

DBCLS Galaxy の利用法

ライフサイエンス統合データベースセンター
山口 敦子

Galaxy とは

Galaxy はゲノムなどの生物学データを対象とした，解析ツール組み合わせインタフェースです。

ペンシルバニア州立大学を中心としたGalaxy team が開発

ユーザは生物学データを，

- ・用意されたツールを組み合わせで**解析**，
- ・ツールの組み合わせや計算履歴の**保存と共有**，
- ・計算履歴，ワークフローの**公開**ができます。

DBCLS Galaxy とは

DBCLS Galaxy は Galaxy をベースとし、主に日本の生物系研究者を対象として、独自のツールや機能を組み込んだ Galaxy です。

<http://galaxy.dbcls.jp/>

注: DBCLS Galaxy の機能をフルに利用するためには、DBCLS OpenID のアカウントを取得する必要があります。
(データ解析だけならば、アカウントなしでもご利用できます)

DBCLS Galaxy の画面

利用可能な
ツールのリスト

ツール操作・結果表示画面

ヒストリーの操作(共有, 新規作成など)
ワークフローの構築
など

Galaxy Analyze Data Workflow Data Libraries Admin Help User

ツール

Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
Regional Variation
Multiple regression
Metagenomic analyses
FASTA manipulation
NGS: QC and manipulation
NGS: Mapping
NGS: SAM Tools
NGS: Peak Calling
EMBOSS
DBCLS
Workflows

DBCLS Galaxy へようこそ! Galaxy は、ゲノムをはじめとした 様々な生物データを、マウスを主とした簡単な操作で複数のツールを組み合わせて、ワークフロー解析できるウェブベースのフレームワークです。ご利用の前に利用規約をご覧ください。

使い方については、
TogoTV :
クリック
そのようなサイトはゲノム中に
24,601ヶ所あることがわかります
データセット 1 との重なりを
'Operate on Genomic Intervals'
から調べましょう

Galaxyを使い、特定の転写因子予測結合領域と遺伝子上流領域の「交差点」をリストアップする
や上部メニューの Help (英語) をご覧ください。

This project is supported in part by NSF, NHGRI, and the Huck Institutes of the Life Sciences.
Galaxy build: \$Rev: 1208 \$
DBCLS Galaxy は文部科学省委託研究開発事業「統合データベースプロジェクト」の成果のひとつであり、ライフサイエンス統合データベースセンターによって運営・管理されています。

ヒストリー
リフレッシュ | すべてをおいたす
Unnamed history
17: Sort on data 16 7,030 lines, format: tabular, database: hg19
情報: save | rerun
16: Group on data 15 7,030 lines, format: tabular, database: hg19
情報: --Group by c4: count[c4] save | rerun
15: Join on data 4 and data 5 16,190 regions, format: interval, database: hg19
情報: save | rerun | BX main | view in GeneTrack

ヒストリー
(解析履歴)

DBCLS Galaxy の特徴

DBCLS Galaxy は日本の生物系研究者を主ターゲットとするため、

- ・ 国内の生物系研究者がよく使う国内外 DB をサポート
(TogoWS経由)

NCBI, EBI, PDB, KEGG などからデータを取得可能

- ・ 日本人向けのカスタマイズ

日本語のメニュー

日本語の文献を検索

など

の機能・ツールが組み込まれている

また、DBCLS で開発された

- ・ テキストマイニング系のツールが組み込まれ、
- ・ DBCLS OpenID で認証する

DBCLS Galaxy の利用例

実際に使ってみましょう

Step0. DBCLS OpenID でログインする

Step1. exon のデータと SNPs のデータを用意する

Step2. 「SNPs の数が多い exon を探す」という解析を
DBCLS Galaxyに用意されたツールを組み合わせ
て行う

Step3. ツールの組み合わせ手順を
ワークフローとして保存する

Step4. 他のユーザと解析履歴, ワークフローを共有する

Step5. 解析履歴, ワークフローを公開する

Step0. DBCLS OpenID でログインする

DBCLS Galaxy ログインページ

OpenID 1.0 を使用したログイン

ログイン

DBCLS OpenID サービスのOpenID (例: <http://openid.dbcls.jp/user/kusako>) が利用可能です。

OpenID 2.0 を使用したログイン

<https://openid.dbcls.jp/> ログイン

DBCLS OpenID サービスのアカウントが利用可能です。

体験版 DBCLS Galaxy

体験版 DBCLS Galaxy: ログイン不要で Galaxy ツールによるゲノム解析とテキスト

利用法

Galaxy とは

Galaxy はゲノム解析のためのウェブアプリケーションです。ゲノム座標データの演算や主要データベースからのデータインポート、ゲノム配列解析、メール経由のデータ共有、データ中心のヒストリ保存、解析ワークフローの管理がおこなえます。解析機能はツールという形で提供されており、それらをつなげるためにユーザーが自由に構築可能なワークフローが提供されています。

DBCLS OpenID 認証画面へ移動

ログインボタンをクリック

DBCLS OpenID Service

ホーム ヘルプ Contact Us

YOUR OPENID:

サインイン

ログイン名とパスワードを入力して下さい

ログイン名

パスワード

サインイン状態を保持する: ☐

サインインする

パスワードを忘れた方はこちら

アカウントを再開する

ログイン名, パスワードを入力してクリック

DBCLS Galaxy へ移動

The screenshot shows the DBCLS Galaxy web interface. On the left is a sidebar with a 'Tools' menu listing various bioinformatics tools like Get Data, Send Data, ENCODE Tools, etc. The main area displays a workflow titled '1. H3K36me3 Search by 0.1' with a list of steps including '1. H3K36me3 Search by 0.1', '2. BED to GFF on data', and '3. H3K36me3 Search by 0.1'. The interface is in Japanese.

Step1. データの用意

exon のデータと SNPs のデータを用意する

Galaxy ツール

Get Data

- Upload File from your computer
- TOGOWS TOOLS
- TOGOWS Search search with a direct-input query
- TOGOWS Search with History search with a query from history pane
- TOGOWS Get Value of a Given Field get the value of a given field for a selected ID
- TOGOWS Get Value of a Given Field on TOGOWS get the value of a given field for a selected ID on TOGOWS
- DBCLS TEXT MINING TOOLS
- TOGOWS Pubmed Get Resource
- MEDLINE Search by a direct-input query
- MEDLINE Search by a query from History pane
- Related PNE articles
- PNE Search PNE Search by Japanese query
- Load requested MEDLINE abstract(s)
- Load NER results
- ORFeil Search ORFeil search with a direct-input query
- ORFeil Search with History ORFeil search with query from a history pane
- ORFeil Search (External Form) Search ORFeil external search form
- Gendoo Gene-to-PMIDs-to-MeSH terms relation table.
- Gendoo Table Gene/MeSH relation table on PMID
- SEMANTIC WEB TOOLS
- Freebase Instance Table
- Freebase MOL Query
- SPARQL Query Tool
- TOOLS OF ORIGINAL GALAXY
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- BX main browser
- Get Microbial Data
- BioMart Central server
- BioMart Test server
- GrameneMart Central server
- Flymine server
- Flymine test server
- modMine server

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data.

clade: Mammal genome: Human assembly: (Feb. 2009 (GRCh37/hg19))

group: Genes and Gene Prediction Tracks track: UCSC Genes add custom tracks

table: knownGene describe table schema

region: genome position chr22:1-51304566 lookup define regions

identifiers (names/accessions): paste list upload list

filter: create

intersection: create

correlation: create

output format: BED - browser extensible data Send output to ☒ Galaxy ☐ GREAT

output file: (leave blank to keep output in browser)

file type returned: ☒ plain text ☐ gzip compressed

get output summary/statistics

To reset all user cart settings (including custom tracks), [click here](#).

右側に UCSC Table Browserが開く

ココ (UCSC Main)

exonデータの取得

Galaxy

clade: Mammal genome: Human assembly: Feb. 2009 (GRCh37/hg19)

group: Genes and Gene Prediction Tracks track: UCSC Genes add custom tracks

table: knownGene describe table schema

region: ☐ genome ☒ position chr22:1-51304566 lookup define regions

output format: BED - browser extensible data Send output to ☒ Galaxy ☐ GREAT

get output
をクリック

Coding Exons
を選択

Send query to Galaxy
をクリック

Home Genomes Genome Browser Blat Tables Gene Sorter

Output knownGene as BED

☐ Include custom track header:

name= tb_knownGene

description= table browser query on knownGene

visibility= pack

url=

Create one BED record per:

- ☐ Whole Gene
- ☐ Upstream by 200 bases
- ☐ Exons plus 0 bases at each end
- ☐ Introns plus 0 bases at each end
- ☒ Coding Exons
- ☐ 3' UTR Exons
- ☐ Downstream by 200 bases

Note: if a feature is close to the beginning or end of a chromosome may be truncated in order to avoid extending past the edge of the chromosome

Send query to Galaxy

Cancel

5: UCSC Main on Human: knownGene (chr22:1-51304566)

13,218 regions, format: bed, database: hg19

情報: UCSC Main on Human: knownGene (chr22:1-51304566)

save | rerun | BX main | view in GeneTrack

1.Chrom	2.Start	3.End	4.Name
chr22	16258185	16258303	uc002slh.1_cds_1_0_chr22_162581
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_162669
chr22	16268136	16268181	uc002slh.1_cds_3_0_chr22_162681
chr22	16269872	16269943	uc002slh.1_cds_4_0_chr22_162698
chr22	16275206	16275277	uc002slh.1_cds_5_0_chr22_162752
chr22	16277747	16277885	uc002slh.1_cds_6_0_chr22_162777

データ取得

SNPsデータの取得

page for the list of contributors and usage restrictions associated with these data.

clade: genome: assembly:

group: track:

table:

output format: Send output to ☒ Galaxy ☐ GREAT

get output
をクリック

Send query to Galaxy
をクリック

Home Genomes Genome Browser Blat Tables Gene

Output knownGene as BED

☐ Include custom track header:

name=
 description=
 visibility=
 url=

Create one BED record per:

☒ Whole Gene
☐ Upstream by bases
☐ Exons plus bases at each end
☐ Introns plus bases at each end
☐ 5' UTR Exons
☐ Coding Exons
☐ 3' UTR Exons
☐ Downstream by bases

Note: if a feature is close to the beginning or end of a chrom they may be truncated in order to avoid extending past the e

4: UCSC Main on Human: snp131 (chr22:1-51304566)

379,047 regions, format: bed, database: hg19

情報: UCSC Main on Human: snp131 (chr22:1-51304566)

[save](#) | [rerun](#) | [BX main](#) | [view in GeneTrack](#)

1.Chrom	2.Start	3.End	4.Name	5	6.Strand
chr22	16050115	16050116	rs77005907	0	-
chr22	16050251	16050252	rs3016036	0	+
chr22	16050352	16050353	rs56342815	0	+
chr22	16050352	16050353	rs2334386	0	+
chr22	16050374	16050375	rs2844882	0	+
chr22	16050407	16050408	rs2844883	0	+

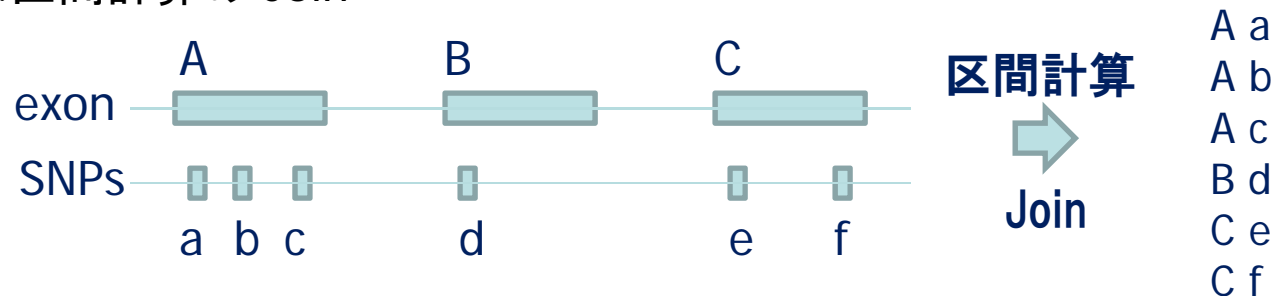
データ取得

Step2. ツールを組み合わせでデータ解析

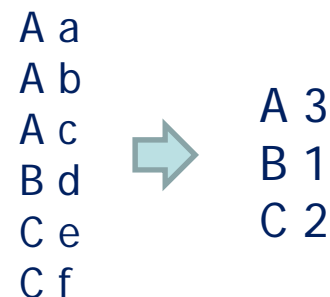
「SNPs の数が多い exon を探す」という解析を
DBCLS Galaxyに用意されたツールを組み合わせで行う

使うツール

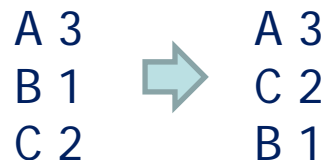
1. 区間計算の Join



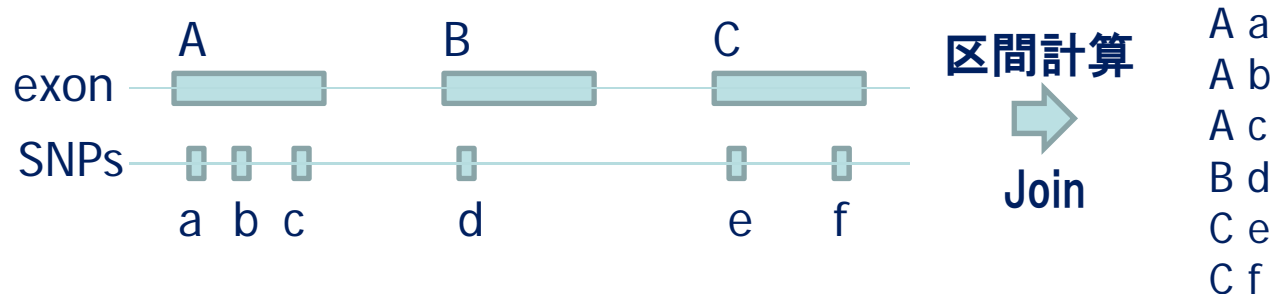
2. グループ化+出現数カウント



3. ソート



Step2-1区間計算の Join



Galaxy

ツール

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression

Operate on Genomic Intervals

- Intersect the intervals of two queries
- Subtract the intervals of two queries
- Merge the overlapping intervals of a query
- Concatenate two queries into one query
- Base Coverage of all intervals
- Coverage of a set of intervals on second set of intervals
- Complement intervals of a query
- Cluster the intervals of a query
- Join the intervals of two queries side-by-side
- Get flanking regions returns flanking regions
- Fetch every

Join

Join: **exonのデータ**
5: UCSC Main on Huma..1-51304566)

First query

with: **SNPsのデータ**
4: UCSC Main on Huma..1-51304566)

Second query

with min overlap:
1 (bp)

Return:
Only records that are joined (INNER JOIN)

Execute

ココ (Join)

Executeをクリック

オーバーラップがある
組み合わせだけ残す

計算結果

15: Join on data 4 and data 5
16,190 regions, format: interval, database: hg19
情報: save | rerun | BX main | view in GeneTrack

1.Chrom	2.Start	3.End	4.Name
chr22	16258185	16258303	uc002aih.1_cde_1_0_chr22_162581
chr22	16266928	16267098	uc002aih.1_cde_2_0_chr22_162669
chr22	16266928	16267098	uc002aih.1_cde_2_0_chr22_162669
chr22	16266928	16267098	uc002aih.1_cde_2_0_chr22_162669
chr22	16266928	16267098	uc002aih.1_cde_2_0_chr22_162669
chr22	16266928	16267098	uc002aih.1_cde_2_0_chr22_162669
chr22	16266928	16267098	uc002aih.1_cde_2_0_chr22_162669
chr22	16266972	16269943	uc002aih.1_cde_4_0_chr22_162699

Step2-2 グループ化＋出現数カウント

Galaxy

ツール

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression

Join, Subtract and Group

- Join two Queries side by side on a specified field
- Compare two Queries to find common or distinct rows
- Subtract V another d
- Group data by a column and perform aggregate operation on other columns.

A a
A b
A c
B d
C e
C f

A 3
B 1
C 2

計算結果

16: Group on data 15
7,030 lines, format: tabular, database: hg
情報: --Group by c4: count[c4]
save | rerun

1	2
uc002slh.1_cds_1_0_chr22_16258186_r	1
uc002slh.1_cds_2_0_chr22_16266929_r	4
uc002slh.1_cds_4_0_chr22_16269873_r	1
uc002slh.1_cds_5_0_chr22_16275207_r	2
uc002slh.1_cds_6_0_chr22_16277748_r	5
uc002slh.1_cds_7_0_chr22_16279195_r	2

ココ(Group)

ココ

Group

Select data: Joinの結果を選ぶ
15: Join on data 4 and data 5
Query missing? See TIP below.

Group by column:
c4 exon の名前を表す列

Ignore case while grouping?:
☐

Operations
Add new Operation
Execute

Operations

Operation 1

Type:
Count

On column:
c4

Round result to nearest integer?:
NO

Remove Operation 1

Add new Operation

Execute

どの列を数えるか

出現数を計算するためにはここをクリック

Executeをクリック

Step2-3 ソート

A 3
B 1
C 2

→

A 3
C 2
B 1

Galaxy

ツール

- [Get Data](#)
- [Send Data](#)
- [ENCODE Tools](#)
- [Lift-Over](#)
- [Text Manipulation](#)
- [Filter and Sort](#)
- [Join, Subtract and Group](#)
- [Convert Formats](#)
- [Extract Features](#)
- [Fetch Sequences](#)
- [Fetch Alignments](#)
- [Get Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Graph/Display Data](#)
- [Regional Variation](#)
- [Multiple regression](#)

ココ

ココ(Sort)

- Filter and Sort**
- Filter data on any column using simple expressions
 - Sort data in ascending or descending order
- Select lines that match an expression

Sort

Sort Query: グループ化の結果を選ぶ
16: Group on data 15

on column:
c2 ソートする列を選ぶ

with flavor:
Numerical sort

everything in:
Descending order

Column selections

Add new Column selection

Execute

Executeを
クリック

計算結果

17: Sort on data 16
7,030 lines, format: tabular, database: hg19
情報:
save | rerun

1	2
uc010gsw.1_cds_1_0_chr22_21480537_x	67
uc002sac.2_cds_0_0_chr22_18834445_x	58
uc003bhh.2_cds_0_0_chr22_46652458_x	46
uc002sac.3_cds_0_0_chr22_20456382_x	41
uc002sug.3_cds_0_0_chr22_21738148_x	41
uc002sug.3_cds_0_0_chr22_21900346_x	41

Step2. ツールを組み合わせでデータ解析

「SNPs の数が多い exon を探す」という解析を
DBCLS Galaxyに用意されたツールを組み合わせで行う

5: UCSC Main on Human: knownGene (chr22:1-51304566)
13,218 regions, format: bed, database: hg19
情報: UCSC Main on Human: knownGene (chr22:1-51304566)
[save](#) | [rerun](#) | [BX main](#) | [view in GeneTrack](#)

1.Chrom	2.Start	3.End	4.Name
chr22	16258185	16258303	uc002slh.1_cds_1_0_chr22_16258185_r
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_16266928_r
chr22	16268136	16268181	uc002slh.1_cds_3_0_chr22_16268136_r
chr22	16269872	16269943	uc002slh.1_cds_4_0_chr22_16269872_r
chr22	16275206	16275277	uc002slh.1_cds_5_0_chr22_16275206_r
chr22	16277747	16277885	uc002slh.1_cds_6_0_chr22_16277747_r

4: UCSC Main on Human: snp131 (chr22:1-51304566)
379,047 regions, format: bed, database: hg19
情報: UCSC Main on Human: snp131 (chr22:1-51304566)
[save](#) | [rerun](#) | [BX main](#) | [view in GeneTrack](#)

1.Chrom	2.Start	3.End	4.Name	5	6.Strand
chr22	16050115	16050116	rs77005907	0	-
chr22	16050251	16050252	rs3016036	0	+
chr22	16050352	16050353	rs56342815	0	+
chr22	16050352	16050353	rs2334386	0	+
chr22	16050374	16050375	rs2844882	0	+
chr22	16050407	16050408	rs2844883	0	+

Join

15: Join on data 4 and data 5
16,190 regions, format: interval, database: hg19
情報:
[save](#) | [rerun](#) | [BX main](#) | [view in GeneTrack](#)

1.Chrom	2.Start	3.End	4.Name
chr22	16258185	16258303	uc002slh.1_cds_1_0_chr22_16258185_r
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_16266928_r
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_16266928_r
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_16266928_r
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_16266928_r
chr22	16266928	16267095	uc002slh.1_cds_2_0_chr22_16266928_r
chr22	16269872	16269943	uc002slh.1_cds_4_0_chr22_16269872_r

グループ化

16: Group on data 15
7,030 lines, format: tabular, database: hg
情報: --Group by c4: count[c4]
[save](#) | [rerun](#)

1	2
uc002slh.1_cds_1_0_chr22_16258185_r	1
uc002slh.1_cds_2_0_chr22_16266928_r	4
uc002slh.1_cds_4_0_chr22_16269872_r	1
uc002slh.1_cds_5_0_chr22_16275207_r	2
uc002slh.1_cds_6_0_chr22_16277748_r	5
uc002slh.1_cds_7_0_chr22_16279195_r	2

ソート

17: Sort on data 16
7,030 lines, format: tabular, database: hg19
情報:
[save](#) | [rerun](#)

1	2
uc010gsw.1_cds_1_0_chr22_21480527_r	67
uc002scc.2_cds_0_0_chr22_18834445_f	58
uc003bhh.2_cds_0_0_chr22_46652458_r	46
uc002sdd.3_cds_0_0_chr22_20456382_r	41
uc002suq.3_cds_0_0_chr22_21738148_f	41
uc002suy.3_cds_0_0_chr22_21900346_r	41

Step2. ツールを組み合わせでデータ解析

今回は触れませんが...

用意されているゲノム解析のツール群に加え、
キーワードから関連遺伝子→タンパク質構造を見たり、
キーワードから PubMed の検索をし、
それらの文献に関連する日本語の文献を検索したり
できます。

Step3. ワークフローの保存

ツールの組み合わせ手順をワークフローとして保存する

The screenshot shows the DBCLS workflow creation interface. On the left, the 'History' panel displays a list of datasets. A blue arrow points to the 'オプション' (Options) button, with a callout box saying 'ココ' (Here). Another blue arrow points to the 'Extract Workflow' option in the dropdown menu, with a callout box saying 'Extract Workflow をクリック' (Click Extract Workflow). On the right, the 'Workflow name' field is set to 'Workflow constructed from history 'Unna...'. Below this, there are buttons for 'Create Workflow', 'Check all', and 'Uncheck all'. The main table lists tools and their associated history items. A blue arrow points from the 'Extract Workflow' option to the 'Tool' column of the table.

Tool	History items created
UCSC Main <i>This tool cannot be used in workflows</i>	1: UCSC Main on Human: knownGene (chr22:1-51304566) <input checked="" type="checkbox"/> Treat as input dataset
BED-to-GFF <input checked="" type="checkbox"/> Include "BED-to-GFF" in workflow	2: BED-to-GFF on data 1
MEDLINE Search by a direct-input query <input checked="" type="checkbox"/> Include "MEDLINE Search by a direct-input query" in workflow	3: MEDLINE Search by a direct-input query
UCSC Main <i>This tool cannot be used in workflows</i>	4: UCSC Main on Human: snp131 (chr22:1-51304566) <input checked="" type="checkbox"/> Treat as input dataset
UCSC Main <i>This tool cannot be used in workflows</i>	5: UCSC Main on Human: knownGene (chr22:1-51304566) <input checked="" type="checkbox"/> Treat as input dataset

ツール選択
ワークフローに使用したいツールを選ぶ

入力選択
各ツールに必要な入力データを選ぶ

Step3. ワークフローの保存

ツールの組み合わせ手順をワークフローとして保存する

MEDLINE Search by a direct-input query
☐ Include "MEDLINE Search by a direct-input query" in workflow

UCSC Main
This tool cannot be used in workflows

UCSC Main
This tool cannot be used in workflows

UCSC Main
This tool cannot be used in workflows

TogoWS Search
☐ Include "TogoWS Search" in workflow

TogoWS Search
☐ Include "TogoWS Search" in workflow

Join
☒ Include "Join" in workflow

Group
☒ Include "Group" in workflow

3: MEDLINE Search by a direct-input query

4: UCSC Main on Human: snp131 (chr22:1-51304566)
☒ Treat as input dataset

5: UCSC Main on Human: knownGene (chr22:1-51304566)
☒ Treat as input dataset

6: UCSC Main on Human: knownGene (chr22:1-51304566)
☒ Treat as input dataset

8: TogoWS Search

12: TogoWS Search

15: Join on data 4 and data 5

16: Group on data 15

The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

Workflow name
SNPsの数が多いexonをchr22から探す

Create Workflow

Tool
UCSC Main

ワークフローに
名前を付ける

Create Workflow
をクリック

Galaxy Analyze Data Workflow Data Libraries Admin Help

Your workflows

Name	# of Steps
TogoWS ▾	3
SNPsの数が多いexonをchr22から探す ▾	6
Workflow constructed from history 'Unnamed hi	
Workflow constructed from history 'Unnamed hi	
Unnamed workflow ▾	
Workflow constructed from history 'Unnamed hi	

Workflows shared with you by
No workflows have been shared with you.

Other options

画面上部の
Workflow メニューで
作ったワークフローを
確認できます

チェックボックスでツールとデータを選択後

ワークフローエディタ

今回は触れませんが...
ヒストリーを使わずワークフローを作るエディタも付いてます

The screenshot displays the Galaxy web interface. On the left, the 'Your workflows' panel lists existing workflows. A blue callout bubble points to the 'Create new workflow' button with the text 'ココをクリック' (Click here). A large blue arrow points from this button to the 'Workflow Canvas' in the center. The canvas shows a workflow with three steps: 'TogoWS Search', 'TogoWS Get Value of a Given Field', and 'Related PNE articles'. The 'Details' panel on the right shows the configuration for the 'Related PNE articles' tool, including input fields for 'PMID list(s) or MEDLINE search result(s)' and 'Entry ID', and a section for 'Edit Step Attributes'.

Galaxy Analyze Data Workflow Data Libraries Admin Help

Your workflows

Create new workflow

Name	# of Steps
TogoWS	3
SNPsの熱が多い exon を chr22 から探す	6
Workflow constructed from history 'Unnamed history'	5
Workflow constructed from history 'Unnamed history'	9
Unnamed workflow	0
workflow constructed from history 'Unnamed history'	7

Workflows shared with you by others

No workflows have been shared with you.

Other options

Configure your workflow menu

Workflow Canvas | TogoWS

TogoWS Search
output (tabular)

TogoWS Get Value of a Given Field
Entry ID
output (tabular)

Related PNE articles
PMID list(s) or MEDLINE search result(s)
output (tabular)

Details

Tool: Related PNE articles

PMID list(s) or MEDLINE search result(s)
Data input 'pmids' (txt)

Edit Step Attributes

Annotation / Notes:

Add an annotation or notes to this step; annotations are available when a workflow is viewed.

What it does

This system provides related Japanese articles for MEDLINE abstract(s). The Japanese articles in the system is Protein, Nucleic acid and Enzyme (PNE) articles. PNE is a journal of Japan publishing review articles in all aspects of biology, and all articles in PNE are written in Japanese. Currently, 2,027 PNE articles are indexed. [Published from 1985 to

Step4. 他のユーザとの共有

特定のユーザと解析履歴を共有する

The image shows a Galaxy web interface with several annotations in Japanese:

- Annotation 1:** A blue box labeled "ココ" (Here) points to the "オプション" (Options) dropdown menu in the top right of the history panel.
- Annotation 2:** A blue box labeled "Share or Publish をクリック" (Click Share or Publish) points to the "Share or Publish" option in the "History Lists" dropdown menu.
- Annotation 3:** A blue box labeled "Share with a user をクリック" (Click Share with a user) points to the "Share with a user" button in the "Sharing and Publishing History" panel.
- Annotation 4:** A blue box labeled "シェアしたいユーザのメールアドレスを入力" (Enter email address of user to share with) points to the input field for "Galaxy user emails with which to share histories" in the "Share 1 histories" dialog.

The "Sharing and Publishing History 'Exon SNPs'" panel contains the following sections:

- Making History Accessible:**
 - Make History Accessible:** Generates a web link that you can share with other people so that they can view this history.
 - Make History Accessible:** Makes the history accessible to other users. You can publish the history to a public section, where it is published by default.
- Sharing History with Specific Users:**

You have not shared this history with any users.

Share with a user

The "Share 1 histories" dialog box shows:

- Share 1 histories**
- Histories to be shared:**

History Name	Number of Datasets
Exon SNPs	17

- Galaxy user emails with which to share histories**
-
- Enter a Galaxy user email address or a comma-separated list of addresses if sharing with multiple users
- Submit**

Step4. 他のユーザとの共有

特定のユーザとワークフローを共有する

ワークフロー画面から、
シェアしたいワークフローを選ぶ

Your workflows

Name

TogoWS ▼

SNPsの数が多いexonをchr22から探す

Workflow construction named history' ▼

Workflow construction named history' ▼

Unnamed workflow

Workflow construction named history' ▼

- Edit
- Run
- Share or Publish
- Clone
- Rename
- Delete

Workflows shared with you by others

No workflows have been shared with you.

Other options

Configure your workflow menu

Sharing and Publishing Workflow 'SNPsの数が多いexonをchr22から探す'

Making Workflow Accessible via Link and Publishing It

This workflow is currently restricted so that only you and the users listed below can access it. You can:

Make Workflow Accessible via Link

Generates a web link that you can share with other people so that they can view and import the workflow.

Make Workflow Accessible and Publish

Makes the workflow accessible via link (see above) and publishes the workflow to Galaxy's [Published Workflow](#) listed and searchable.

Sharing Workflow with Specific Users

You have not shared this workflow with any users.

Share with a user

[Back to Workflows List](#)

あとはヒストリー(計算履歴)と同様

Step5. 解析履歴, ワークフローの公開

解析履歴を公開する

The image shows a screenshot of the Galaxy web interface. On the left, a 'History' panel is visible with a dropdown menu open. A blue arrow points to the 'オプション' (Options) button, with a callout box saying 'ココ' (Here). Another blue arrow points to the 'Share or Publish' option in the dropdown menu, with a callout box saying 'Share or Publish をクリック' (Click Share or Publish). The right side of the image shows a panel titled 'Sharing and Publishing History 'Exon SNPs''. This panel contains instructions on how to share history. Two blue arrows point from the 'Share or Publish' menu option to the 'Make History Accessible via Link' and 'Make History Accessible and Publish' buttons in the panel. To the right of these buttons, there are two callout boxes: '公開のための URL 作成' (Create URL for public) and '公開のための URL 作成と 公開リストへ 掲載' (Create URL for public and post to public list).

Sharing and Publishing History 'Exon SNPs'

Making History Accessible via Link and Publishing It

This history is currently restricted so that only you and the users listed below can access it. You can:

Make History Accessible via Link
Generates a web link that you can share with other people so that they can view and import the history.

Make History Accessible and Publish
Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Sharing History with Specific Users

You have not shared this history with any users.

Share with a user

[Back to Histories List](#)

公開のための URL 作成

公開のための URL 作成と 公開リストへ 掲載

Step5. 解析履歴, ワークフローの公開

解析履歴を公開する

公開のためのURL作成と公開リストへ掲載

Sharing and Publishing History 'Exon SNPs'

Making History Accessible via Link and Publishing It

This history **accessible via link and published**.

Anyone can view and import this history by visiting the following URL:

<http://galaxy.dbcls.jp/u/atsuko/h/exon-snps>

This history is publicly listed and searchable in Galaxy's **Published Histories** section.

You can:

Unpublish History

Removes history from Galaxy's **Published Histories** section so that it is not publicly listed or searchable.

Disable Access to History via Link and Unpublish

Disables history's link so that it is not accessible and removes history from Galaxy's **Published Histories** section so that it is not publicly listed or searchable.

公開URL

公開された計算履歴リスト

Published Histories | atsuko | Exon SNPs

import and start using history

Galaxy History 'Exon SNPs'

Description/Notes: None

Dataset	Description/Notes
1: UCSC Main on Human: knownGene (chr22:1-51304566)	None
2: BED-to-GFF on data 1	None
3: MEDLINE Search by a direct-input query	None
4: UCSC Main on Human: snp131 (chr22:1-51304566)	None
5: UCSC Main on Human: knownGene (chr22:1-51304566)	None
6: UCSC Main on Human: knownGene (chr22:1-51304566)	None
8: ToGoWS Search	None
12: ToGoWS Search	None
15: Join on data 4 and data 5	None
16: Group on data 15	None
17: Sort on data 16	None

Galaxy

Analyze Data

Workflow

Data Libraries

Admin

Help

User

Published Histories

search



| Advanced Search

Name	Annotation	Owner	Community Tags	Last Updated ↑
Twitter Nortify		atsuko		less than a minute ago
Exon SNPs		atsuko		17 minutes ago

Step5. 解析履歴, ワークフローの公開

ワークフローを公開する

ワークフロー画面から,
シェアしたいワークフローを選ぶ

Your workflows

Name

TogoWS ▼

SNPsの数が多いexonをchr22から探す

Workflow construction named history' ▼

Workflow construction named history' ▼

Unnamed workflow

Workflow construction named history' ▼

- Edit
- Run
- Share or Publish
- Clone
- Rename
- Delete

Workflows shared with you by others

No workflows have been shared with you.

Other options

Configure your workflow menu

Sharing and Publishing Workflow 'SNPsの数が多いexonをchr22から探す'

Making Workflow Accessible via Link and Publishing It

This workflow is currently restricted so that only you and the users listed below can access it. You can:

Make Workflow Accessible via Link

Generates a web link that you can share with other people so that they can view and import the workflow.

Make Workflow Accessible and Publish

Makes the workflow accessible via link (see above) and publishes the workflow to Galaxy's [Published Workflow](#) listed and searchable.

Sharing Workflow with Specific Users

You have not shared this workflow with any users.

Share with a user

[Back to Workflows List](#)

あとはヒストリー(計算履歴)と同様

まとめ

DBCLS Galaxy はゲノムなどの生物学データを対象とした、解析ツール組み合わせインタフェースで、これを使うと、

- ・用意されたツールを組み合わせ
生物学データを**解析**,
- ・ツールの組み合わせや計算履歴の**保存**
- ・ユーザ間の計算履歴・ワークフローの**共有**,
- ・計算履歴・ワークフローの**公開**ができます。

今後の予定

データライブラリを整備

LSDBの他のツールとの連携 & 組み込み

日本語ドキュメントの充実

組み込みツール, ドキュメント化などについて,
ぜひご意見・ご要望をお寄せ下さい.
support@dbcls.rois.ac.jp