Perl for Bioinformatics

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Informatics in the genomic setting involves the storage, search, and manipulation of textual data such as DNA 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.)

This short book introduces Perl to the bio or computer scientist 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. Chapter 6 covers subroutines. 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 7 presents several Perl scripts for various common bioinformatics tasks. Chapter 8 covers the BioPerl project.

Chapter 9 presents some modules, with examples from bioinformatics.

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Precisely why? Because this Perl for Bioinformatics is an unordinary book that the inside of the guide waiting for you to snap that but latter it will jolt you with the secret the item inside. Reading this book next to it was fantastic author who all write the book in such remarkable way makes the content inside easier to understand, entertaining means but still convey the meaning fully. So , it is good for you because of not hesitating having this anymore or you going to regret it. This amazing book will give you a lot of rewards than the other book get such as help improving your ability and your critical thinking approach. So , still want to postpone having that book? If I were you I will go to the e-book store hurriedly.

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