BioRuby project update

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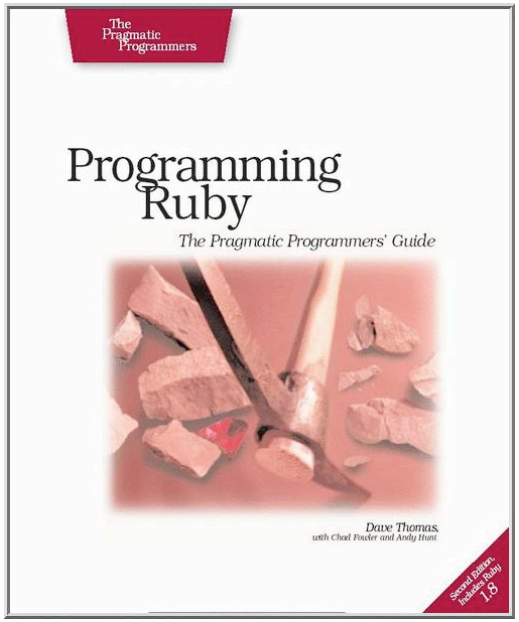
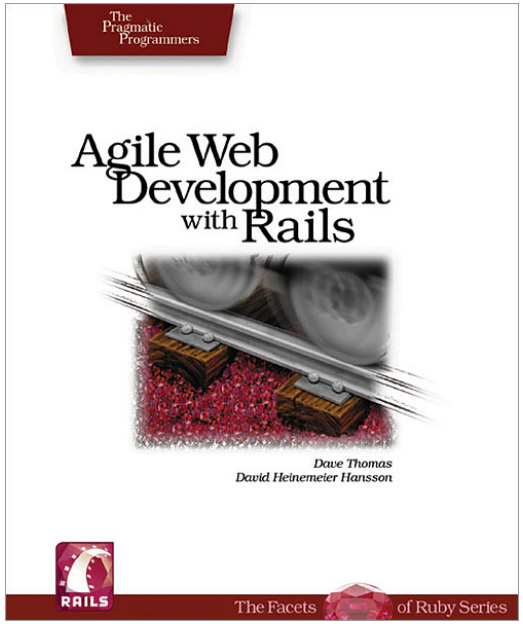
Introduction

- 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  - Originally made in Japan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 miniutes, no '--force' required :-)

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

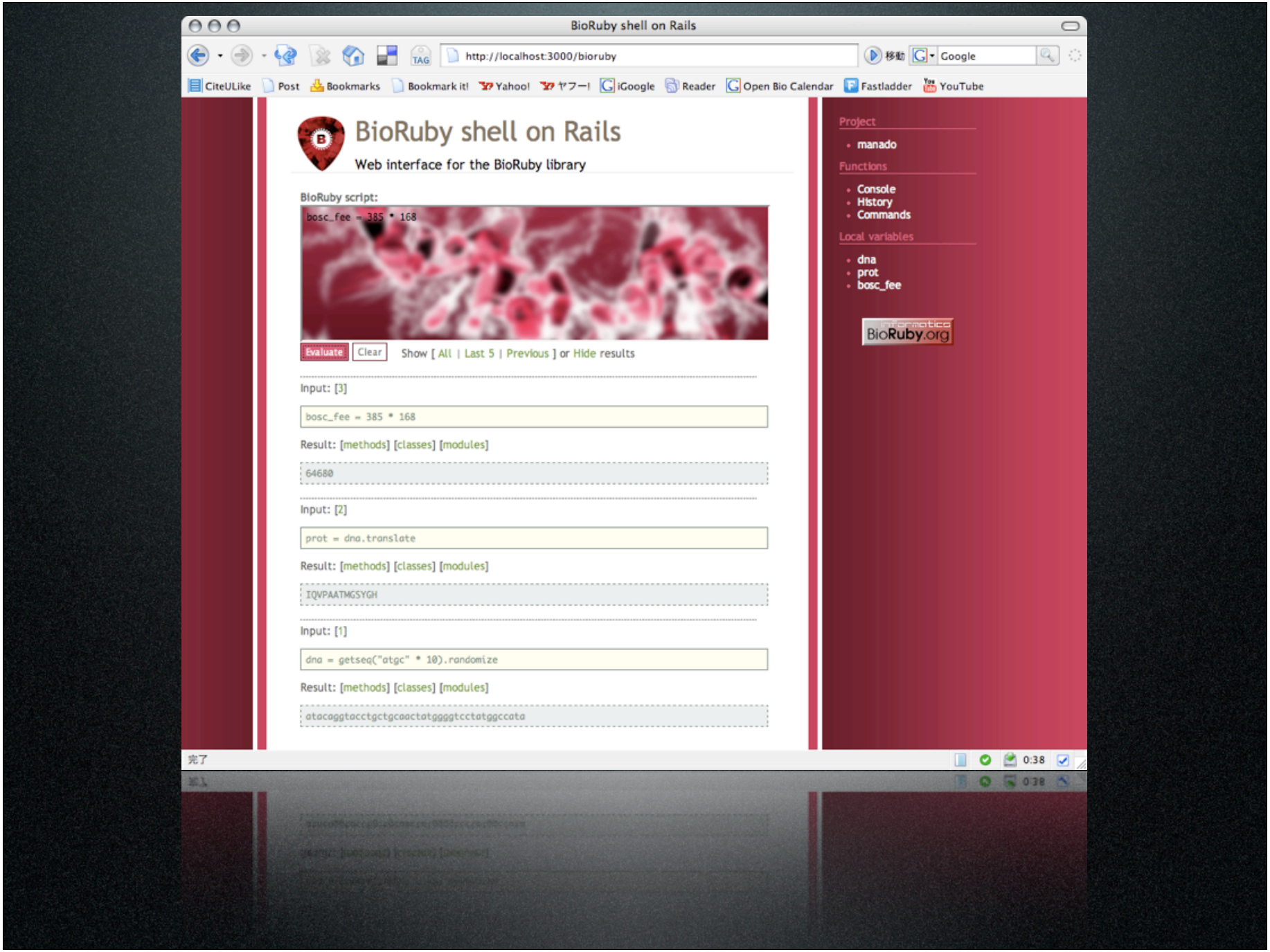
- Bio::Command to provide transparenet HTTP proxy access
- Bio::KEGG::* - followed recent changes
- Bio::Alignment - added support for Phylip, Molphy, GCG MSF formats
- New methods
  - Bio::SOAPWSDL, Bio::BLAT, Bio::MAFFT, Bio::ClustalW, Bio::PROSITE, Bio::KEGG::KGML, Bio::Sequence::NA
  - Bio::AminoAcids 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
http://localhost:3000/bioruby
Google
CiteULike
Post
Bookmarks
Bookmark it!
Yahoo!
ヤフー!
iGoogle
Reader
Open Bio Calendar
Fastladder
YouTube
BioRuby shell on Rails
Web interface for the BioRuby library
BioRuby script:
bosc_fee = 385 * 168
Evaluate
Clear
Show [All | Last 5 | Previous] or Hide results
Input: [3]
bosc_fee = 385 * 168
Result: [methods] [classes] [modules]
64680
Input: [2]
prot = dna.translate
Result: [methods] [classes] [modules]
IQVPAATMGSYGH
Input: [1]
dna = getseq("atgc" * 10).randomize
Result: [methods] [classes] [modules]
atacaggtacctgctgcaactatggggtcctatggccata
Project
manado
Functions
Console
History
Commands
Local variables
dna
prot
bosc_fee
BioRuby.org
完了
0:38

Installation

- Installing Ruby (few minutes) http://www.ruby-lang.org/

```
% ./configure
% sudo make install
```

- Installing RubyGems (few seconds) http://rubyforge.org/projects/rubygems/

```
% sudo ruby setup.rb
```

- Installing Ruby on Rails (few minutes) http://rubyforge.org/projects/rsruby/

```
% sudo gem install rails -y
```

- Installing BioRuby (few seconds) http://bioruby.org/

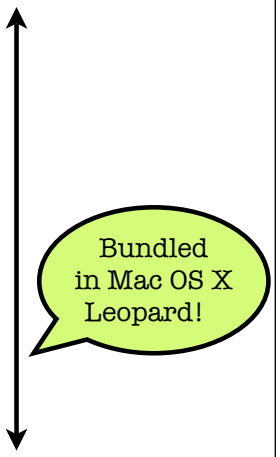
```
% sudo gem install bioruby
```

- Installing RSRuby (few seconds) http://rubyforge.org/projects/rsruby/

```
% 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
```



Future plans

- Integration with Ruby on Rails
  - Data models
  - Web service
  - Visualization
- Documentation
- Publication

http://bioruby.org/