

Summary

- DNA Data Bank of Japan (DDBJ) provides Web-based systems for biological analysis, called Web APIs for biology (WABI).
- Each Web service and workflow can be used as a complete service or a building block for programmers to construct more complex information processing systems.
- Workflow navigation system aims to help non-programming biologists perform analysis tasks by providing next applicable services on Web browsers according to the output of a previously selected service.

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Services at DDBJ	Programming	Customization
Web APIs	Need	Very flexible
Workflows	No need	Impossible
Workflow Navigation System	No need	Flexible

DDBJ Web APIs for Biology (DDBJ WABI)

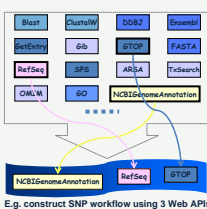
<http://www.xml.nig.ac.jp/>



- Web APIs are the interfaces for programs to access Web services on the Internet.
- Web APIs are building blocks for the developments of workflows.
- Web APIs are implemented by both REST and SOAP.
- DDBJ provides 129 methods (APIs) from 21 categories (services).

Provided Web APIs

Service name (# of Web APIs)	Service description
DDBJ(7), ARSA(4), GetEntry(44),	Keyword search and data retrieval against 20 public databases
Blast(6), ClustalW(4), Fasta(5), VecScreen(4)	Analysis functions such as homology search and multiple alignments
Gib(11), Gtop(3), GTPS(8), GIBV(8), GIBENV(1), GIBIS(1), SPS(2)	DDBJ original database system (microbial/virus genome, insertion sequence, environmental sequence, re-evaluation of ORF in genome, protein structure)
TxSearch(5), RefSeq(1), GO(3), Ensembl(4), OMIM(2), NCBIgenomeAnnotation(4)	Useful databases developed by other institutes.



How to Use DDBJ Web APIs

An example of retrieving a DNA sequence entry for an accession number from the REST server

```
use LWP::UserAgent;
$ua = new LWP::UserAgent;

# make a request
$req = new HTTP::Request POST => 'http://xml.nig.ac.jp/rest/Invoke';
$req->content_type('application/x-www-form-urlencoded');

# set parameters and retrieve a DDBJ entry in a FASTA format
$req->content('service=GetEntry&method=getDDBJEntry&accession=AB000100');

# sent the request and get response
$res = $ua->request($req);

# show response
print $res->content;
```

DDBJ Workflows

- A workflow is a predefined series of applications of Web APIs.
- Typical analysis procedures can be carried out without any programming.
- DDBJ currently provides 8 workflows.

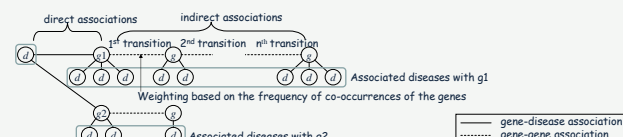
Workflow	Description
Homology workflow	Search other species which have genes similar to human genes.
Human chromosome gene workflow	Show the number of genes on each chromosome.
Nucleotide frequency workflow	Report the pattern of nucleotide frequency distribution.
Blast-ClustalW workflow	Run blastn and compare alignment regions of high similar sequences.
BLAST workflow	Run multiple BLAST against DDBJ, UniProtKB/Swiss-Prot, and PDB.
Splicing workflow	Compare the similarities between splicing structure and homology.
OMIM workflow	Compare the similarities of human disease genes among eukaryotes.
SNP workflow	Extract the relation between a human gene and SNP.
Disease-related gene workflow	Extract a group of associated genes with a given disease.

How to Use DDBJ Workflows

- Click on [Workflow] of WABI top page <http://www.xml.nig.ac.jp/>.
- Click on [SNP workflow].
- Input a keyword about human genes (e.g. "transporter") and click on [Search].
- Information on protein 3D structures and disorder regions for the genes is shown in a table like below.

Disease-related Gene Workflow

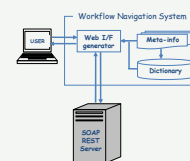
- We are developing an information retrieval system named BDSS (Drug Discovery and Diagnostic Support System), which presents associations among genes, diseases, and chemicals.
- We propose a specificity-based ranking method that ranks a gene which causes a given disease but does not cause other diseases at the top. Our ranking policy is useful for drug discovery and diagnosis.



DDBJ Workflow Navigation System

<http://cyclamen.ddbj.nig.ac.jp/>

- A workflow navigation system dynamically presents users a list of services that are executable as a next step according to results of a service.
- Users only need to select a service (follow a Web link) which they would like to execute from the list of executable services.
- A list of services is generated from dictionaries and meta-information of services.



How to Use DDBJ Workflow Navigation System

For example, if you want to retrieve DDBJ entry and then execute BLAST search,

- Click on [Keyword search] tab of the workflow navigation system top page.
- Click on [DDBJ].
- Click on [FlatFile].
- Input an accession number and click on [submit]. Then, a result about the DDBJ entry is displayed.
- Click on [BLAST against DDBJ by DNA sequence] in [Next flow] tab.
- Jump to the BLAST search page, where [sequence] field is automatically filled with the result of the previous service.
- Check the options and Click on [submit]. Then you can obtain the BLAST result.

CookBook

- Provide wiki-style Web pages to share know-how in usage of WABI services, such as "How can we execute phrase search by ARSA?" and "How can we retrieve BLAST result with an XML format?". Example programs are also available.