BioRuby

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Background

1. *Too many* DB formats exist (GenBank, SWISS-PROT, KEGG, etc.).
2. The interfaces for tools are often *unfriendly* for batch processing (FASTA, BLAST, CLUSTALW, etc.).
3. Object-oriented design is very useful for an *unified interface*, regardless of underlying data objects!

Overview of Ruby

- Interpreted scripting language for quick and easy object-oriented programming.
- Complete, full, pure object oriented language: *All data are objects*.
- Simple, straight-forward, extensible, and portable.
- Very popular, especially in Japan. In part, because the author "Matz" is Japanese.
- Totally free.

Hello World

Ruby	`puts 'Hello'`
C	`main(){puts("Hello");}`
Perl	`print "Hello\n";`
Python	`print "Hello"`
Tcl	`puts "Hello"`
BASH	`echo Hello`

Serious Example

```perl
# Perl
package Foo;
sub new {
    my $self = shift;
    bless { 'foo' => 0 }, $self;
}
sub add {
    my $self = shift;
    my $arg = shift;
}
sub output {
    my $self = shift;
    print $self->{'foo'}, "\n";
}

package main;
$foo = new Foo;
$foo->output;
$foo->add(10);
$foo->output;
```

```ruby
# Ruby
class Foo
  def initialize
    @foo = 0
  end
  def add(arg)
    @foo += arg
  end
  def output
    puts @foo
  end
end

foo = Foo.new
foo.output
foo.add 10
foo.output
```

What is BioRuby

- The aim is to provide *"open source" resources* for bioinformatics.
- Based on the pure object-oriented language *Ruby*.
- Creating applications, as well as libraries.
- Licensed under the term of *LGPL*.

Why BioRuby

- Ruby has *good readability*, so your code won't be write-only code.
- Ruby is *easily extensible* by Ruby itself (i.e. overriding methods) and by dynamically loadable C modules.
- Ruby's object-oriented design support is straightforward and complete.
- We love Ruby ! Programming with Ruby is *quite delightful* !

Current Status

DB parsers

GenBank, GenBank location, DDBJ, KEGG/GENES, KEGG/GENOME, PROSITE, TRANSFAC, LITDB, and Gene Ontology classes.

Data modules

Amino Acids, Nucleic Acids, Codon Table, and KEGG organisms modules.

Tool support

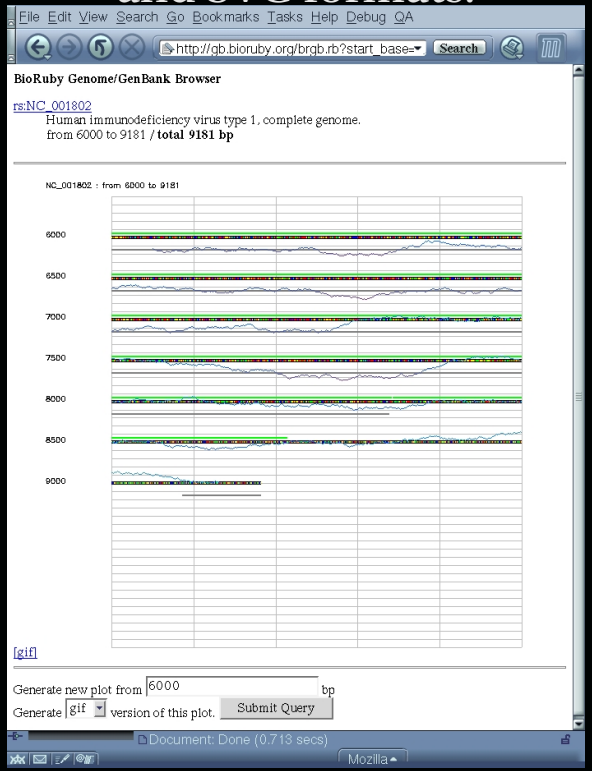
FASTA and SSEARCH.

Misc

DBGET module, Sequence class, modules for Hierarchical Clustering and Smith-Waterman algorithm alignment, Matrix class for Bioinformatics, etc.

Application

BioRuby Genome Browser is an example of BioRuby applications, which supports GIF, PNG and SVG formats.



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