may not have been anticipated when the web interface was constructed, others perhaps were too complex to support for use over the web. Perl is an ideal language for such needs. With Perl one will sometimes be able to solve a data search or manipulation problem in a matter of hours if not minutes. (Solving the same problem in C/C++/Java could take much, much longer.) Here are some particular problems in this setting for which Perl is a great fit.

- Searching sequence databases with regular expression patterns.
- Parsing entries in databases (e.g., reading a Genbank entry of a gene and extracting its exons).
- Converting database entries from one format to another (e.g., converting from Genbank to EMBL format).
- Using standard sequence analysis tools written in Perl. (See the various Perl packages supported by the BioPerl project.) (For the second edition: As it turns out, Perl is a great language also for rapid development of various sophisticated algorithms used in bioinformatics, especially those in sequence analysis. This can be useful for students in a course who quickly want to implement such algorithms and do real things with them. It can also be good in a scientific or professional setting where biologists want certain questions answered, and their computer colleagues can quickly put together Perl scripts to do what they want.) This short book introduces Perl to the bio or computer scientist who is

interested in or working in bioinformatics. Chapter 1 covers data types. Chapter 2 covers control structures. Chapter 3 covers input and output. Chapter 4 covers regular expressions. Chapter 5 covers handy functions on strings. All these chapters contain illustrative examples from bioinformatics. These chapters cover only those features of Perl that are particularly important to know in the context of search and manipulation of biomolecular data. In particular, Unix-specific features such as those involving Unix file, directory and process management are omitted. Chapter 6 touches on subroutines. Chapter 7 presents several Perl scripts for various common bioinformatics tasks (there are some additions in the second edition). Chapter 8 - a relatively big new chapter added in the second edition - describes several bioinformatics algorithms such as those used in fragment assembly, heuristic local alignment, automated motif discovery, classification of sequences, optimal sequence-to-sequence alignment, optimal sequence-to-profile alignment, heuristic multiple alignment, profile hidden Markov models, and phylogenetic analysis and presents Perl scripts for them. Chapter 9 covers the BioPerl project. Chapter 10 covers some Perl modules of use in bioinformatics.

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