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PROJECTS

KEGG, TogoWS, BioRuby

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Research interests

TogoDB

deploy your DB in 5min

Your data in CSV

upload

configure

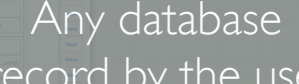
TogoWS

integrated REST/SOAP services

endpoint

Can be accessed with REST API as Linked Data

deploy



Any database record by the user

<http://togows.dbcls.jp/entry/togodb-foobardb/123.rdf>

http://togodb.dbcls.jp/foobardb/show/123

On-the-fly to Linked Data

TogoWS REST interface

Retrieve/parse entries

```
/entry/database/entry_id[,entry_id2,...][[/field][.format]]
http://togows.dbcls.jp/entry/uniprot/A1AG1_HUMAN,A1AG1_MOUSE
http://togows.dbcls.jp/entry/uniprot/A1AG1_HUMAN,A1AG1_MOUSE.fasta
http://togows.dbcls.jp/entry/uniprot/A1AG1_HUMAN,A1AG1_MOUSE.gff
http://togows.dbcls.jp/entry/pubmed/16381885
http://togows.dbcls.jp/entry/pubmed/16381885/authors
http://togows.dbcls.jp/entry/pubmed/16381885/authors.json
database:
KEGG: gene, orthology, enzyme, compound, drug, glycan, reaction
DDBJ: ddbj, dad
PDBj: pdb
NCBI: gene, genome, genomeprj, geo, journals, mesh, nucleotide, omim,
pmc, protein, pubmed, taxonomy, cdd, popset, snp, unigene,
homologene, nuccore, nuceast, nucgss, unists
EBI: biomodels, chebi, ensembl, go, interpro, reactome, uniprot,
uniparc, uniref100, uniref90, uniref50, msdchem, msdpdb
format:
rdf, ttl, xml, json, gff, fasta etc.
```

Search entries

```
/search/database/query+string[/offset,limit][.format]
http://togows.dbcls.jp/search/uniprot/lung+cancer/count
http://togows.dbcls.jp/search/uniprot/lung+cancer/1,10
```

Convert data format

```
/convert/source.format
http://togows.dbcls.jp/convert/blast.gff
source: genbank, blast, fasta, ps1, sim4, hmmer, exonerate, wise etc.
format: gff etc.
```

Data sources



TogoWS
+
BioRuby, BioPerl



Linked Data

In BioHackathon 2010



- ☐ BioRuby extension - Support for Semantic Web
- ☐ RDF converters for TogoWS (ActiveRDF?)
- ☐ Modular system (BioRuby shell plug-in)



- ☐ Integration of data from KEGG Ortholog Clusters (OC) and KEGG MODULE with Semantic Web technology
- ☐ Phylogenetic profile
- ☐ KEGG in RDF, BioPAX



- ☐ Genome annotation + NGS data
- ☐ Queries to Semantic Web