

Perl & BioPerl

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Perl

- Perl is a family of two high-level, general-purpose, interpreted, dynamic programming languages. "Perl" refers to Perl 5, but from 2000 to 2019 it also referred to its redesigned "sister language", Perl 6, before the latter's name was officially changed to Raku in October 2019.

Frontend & Backend

- The terms “front-end” and “back-end” refer to where the code runs in the client-server model . In a traditional client-server application, Perl can be used to write either the client (front end) or the server (back end).

Advantages of Perl

- Perl Provides supports for cross platform and it is compatible with mark-up languages like HTML, XML etc.
- It is very efficient in text-manipulation i.e. Regular Expression. ...
- It is free and a Open Source software which is licensed under Artistic and GNU General Public License (GPL).

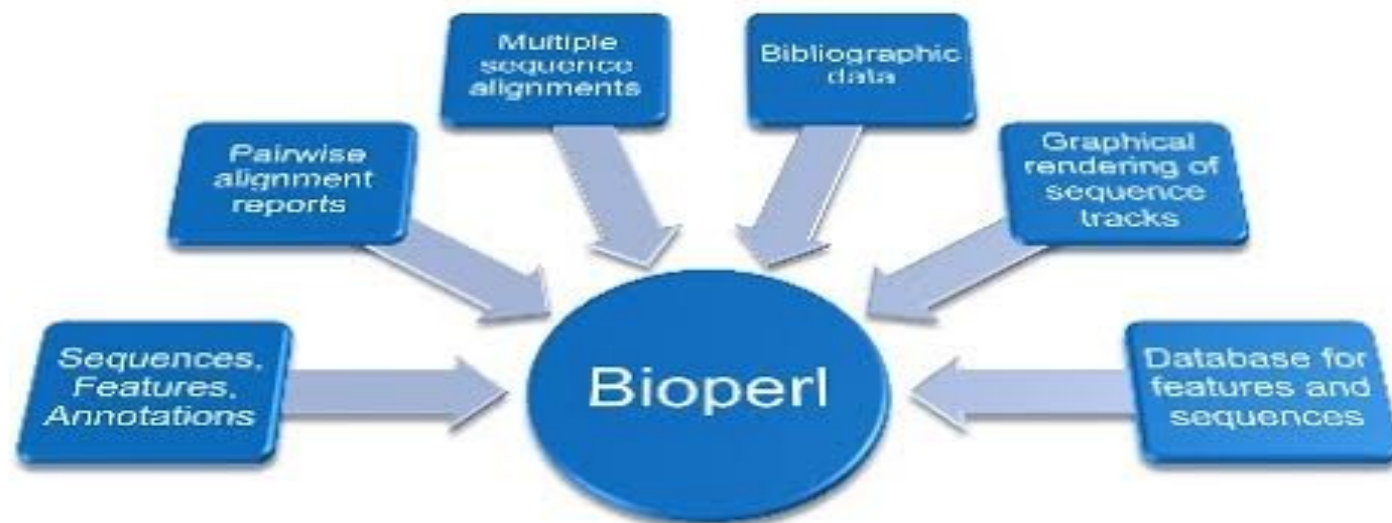
Perl Now day

- It's still worth learning, at least at a basic level, such as in Learning Perl . It's the source of pretty much all the regular expression parsers you see in Python, Ruby, etc. (PCRE = Perl-Compatible Regular Expressions). It's not a popular language these days, because it's hard to work collaboratively in Perl.

Python or Perl

- Python's Clean vs Perl's Complex Syntax.
Python takes a huge advantage over Perl when it comes to code readability. ... On the other hand, Perl borrows its syntax from various programming languages like C, shell scripting and even awk and sed filters when it comes to regular expressions.

Major Domains Covered



Bio Perl

- Bioperl provides an easy-to-use, stable, and consistent programming interface for bioinformatics application programmers. The Bioperl modules have been successfully and repeatedly used to reduce otherwise complex tasks to only a few lines of code.

Application of BioPerl

- Bioperl is a tool kit for bioinformatics software development. It is a suite of Perl modules designed to parse and manipulate various types of data that one uses in bioinformatics. This includes sequences, annotations, sequence alignments, and parsers for the many different file formats for these data.

BioInformatics and Programming

- In the recent years, Bioinformatics and computational biology are two of some important and active research disciplines. Finding insights into biology, information technology tools in the form of programming languages suitable for biology along with data mining tools and techniques are deployed. This work explores the performances of BioPerl, Biojava, BioPython, BioRuby, BioSmalltalk under Bio* projects for executing bioinformatics tasks.

Influence on the Human Genome Project

- The Human Genome Project faced several challenges during its lifetime. A few of these problems were solved when many of the genomics labs started to use Perl. The process of analyzing all of the DNA sequences was one such problem. Some labs built large monolithic systems with complex relational databases that took forever to debug and implement, and got surpassed by new technologies.

- Several related bioinformatics libraries implemented in other programming languages exist as part of the Open Bioinformatics Foundation, including:
- Biopython
- BioJava
- BioRuby
- BioPHP
- BioJS
- Bioconductor

Reference

- <https://en.wikipedia.org/wiki/BioPerl>
- https://www.researchgate.net/publication/322987758_Performance_Evaluation_of_BioPerl_Biojava_BioPython_BioRuby_and_BioSmalltalk_for_Executing_Bioinformatics_Tasks
- <https://www.slideshare.net/bcbbslides/intro-to-perl-and-bioperl>
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC187536/>

Thank You