GEMBASSY: an EMBOSS associated software package for genome analysis using G-language SOAP/REST web services

http://www.g-language.org/gembassy
http://github.com/celery-kotone/GEMBASSY/

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EMBOSS Associated Software (EMBASSY) Package
- 53 tools wrapping G-language REST/SOAP Web Services
- Available from website, GitHub, and EMBOSS Explorer
- GNU General Public License version 2

http://soap.g-language.org/gembassy/emboss_explorer
G-language GAE

- G-language Genome Analysis Environment
- Current version: 1.8.13
- > 100 methods
  - Codon bias
  - Strand bias
- Sequence composition
- Visualization
G-language Server

REST/SOAP CGI

Response

Analyses

G-language GAE

Request

User

Get Sequence

Databases

European Molecular Biology Laboratory

Heidelberg Grenoble Hamburg Hinxton Monterotondo

NCBI

DDBJ

DNA Data Bank of Japan

G-language SOAP Service WSDL File:

- http://soap.g-language.org/g-language.wsdl

EMBOSS (> 6.5.7)

gSOAP Toolkit (version 2.8)

libcurl-devel (> 7.29.0)

G-language SOAP Service WSDL File:

- http://soap.g-language.org/g-language.wsdl

Mac OS X/UNIX
Working with GEMBASSY

% seqret -feature refseqn:NC_000964 -osformat genbank
Read and write (return) sequences
output sequence(s) [nc_000964.genbank]: nc_000964.gbk
% ggcskew nc_000964.gbk
Calculates the GC skew of the input sequence
Created ggcskew.ps

% ggenomemap3 nc_000964.gbk

% gcircularmap nc_000964.gbk
Identify predicted highly expressed gene
Codon usage output file [nc_000964.gphx]:

% grep ^0 nc_000964.gphx |
  sort -t , -k 3 -nr |
  cut -d , -f 6 > genes_sorted.txt

% head -n 100 genes_sorted.txt > top_genes.txt

% tail -n 100 genes_sorted.txt > bottom_genes.txt
% genret nc_000964.gbk @<top|bottom>_genes.txt
before_startcodon [<top|bottom>_before_startcodon.fasta

emna -> extractalign -> kweblogo
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ISMB Posters

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