BioRuby project update

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Introduction

- BioRuby - bioinformatics library for Ruby language
  - Object oriented scripting language
  - Originally made in Japan
  - Getting popular by "Ruby on Rails" web development framework
History

• 1993 Ruby language is born
• 1996 BioPerl project started
• 1999 BioPython, BioJava projects started
• 2000 BioRuby project started
• 2002 BioHackathon #1, #2
• 2003 BioHackathon #3
• 2006 BioRuby 1.0 released
• 2006 Phyloinformatics Hackathon #1 (at NESCent)
• 2007 BioRuby 1.1 released
Functionality

• As a library
  • Bioinformatics analysis (2000-2007)
    • Sequences, Pathways, References etc.
    • Databases, Applications, and Web services
  • Chemoinformatics analysis combined with ChemRuby (2005)
  • Phyloinfomatics analysis (2006)

• As an application
  • Interactive shell (2006)
  • Web application development with Ruby on Rails (2007)
Strength

• Up-to-date support for the KEGG database
  • Pathways, Organisms, Genes, Compounds, Enzymes, Drugs etc.
    http://www.genome.jp/kegg/
  • Web services (SOAP/WSDL library is bundled with Ruby)
    • DDBJ XML, EBI web service, KEGG API etc.
      http://xml.nig.ac.jp/
      http://www.ebi.ac.uk/Tools/webservices/
      http://www.genome.jp/kegg/soap/
  • Web applications (Ruby on Rails made development easy)
    • MPI bioinformatics toolkit, KEGG on Rails etc.
      http://toolkit.tuebingen.mpg.de/
      http://dev.kegg.jp/

• Very easy to install (less than few minutes, no '--force' required :-)
http://toolkit.tuebingen.mpg.de/
http://dev.kegg.jp/
BioRuby 1.1

- Released today! (2007/7/19)

  - http://bioruby.org/

  - http://bioruby.org/archive/bioruby-1.1.0.tar.gz

  - http://rubyforge.org/projects/bioruby/

  - http://rubyforge.org/frs/download.php/22958/bio-1.1.0.gem
What's new?

- License is changed to Ruby's
  - Distributed under the same terms as Ruby
- Phyloinfomatics modules
  - Bio::Tree, Newick, NEXUS etc.
- BioRuby plugin generator for Ruby on Rails
  - bioruby --rails
New modules

- Bio::Tree - Phylogenetic tree class by Naohisa Goto
- Bio::Newick - Newick tree format parser/formatter by Daniel Amelang
- Bio::NEXUS - NEXUS tree format parser/formatter by Christian M Zmasek
- Bio::Phylip - Phylip alignment/matrix parser by Naohisa Goto
- Bio::GCG::Msf - MSF alignment parser by Naohisa Goto
- Bio::Ensembl - Ensembl Genome Browser client by Mitsuteru Nakao
- Bio::PTS1 - Peroxisomal targeting signal predictor by Mitsuteru Nakao
- Bio::Iprscan - InterPro scan parser by Mitsuteru Nakao
- Bio::SOFT - NCBI GEO SOFT parser by Trevor Wennblom
- Bio::Lasergene - DNASTar Lasergene sequence parser by Trevor Wennblom
- Bio::RestrictionEnzyme - REBASE based utilities by Trevor Wennblom
- Bio::Map - Linkage maps and markers by Jan Aerts
- Bio::Muscle, Bio::Probcons, Bio::Tcoffee by Jeffrey Blakeslee
Enhancements

- Bio::Command to provide transparent HTTP proxy access
- Bio::KEGG::* - followed recent changes
- Bio::Alignment - added support for Phylip, Molphy, GCG MSF formats
- New methods
  - Bio::SOAPWSDL, Bio::BLAT, Bio::MAFFT, Bio::ClustalW, Bio::PROSITE, Bio::KEGG::KGML, Bio::Sequence::NA
  - Bio::AminoAcids support for Pyrrolysine, Selenocysteine etc.
- BioRuby shell plugins
  - soap, blast, psort, codon, seq
  - Bio.shell methods
Bug fixes

- Bio::PDB by Mikael Borg
- Bio::DAS by Dave Thorne
- Bio::SQL by Raoul Jean Pierre Bonnal
- Bio::GFF3 by Hien Le
- Bio::Blast::Fastacmd by Shuji Shigenobu
- Bio::Fasta by Fredrik Johansson
- Bio::FlatFile by Naohisa Goto
Phyloinformatics Hackathon

- NESCent (Dec 2006)

Objectives

- Phylogenetic tree - Bio::Tree

- Phyloinformatics formats - NEXUS, Newick etc.

- Interface for interactive analysis - BioRuby on Rails
BioRuby shell on Rails

Web interface for the BioRuby library

BioRuby script:

```ruby
basc_fee = 395 * 168
```

Result:

```
methods  classes  modules
```

Input: [3]

```
basc_fee = 395 * 168
```

Result:

```
methods  classes  modules
```

Input: [3]

```
prot = dna.translate
```

Result:

```
methods  classes  modules
```

Input: [1]

```
dna = getseq("etgc", 38).randomize
```

Result:

```
methods  classes  modules
```

```
Installation

- Installing **Ruby** (few minutes)  
  % ./configure  
  % sudo make install

- Installing **RubyGems** (few seconds)  
  % sudo ruby setup.rb

- Installing **Ruby on Rails** (few minutes)  
  % sudo gem install rails -y

- Installing **BioRuby** (few seconds)  
  % sudo gem install bioruby

- Installing **RSRuby** (few seconds)  
  % export R_HOME="/Library/Frameworks/R.framework/Resources"
  % sudo gem install rsruby -- --with-R-dir=$R_HOME
  or
  % ruby setup.rb config -- --with-R-dir=$R_HOME
  % ruby setup.rb setup
  % sudo ruby setup.rb install

Bundled in Mac OS X Leopard!
Future plans

• Integration with Ruby on Rails
  • Data models
  • Web service
  • Visualization
• Documentation
• Publication
http://bioruby.org/