

Bioinformatics Open Source Conference, June 23-24 2005, Detroit

BioRuby 2005

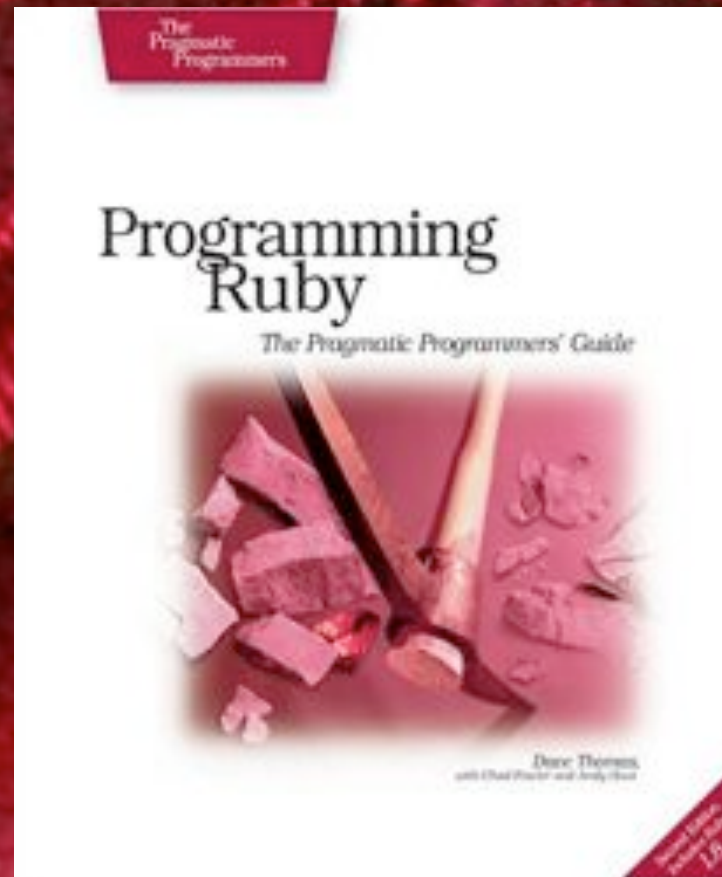
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<http://bioruby.org/>

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What's BioRuby?

- BioPerl for the Ruby programmer



BioRuby updates

- **BioRuby 0.6.2** released
 - Sim4, BLAT, Spidey parsers are added
 - Unit tests is being added by Moses Hohman
 - KEGG GLYCAN database is supported
- KEGG API 4.0 released (tested with **BioRuby**)
 - APIs for LIGAND, GLYCAN, REACTION databases
 - Colored PATHWAY in HTML format is available

What's coming next?

- **BioRuby** 0.6.3 will be released soon
 - Bug fixes
 - We will not continue to support Ruby 1.6
 - RubyGems for easy installation
 - `% gem install bioruby`
- **ChemRuby** project started
 - Nobuya Tanaka (KEGG lab.)
- Financial support for developing docs/tests and integration of Bio and Chem -Ruby

Ruby1.8
inside!



Exploratory Software Project

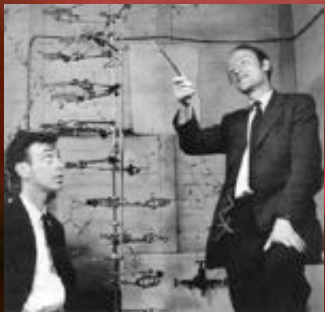
- 1 year financial support from IPA
 - Infotech Promoting Agency, Japan

IPA

- **"BioRuby + ChemRuby"**
 - 4 core developers
 - documentations, unit tests
 - develop new features
 - integration of these projects

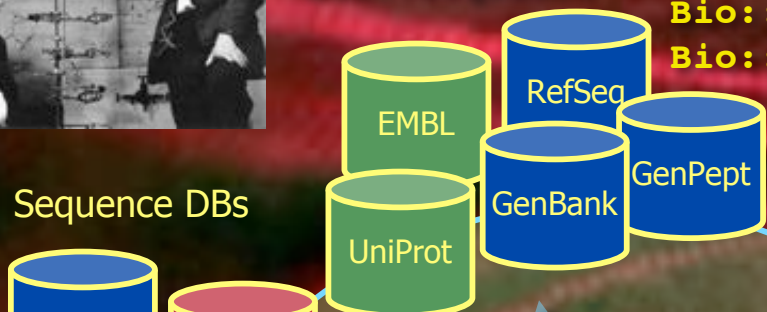
Bio(Chem)RubyHackathon every month!?

Bio + Chem informatics

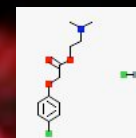
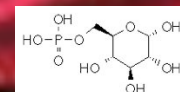


Bio::Sequence

Bio::GenBank,
Bio::EMBL etc.



LIGAND



Sequence DBs



Bio::Flat (BDB)
Bio::Fetch (HTTP)
Bio::SQL (RDB)



Compound DBs

Various format

Bio::Reference

Bio::DAS
(REST CGI)

Bio::KEGG::API
(SOAP/WSDL)



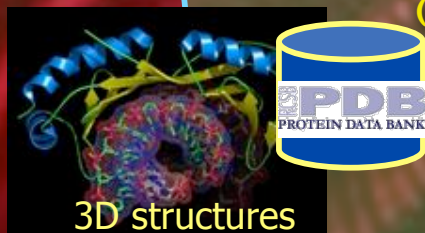
E-Utills
(CGI)



Bio::Pathway



Softwares



3D structures

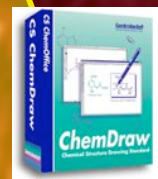
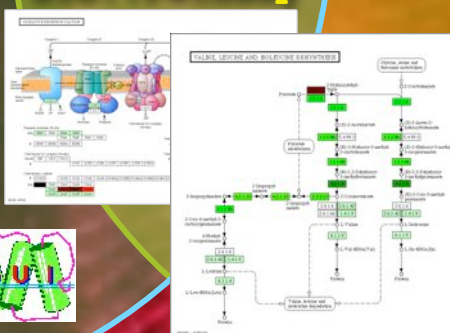
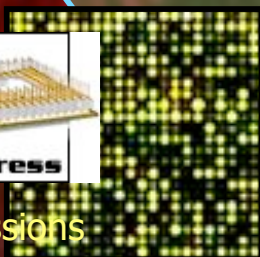
Bio::BLAST,
Bio::HMMER etc.



BLAST

Softwares

Gene expressions



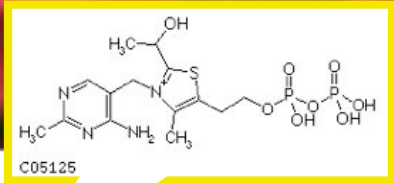


in KEGG lab,

Katayama: developing KEGG API, KEGG DAS etc.

Tanaka: developing algorithms for structure search etc.

ChemRuby



Connect seamlessly..

BioRuby + KEGG API

```

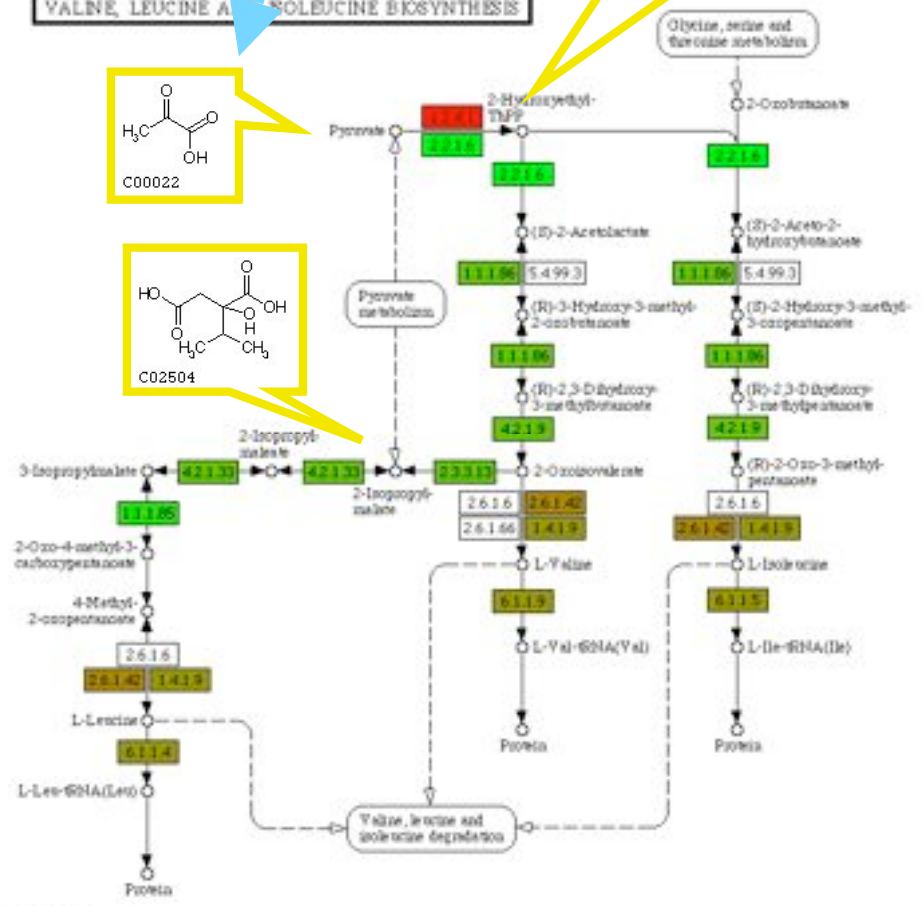
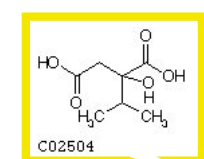
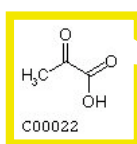
korg = "bsu"

serv = Bio::KEGG::API.new

list = serv.list_pathways(korg)
list.each do |path|
  pathway = path.entry_id
  fg_list = Array.new
  bg_list = Array.new
  genes = serv.get_genes_by_pathway(pathway)
  genes.each do |gene|
    fg_list << "#000000"
    bg_list << exp2rgb(gene) || "#cccccc"
  end
  url = serv.color_pathway_by_objects(pathway,
  serv.save_image(url)
end

```

VALINE, LEUCINE AND ISOLEUCINE BIOSYNTHESIS



More info?

- <http://bioruby.org/>
- staff@bioruby.org
 - Toshiaki Katayama
 - Mitsuteru Nakao
 - Naohisa Goto
 - Nobuya Tanaka

BioPerl

BioRuby

BioRuby



BioRuby

ChemRuby