Bio**Ruby** : Object Oriented Open Source Library for Bioinformatics

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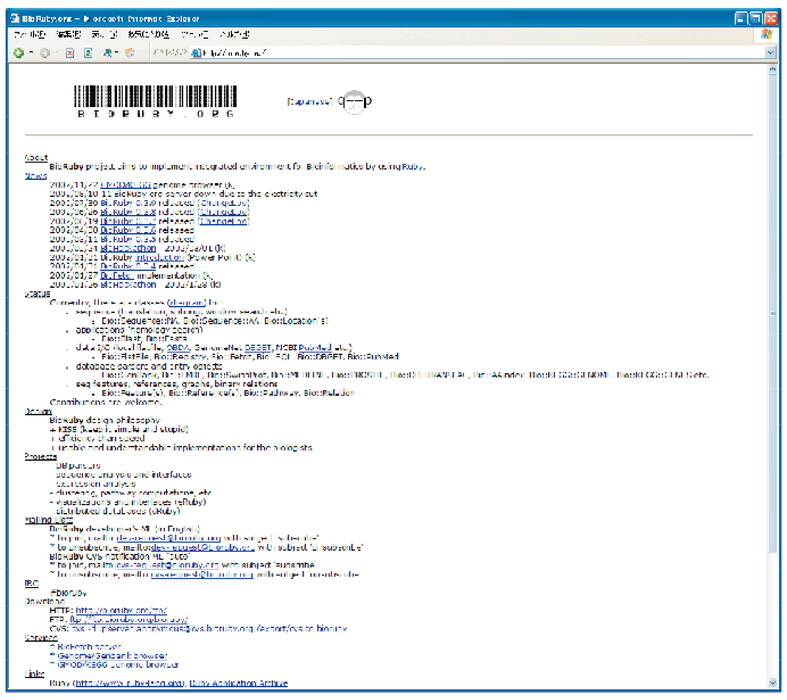
Scope

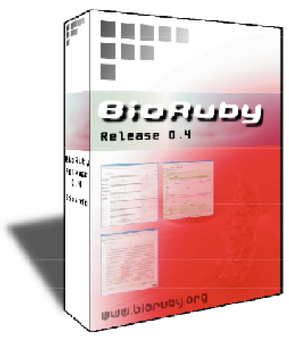
Bio**Ruby** is a class library written in Ruby – an object oriented scripting language – for the daily bioinformatics tasks including biological database access, fetch and parse the entries, execute sequence analysis applications and parse the result in a unified way. Both of the Ruby and BioRuby projects are started in Japan.

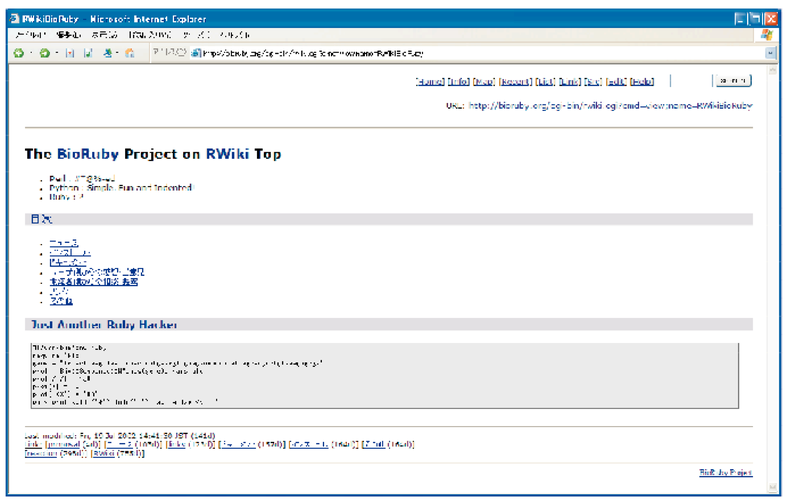


History

1995/12/21 Ruby language (0.95) was opened to public (fj.sources)
2000/11/21 Bio**Ruby** project started
2001/03/18 mailing list started
2001/06/21 bioruby-0.1
2001/07/13 http://gb.bioruby.org launched
2001/07/19 ISMB/BOSC2001 lightning talks
2001/10/24 bioruby-0.3 w/ CVS repository
2002/01-02 BioHackathon w/ BioFetch server
2002/07/18 http://q–p.bioruby.org launched
2002/08/02 BOSC Japan 2002 w/ BioBlog server
2002/11/22 http://gmod.bioruby.org launched
2002/12/xx bioruby-0.4 released

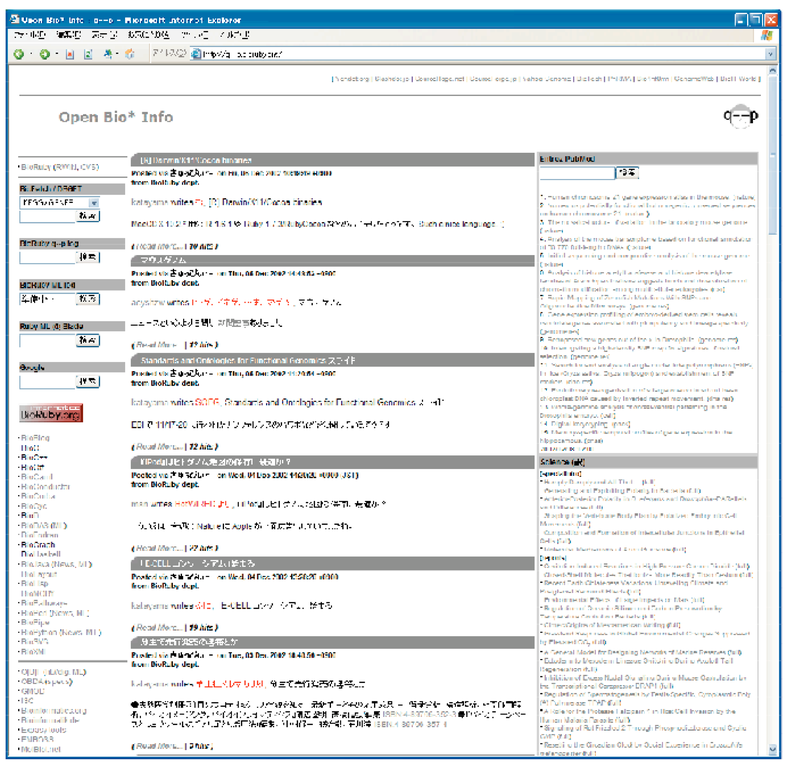
http://bioruby.org/





Open Bio* related projects

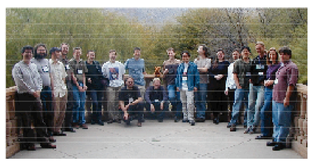
BioPerl by Ewan, Jason, Heikki et al.
BioPython by Andrew, Brad et al.
BioJava by Thomas, Matthew et al.
OmniGene by Brian et al.
BioMOBY by Mark et al.
GMOD by Lincoln et al.
BioSQL by Hilmar, Chris et al.
BioPipe by Elia et al.
BOS by Martin et al.
EMBOSS etc...



BioHackathon

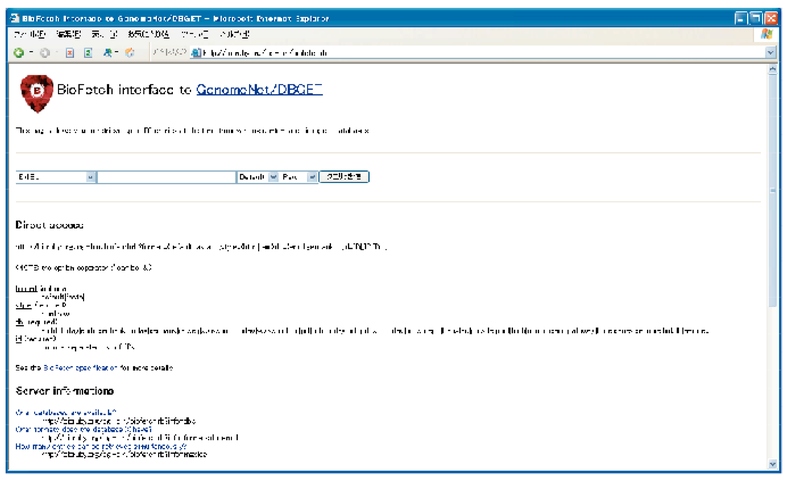
Invite only annual hacking event with commercial support where the Open Bio* developers meet face-to-face to develop common infrastructures for the Open Bio* and the bioinformatics community.

2002/01/26-28 the 1st BioHackathon held in Tucson, Arizona, U.S.A.
AZ portion - mainly sponsored by O'Reilly
2002/02/24-01 2nd part of the event held in Cape Town, South Africa
CT portion - mainly sponsored by Electric Genetics

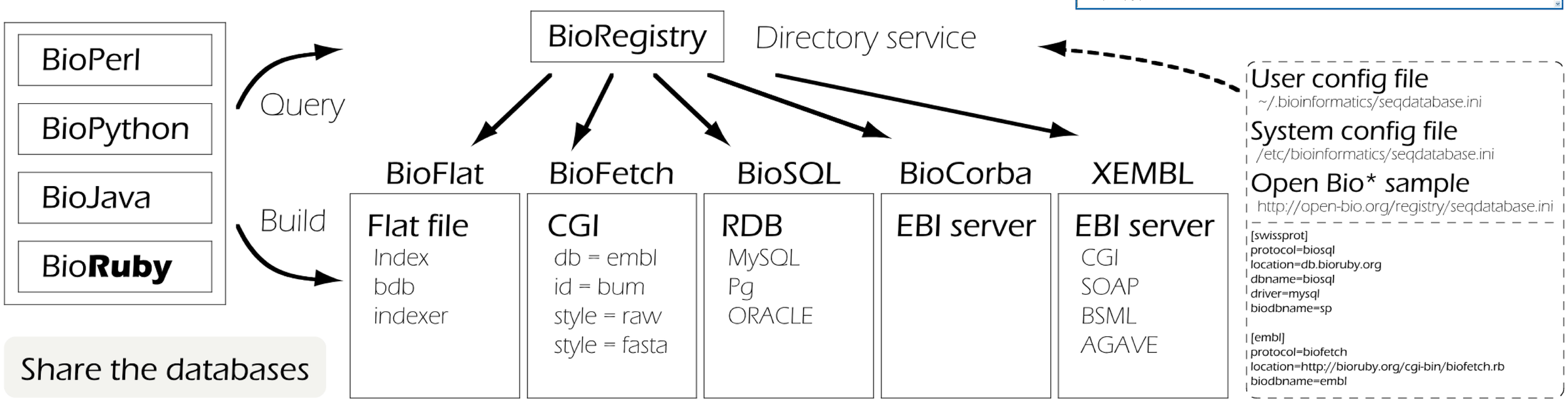


Result :
Implement OBDA specs defined during the Hackathon.
– topics on ontology, graph, biblio are also discussed.

2003/02/xx-xx BioHackathon 2003 will be held in Singapore



OBDA - Open Bio* sequence Database Access



Share the databases

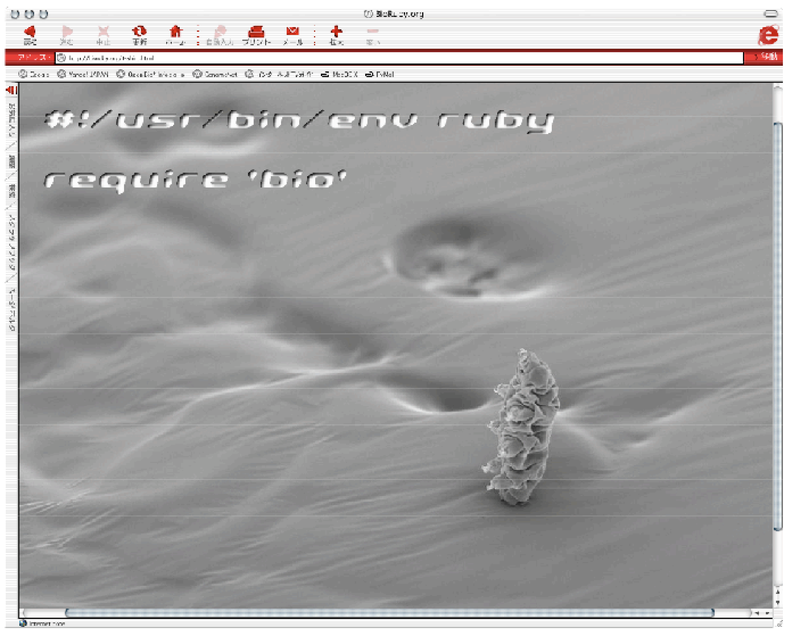
BioRuby getting started

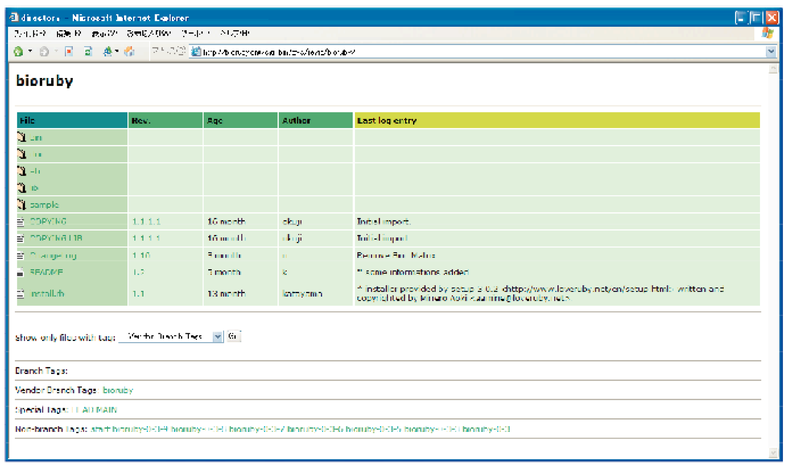
Stable release :

```
% lftpget ftp://ftp.bioruby.org/bioruby/bioruby-0.4.0.tar.gz
% tar zxvf bioruby-0.4.0.tar.gz
% cd bioruby-0.4.0
% ruby install.rb config
% ruby install.rb setup
% su
# ruby install.rb install
```

Cutting edge version :

```
% cvs -d ':pserver:anonymous@cvs.bioruby.org:/export/cvs' login
CVS password: ( just hit return )
% cvs -d ':pserver:anonymous@cvs.bioruby.org:/export/cvs' checkout bioruby
% cd bioruby
following installation procedure is same as above
```





Bio::* classes

Bio::Sequence, Bio::Location, Bio::Feature classes

treat nucleic acid and amino acid sequences, calculate compsitions, reverse complement, translation, window search, splicing, sequence annotation from feature table, etc.

Bio::DB classes (GenBank/EMBL/KEGG etc.)

parsers for various databases (currently supports >20 database formats)

Bio::Blast, Bio::Fasta, Bio::HMMER, Bio::EMBOSS classes

application wrappers and report parsers (supports local and remote execution)

Bio::Reference, Bio::PubMed classes

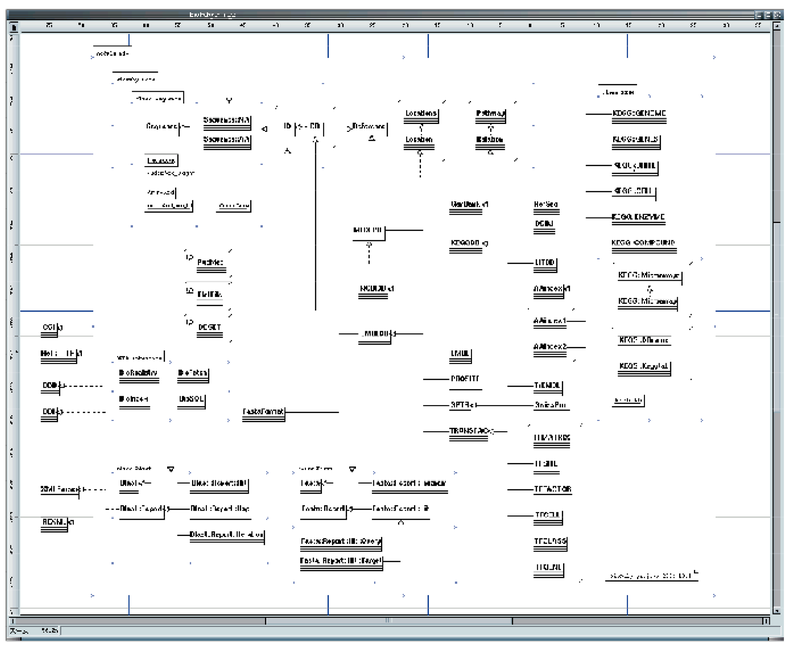
store and reformat the reference information, query the NCBI/PubMed database

Bio::Registry, Bio::SQL, Bio::Fetch, Bio::Flat classes

OBDA sequence database accessing interfaces

Bio::Pathway, Bio::Relation classes

graph computation and binary relations



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,"g"=>4,"t"=>3}
puts gene.gc                  # --> 55.6
prot = gene.translate
puts prot                     # --> "GIW"
puts prot.molecular_weight    # --> 374.45
```

Running Blast

```
#!/usr/bin/env ruby
require 'bio'
fastafile = ARGV.shift
bl = Bio::Blast.local('blastp', fastafile)
ff = Bio::FastaFormat.open(fastafile)
ff.each do |entry|
  puts entry.entry_id
  report = factory.query(entry)
  report.each do |h|
    puts [h.query_id, h.target_id, h.evalue].join("\t")
  end
end
```

Flat file database access

```
#!/usr/bin/env ruby
require 'bio'
ff = Bio::GenBank.open("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

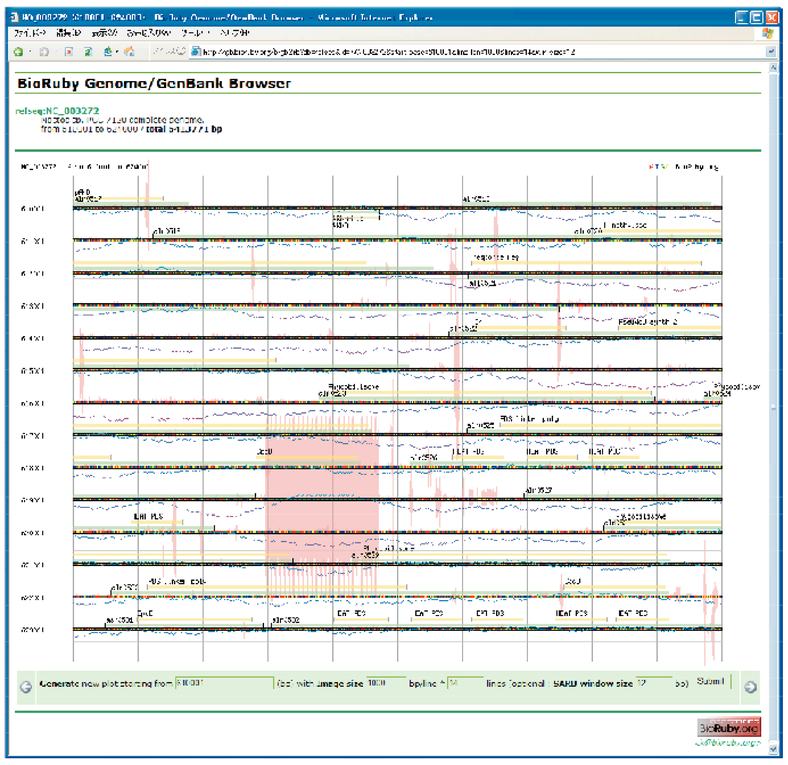
```
#!/usr/bin/env ruby
require 'bio'
registry = Bio::Registry.new
db = registry.db("swissprot")
puts db.fetch("TETW_BUTFI")
```

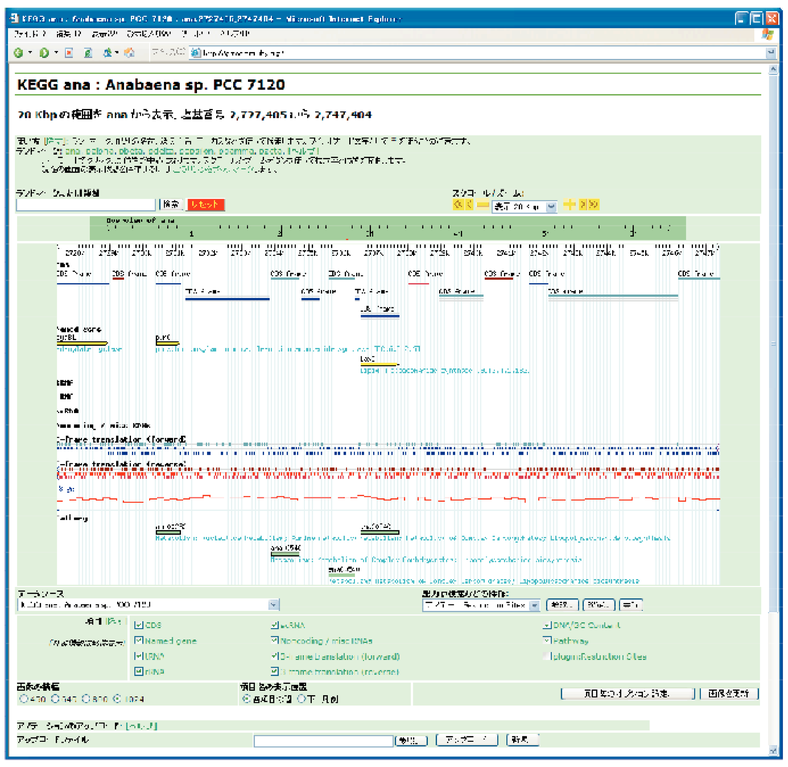
'bioflat' command

```
% bioflat --makeindex gbphg \
          --format genbank gbphg.seq
% bioflat gbphg AB048798
```

'biofech' command

```
% biofetch eco b0001
```





Future work

- Documentation
- Alignment classes
- NCBI / E-utils
- SOAP (DAS, XEMBL, BQS, NIG), CORBA
- Pfam, InterPro, GO, GFF, BSML, AGAVE
- Pathway computation / SSDB
- 3D structure / PDBj

What's coming next ...

- Demo in Tokutei sympo
- BioHackathon2003
- BIP2003
- BOSC2003