BioRuby : Open-source Bioinformatics Library

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Summary

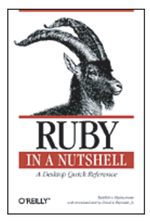
BioRuby is an open-source project which aims to provide a reusable library for biological tasks for the Ruby language. Ruby is an interpreted object-oriented scripting language wih a simple and powerful syntax and native object-oriented programming support. Ruby was started by a Japanese author and is now accepted not only by Japanese but also by many professional programmers around the world as a highly productive language.

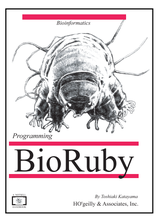
Ruby has many advantageous features to process text files and for system management tasks, which are frequently needed for bioinformatics tools. Compared to other languages, it has native support for object-oriented programming with a simple but powerful syntax, with which we can easily describe and manipulate complicated biological data structures efficiently. These are the main reason why we decided to implement a bioinformatics library in Ruby, even though BioPerl, BioJava, and BioPython were developed previously.

BioRuby project was started in late 2000, and is still in progress. Currently, in version 0.5.3 (latest release), there are over 80 files and 15,000 lines (except comment-only lines). BioRuby is available as free software and is licensed under the LGPL.

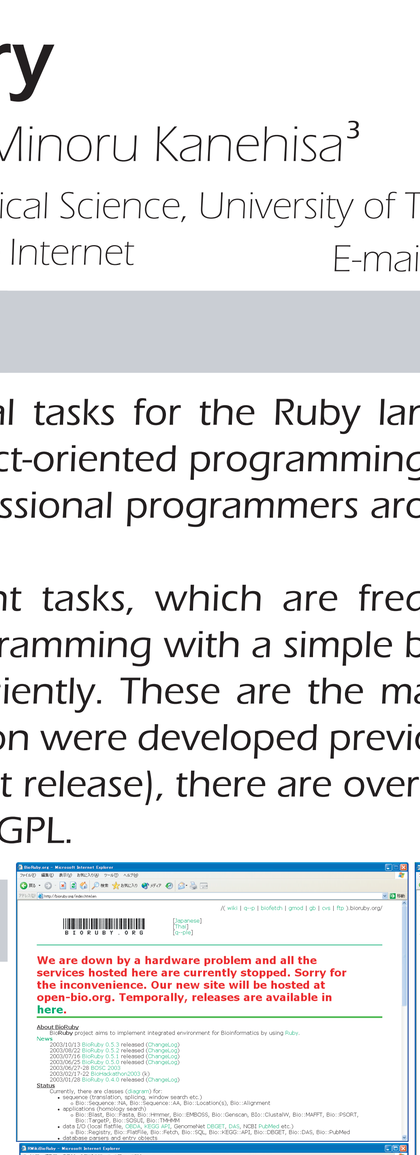
History

(1995/12/21 Ruby language (0.95) was opened to public (fj.sources))
2000/11/21 BioRuby project started
2001/03/18 mailing list started
2001/06/21 bioruby-0.1
2001/07/19 ISMB/BOSC2001 lightning talks
2001/10/24 bioruby-0.3 w/ CVS repository
2002/01-02 BioHackathon w/ BioFetch server
2002/12/16 GIW2002 software demonstration
2003/01/28 bioruby-0.4.0 released
2003/02/17 BioHackathon 2003
2003/06/25 bioruby-0.5.0 released
2003/06/27 ISMB/BOSC2003 talks
2003/07/16 bioruby-0.5.1 released
2003/08/22 bioruby-0.5.2 released
2003/10/13 bioruby-0.5.3 released





http://bioruby.org/



Classes in BioRuby

Basic data structures

	Bio::Sequence::NA	Nucleic acid sequences
	Bio::Sequence::AA	Amino acid sequences
	Bio::Locations	Locations
	Bio::Features	Annotations
	Bio::Reference	Literatures
	Bio::Relation	Graphs / Relations
	Bio::Pathway	Pathways
NEW	Bio::Alignment	Alignments

Wrappers and parsers for bioinformatics tools

updated	Bio::Blast	BLAST (similarity search)
	Bio::Fasta	FASTA (similarity search)
	Bio::HMMER	HMMER (similarity search)
NEW	Bio::ClustalW	CLUSTAL W (multiple alignment)
NEW	Bio::MAFFT	MAFFT (multiple alignment)
NEW	Bio::PSORT	PSORT (protein subcellular localization)
NEW	Bio::TargetP	TargetP (protein subcellular localization)
NEW	Bio::SOSUI	SOSUI (transmembrane helix prediction)
NEW	Bio::TMHMM	TMHMM (transmembrane helix prediction)
NEW	Bio::GenScan	GenScan (gene finding)
	Bio::EMBOSS	EMBOSS (analysis package)

Databases and sequence file formats

	Bio::FastaFormat	FASTA format
	Bio::GenBank	GenBank / DDBJ
	Bio::EMBL	EMBL
	Bio::SPTR	SwissProt and TrEMBL
NEW	Bio::NBRF	PIR
NEW	Bio::PDB	Protein Data Bank
	Bio::PROSITE	PROSITE motifs
	Bio::AAindex	AAindex
NEW	Bio::GO	Gene Ontology
NEW	Bio::GFF	General Feature Format
	Bio::KEGG::GENES	KEGG GENES
	Bio::KEGG::GENOME	KEGG Genomes
NEW	Bio::KEGG::KO	KEGG Orthorogy
	Bio::KEGG::ENZYME	KEGG enzyme
	Bio::KEGG::COMPOUND	KEGG compound
	Bio::KEGG::CELL	KEGG CELL
	Bio::KEGG::Microarrays	KEGG microarrays
	Bio::KEGG::BRITE	Biomolecular Reactions
	Bio::LITDB	Protein/peptide literature database
	Bio::TRANSFAC	The transcription factor database
NEW	Bio::FANTOM	Functional annotation of mouse
	Bio::MEDLINE	MEDLINE bibliographic database

File, network, and database I/O

	Bio::Registry	OBDA Registry service
	Bio::SQL	OBDA BioSQL RDB schema
	Bio::Fetch	OBDA BioFetch via HTTP
	Bio::FlatFileIndex	OBDA flat file indexing system
	Bio::FlatFile	Flat file reader with data □□ □ □ format autodetection
	Bio::PubMed	NCBI PubMed service
NEW	Bio::DAS	Distributed Annotation System
NEW	Bio::KEGG::API	SOAP/WSDL interface in KEGG
NEW	Bio::DDBJ::XML	DDBJ web services

Command-line applications

NEW	biogetseq	OBDA Resistry sequence retrieval
	biofetch	OBDA BioFetch sequence retrieval
	bioflat	Creates/searches ODBA flat file index

Sample / Miscellaneous

NEW	goslim.rb	GO slim histgram
NEW	tdiary.rb	Plug-in for tDiary

NEW : newly added in 2003
updated : significant improvement
(Some classes are not listed here.)

Sample codes

Sequence manipulation

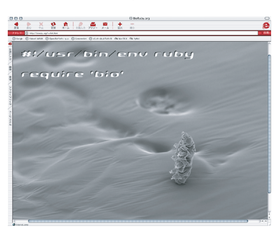
```
#!/usr/bin/env ruby
require 'bio'
gene = Bio::Sequence::NA.new("ggtatctgg")
puts gene.complement□□ # –> "ccagatacc"
puts gene.composition□□ # –> {"a"=>1,"c"=>1, ...
puts gene.gc□□ □ □ □ □ # –> 55.6
prot = gene.translate□□ □ # –> Bio::Sequence::AA
puts prot□□ □ □ □ □ □ □ □ # –> "GIW"
puts prot.molecular_weight□ # –> 374.45
```

Flat file database access

```
#!/usr/bin/env ruby
require 'bio'
ff = Bio::FlatFile.auto("gbbct1.seq")
ff.each do |gb|
  gb.each_gene do |f|
    pos = f.position
    title = gb.entry_id + pos
    puts gb.seq.splicing(pos).to_fasta(title)
  end
end
```

Entry fetch by OBDA

```
#!/usr/bin/env ruby
require 'bio'
registry = Bio::Registry.new
db = registry.db("swissprot")
puts db.fetch("TETW_BUTFI")
```



'bioflat' command

```
% bioflat –create –location ./ \
        –dbname gbphg \
        gbphg.seq
% bioflat gbphg AB048798
```

'biofech' command

```
% biofetch eco b0001
```

'biogetseq' command

```
% biogetseq –dbname eco \
□□ □ b0001 b0002
```