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AFFILIATION

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PROJECTS

KEGG, TogoWS, BioRuby

Research interests

TogoDB

deploy your DB in 5min



upload

The screenshot shows the TogoDB web application. On the left, a file upload dialog is open, prompting for a CSV file named 'toge'. The 'Import' tab is selected. In the center, the 'Database Browser' shows a table named 'institute_dictionary' with two entries: 'katom' and 'katana'. On the right, a 'Settings for /katom' dialog is open, displaying column options for various fields like 'seqid', 'frame', 'orf', 'cric64', etc.

configure

TogoWS

integrated REST/SOAP services

The screenshot shows the TogoWS web interface. It features a main dashboard with a green and blue design, displaying the message 'Integration of the bioinformatics web services'. Below the dashboard, there's a 'Related resources' section listing various databases and services, and a 'Summary of TogoWS services' section. A large callout bubble on the right side states 'Can be accessed with REST API as Linked Data'.

endpoint

This screenshot shows a detailed REST API endpoint for a specific record. The URL is 'http://togodb.dbcls.jp/foobardb/show/123'. The page displays a table of sequence data with columns like 'SeqID', 'Frame', 'ORF', 'Length', 'TargetID', 'Ain_Length', 'Evalue', 'Score', and 'Accession'. Below the table, there's a detailed view of a sequence record, including its structure and associated domains and motifs.

deploy

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

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

Any database
record by the user

On-the-fly to Linked Data

TogоЮS 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, nucest, 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, psl, sim4, hmmer, exonerate, wise etc.
  format: gff etc.
```

Data sources



TogоЯS
+
BioRuby, BioPerl



Linked Data

In BioHackathon 2010



- BioRuby extention - 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

