

DRA と DDBJパイプライン入門

中村 保一

Aug 24, 2017

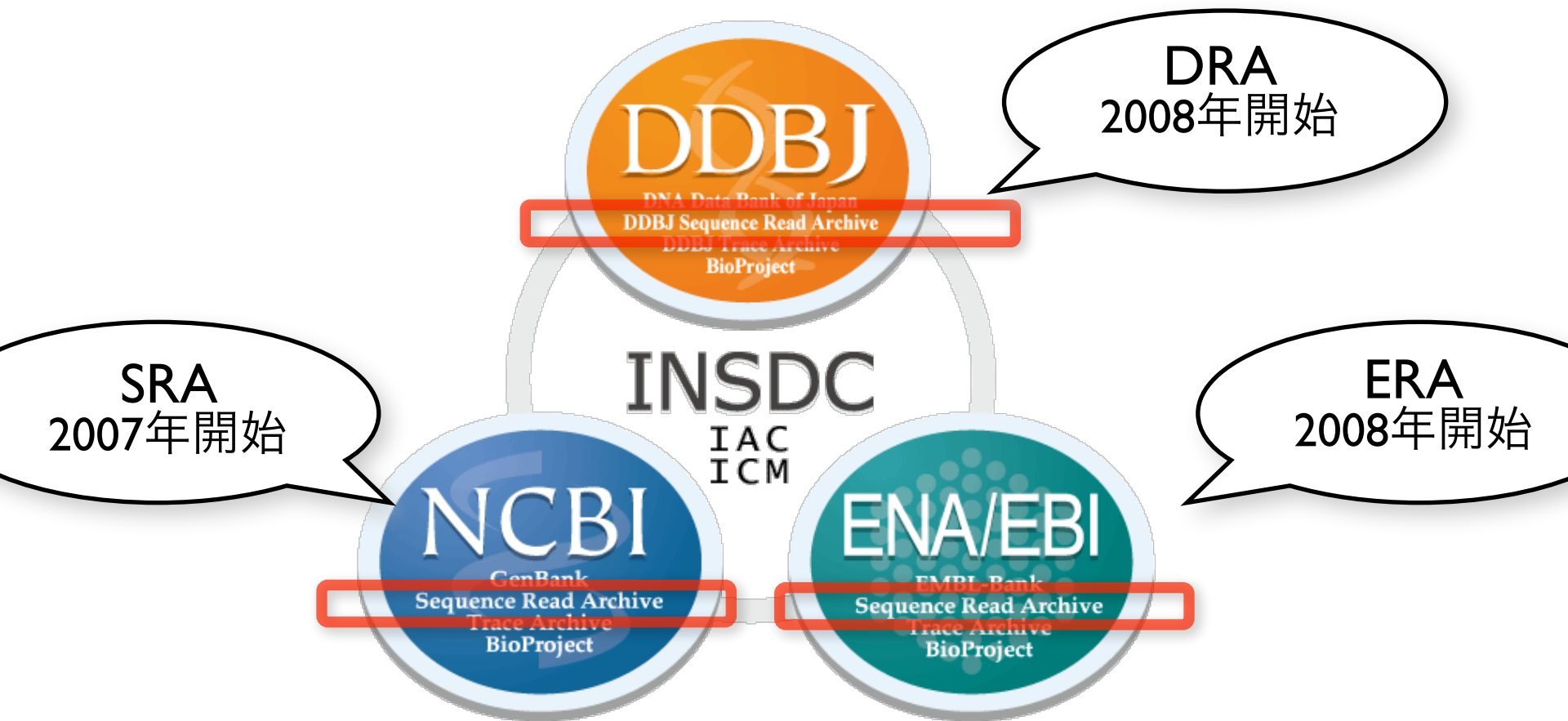
石川県立大学

DRA

DDBJ Sequence Read Archive

DDBJ Sequence Read Archive (DRA)

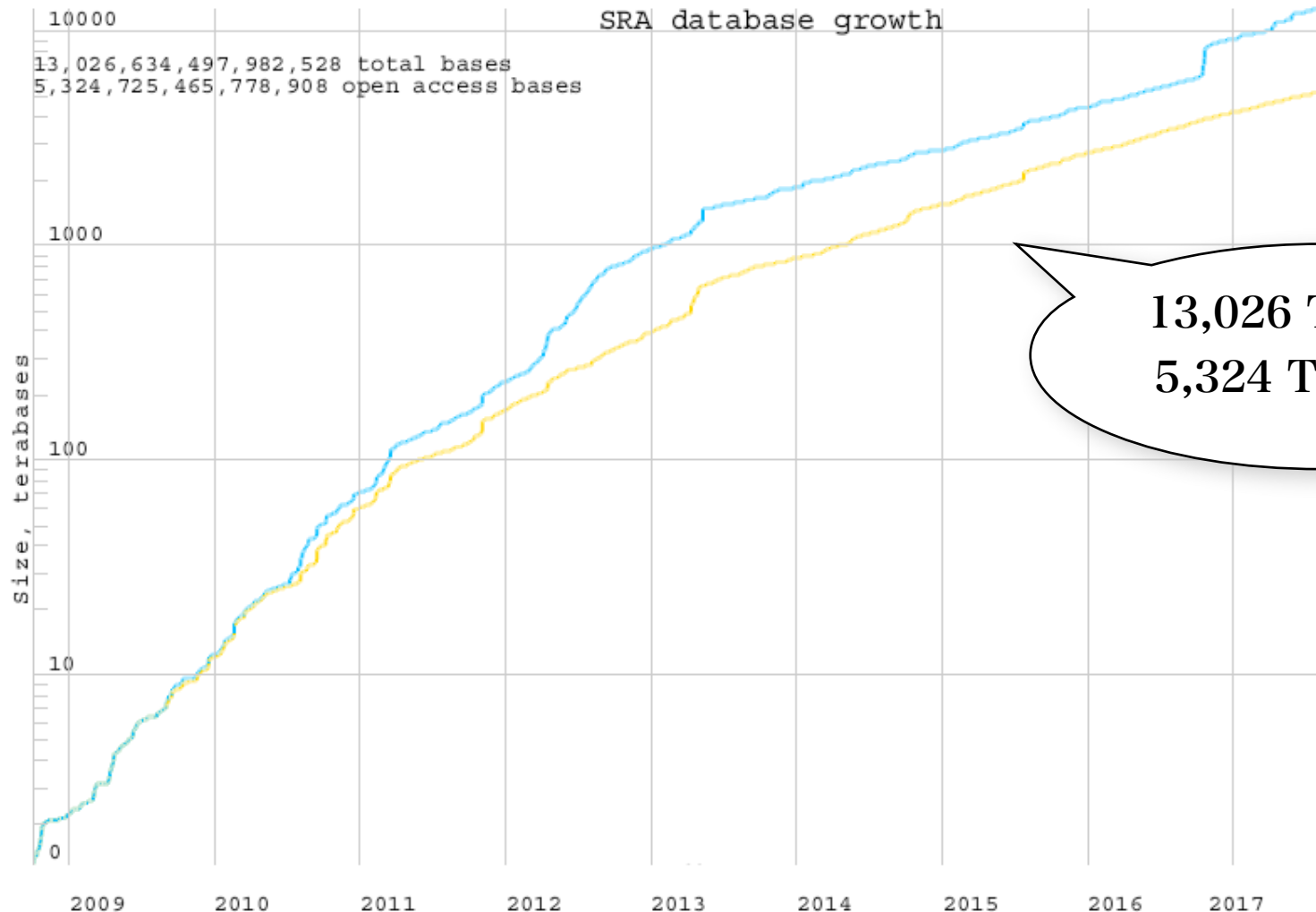
新世代シーケンサから出力される配列や
アライメントデータを登録・公開



International Nucleotide Sequence Databank Collaboration

SRA growth (NGS row/bam data amount)

NCBI Sequence Read Archive



13,026 TB total
5,324 TB open

DRAウェブサイト ⇒ [DRA] で検索

<http://trace.ddbj.nig.ac.jp/dra/>

登録関係情報



Sequence Read Archive

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Google™ カスタム検索



解析パイプライン

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DDBJ Sequence Read Archive (DRA) は, the 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD® System などの次世代シーケンサからの出力データ (Raw Data) を蓄積・提供するためのデータベース (Nucleotide Sequence Database Collaboration (INSDC) のメンバーであり、国際的な Sequence Read Archive (ERA) との国際協力のもと、運営されています。従来のキャピタシオン式シーケンサからの出力データも DRA に登録してください。

データ検索

データ取得



検索

データをキーワード、生物名、シーケンサなどで検索する



登録

新型シーケンサからの生データやアライメントデータを登録する



動画マニュアル

DRA の利用方法や登録方法を解説している動画をみる

DRA: 新型シーケンサデータを保存・共有

Sequence Read Archive

Home Submission **Search** Download Pipeline About DRA

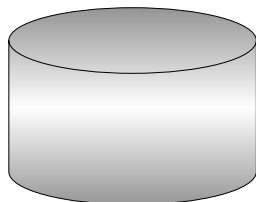
DDBJ Sequence Read Archive (DRA) は Roche 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD® Sなどの次世代シーケンサからの出力データのためのデータベースです。DRA は International Nucleotide Sequence Database Collaboration (INSDC) のメンバーであり、NCBI Sequence Read Archive (SRA) と EBI Sequence Read Archive (ERA) との国際協同で、運営されています。従来のキャピラリー式シーケンサからの出力データは DDBJ Trace Archive に登録ください。


検索
データをキーワード、生物名、シーケンサなどで検索する


登録
新型シーケンサからの生データやアライメントデータを登録する


動画マニュアル
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研究者



インターネットを通じて、登録・公開したデータを、別の研究者が再利用できる

Released Data

search result : 30

Accession	Study Title	Organism(s)	Center Name	Release Date
DRA000001	Whole genome sequencing of <i>Bacillus subtilis</i> subsp. natto BEST195	<i>Bacillus subtilis</i> subsp. natto	KEIO	2010-03-26
DRA000002	Whole genome resequencing of <i>Bacillus subtilis</i> subsp. subtilis str. 168	<i>Bacillus subtilis</i> subsp. subtilis str. 168	KEIO	2010-03-26
DRA000010	Whole genome shotgun sequences of <i>Oryza sativa</i> japonica variety, Koshihikari	<i>Oryza sativa</i> Japonica Group	NIAS	2010-03-31
DRA000030	Whole-genome DNA methylation analysis in human breast cancer cell lines using MeDIP-seq	<i>Homo sapiens</i>	KUGSPS	2010-03-01
DRA000039	genetic variation detected in 206 <i>Klebsiella pneumoniae</i> plasmids	<i>Klebsiella pneumoniae</i>	WMC	2009-12-14
DRA000067	<i>B. anthracis</i> BA103 genome analysis	<i>Bacillus anthracis</i>	NIID	2010-04-22
DRA000068	<i>B. anthracis</i> BA104 genome analysis	<i>Bacillus anthracis</i>	NIID	2010-04-22
DRA000069	Whole SNPs analysis of ciprofloxacin resistance among <i>B. anthracis</i> strains	<i>Bacillus anthracis</i>	NIID	2010-04-22
DRA000070	Whole SNPs analysis of ciprofloxacin resistance among <i>B. anthracis</i> strains	<i>Bacillus anthracis</i>	NIID	2010-04-22
DRA000155	CAGE analysis of whole adult brain and whole embryo rat transcriptome	<i>Rattus norvegicus</i>	RIKEN_OSC	2010-03-17
DRA000169	Linking new promoters to functional transcripts in small samples with nanoCAGE and CAGEscan	<i>Homo Sapiens</i>	RIKEN_OSC	2010-06-08
DRA000205	A comprehensive survey of 3' animal mRNA modification events and a possible role for 3' adenylation in modulating mRNA targeting effectiveness	<i>Homo Sapiens</i>	RIKEN_OSC	2010-07-23
DRA000220	Whole genome sequencing of <i>Oryzias latipes</i> Hd-R	<i>Oryzias latipes</i>	KEIO-SM	2010-08-16
SRA000252	<i>Toxoplasma gondii</i> transcript sequencing project	<i>Toxoplasma gondii</i>	UT-MGS	2009-07-01
SRA000253	<i>Glossina morsitans</i> transcript sequencing project	<i>Glossina morsitans</i>	UT-MGS	2009-07-01
SRA000254	<i>Glossina morsitans</i> transcript sequencing project	<i>Glossina morsitans</i>	UT-MGS	2009-06-25
SRA000255	<i>Anopheles stephensi</i> transcript sequencing project	<i>Anopheles stephensi</i>	UT-MGS	2009-07-01
SRA000256	<i>Cryptosporidium parvum</i> transcript sequencing project	<i>Cryptosporidium parvum</i>	UT-MGS	2009-07-01
SRA000257	<i>Plasmodium yoelii</i> transcript sequencing project	<i>Plasmodium yoelii</i>	UT-MGS	2009-09-22

ページ表示を止めた

FTP ディレクトリ /ddbj.database/dra/ / ftp.ddbj.nig.ac.jp

この FTP サイトはエクスプローラーでは表示するには、ページをクリックして、エクスプローラーで FTP サイトを開くをクリックしてください。

```
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Welcome to DDBJ FTP Archive, running on ftp.ddbj.nig.ac.jp!
-----
Please contact ddbj@ddbj.nig.ac.jp when you have any problem for getting
access to this archive, downloading the data, and etc.
-----
Termination of DDBJ-XML output format.
Here is the announcement.
http://www.ddbj.nig.ac.jp/whatnew/2010/100825-e.html
-----
A new directory, "patent", was made under "ddbj.database".
Now, all of patent amino acid sequence data for JPO and KIPD are
included in the new "patent" directory.
-----
For details, please read the README.TXT in this directory.
-----
Distributions of the latest DDBJ release and newly-arrived/updated
entries after that release can be retrieved at the following FTP
sites.
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DDBJ Flat file
ftp://ftp.ddbj.nig.ac.jp/ddbj.database/ddbj/
ftp://ftp.ddbj.nig.ac.jp/ddbj.database/ddbjnew/
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DDBJ Flat file(1PA)
ftp://ftp.ddbj.nig.ac.jp/ddbj.database/1pa/ddbj/
ftp://ftp.ddbj.nig.ac.jp/ddbj.database/1pa/ddbjnew/
-----
1KSD-XML
ftp://ftp.ddbj.nig.ac.jp/ddbj.database/ddbj/xal/insdxml_current/
ftp://ftp.ddbj.nig.ac.jp/ddbj.database/ddbjnew/xal/insdxml_current/
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It was last modified on Fri Feb 26 2010.
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公開データの DRA Search での検索

公開データは EBI SRA / NCBI SRA と共有されています

DRA Search [Send Feedback](#) [Search Home](#) [DRA Home](#)

Accession :

OR

Organism : StudyType :

CenterName : Platform :

Show records Sort by

Statistics

Released Entries

Type	Count
Submission	23770
Study	3423
Experiment	29624
Sample	111241
Run	71620

Organism

#	Organism Name	Study
1	Homo sapiens	293
2	metagenome sequence	169
3	Mus musculus	163
4	Drosophila melanogaster	121
5	marine metagenome	79
6	Caenorhabditis elegans	39
7	Arabidopsis thaliana	38
8	synthetic construct	37
9	Saccharomyces cerevisiae	35
10	Panicum virgatum	21

Show records Sort by

Search Results (358 studies)

#	STUDY	SUBMISSION	STUDY_TITLE	STUDY_TYPE	ORGANISM	CENTER_NAME
1	DRP000003	DRA000003	Comprehensive identification and characterization of the nucleosome structure	Transcriptome Analysis	Homo sapiens	UT-MGS
2	DRP000004	DRA000004	Comprehensive identification and characterization of the transcripts, their expression lev	Transcriptome Analysis	Homo sapiens	UT-MGS
3	DRP000005	DRA000005	Comprehensive characterization of expression lev			
4	DRP000006	DRA000006	Comprehensive characterization of expression lev			
5	DRP000007	DRA000007	Comprehensive characterization of polymerase II			
6	DRP000008	DRA000008	Comprehensive characterization of polymerase II			
7	RNAseq	34				
8	Population Genomics	31				
9	Gene Regulation Study	24				
10	Cancer Genomics	14				

DRP000003

Study Detail

Title	Comprehensive identification and characterization of the nucleosome structure
Abstract	Comprehensive identification and characterization of the nucleosome structure in mammalian genes were attempted. We used Nucleosome-Seq method, in which next gene sequencing technology and microcococcus nuclease digestion assay were combined.
Description	Although recent studies have revealed that the majority of human genes are subjected to regulation of alternative promoters (APs), the biological relevance of this phenomenon remains unclear. In order to understand biological significance of the presence of diverg .. [more]
Project ID	34559
Center Name	UT-MGS (University of Tokyo, Medical Genome Sciences)

Navigation

Submission	DRA000003	FTP
Experiment	DRX000003	FASTQ SRALite
Sample	DRS000003	

生物名 etc での絞り込み

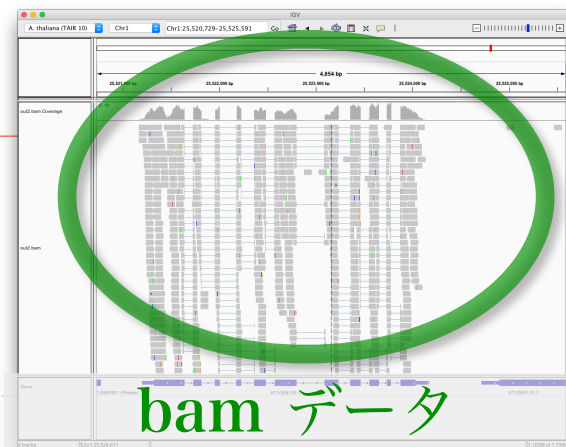
検索結果リスト

ダウンロード

詳細 (メタデータ記述)

DRA の中身

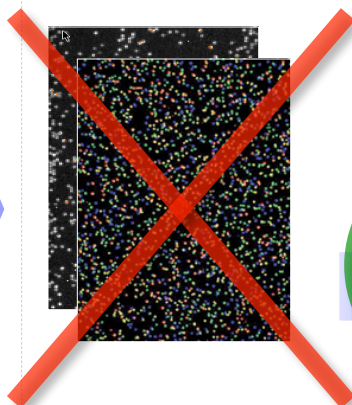
~~配列のみ~~



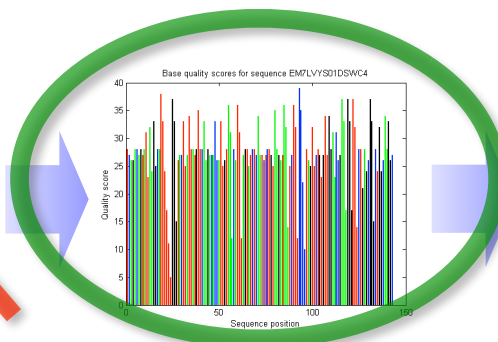
アラインメントデータ



NGS



画像データ



1次データ

ベースコール
Quality etc

```
@SRR001654.1 9460:7:1:830:763 length=36
GTCAATATTAATCATACCAATATACTCAAAAAATAA
+SRR001654.1 9460:7:1:830:763 length=36
I+&*4)%+5'#%/) &$%$#%"#&%%"$%#%!"
@SRR001654.2 9460:7:1:402:781 length=36
GCTCTAAAAAGCAAAATTCAGTCTTCAAAATAATTC
+SRR001654.2 9460:7:1:402:781 length=36
II+($%+%'&+*-0+/*("%&+""&"("$""#%&$
@SRR001654.3 9460:7:1:433:775 length=36
GTGCTTTT TTTTCAGGAAGTTGCTCTCTCTATC
+SRR001654.3 9460:7:1:433:775 length=36
II3DI>IIIIIIII...&%&19)."+%,$"&@N%#
```

fastq データ

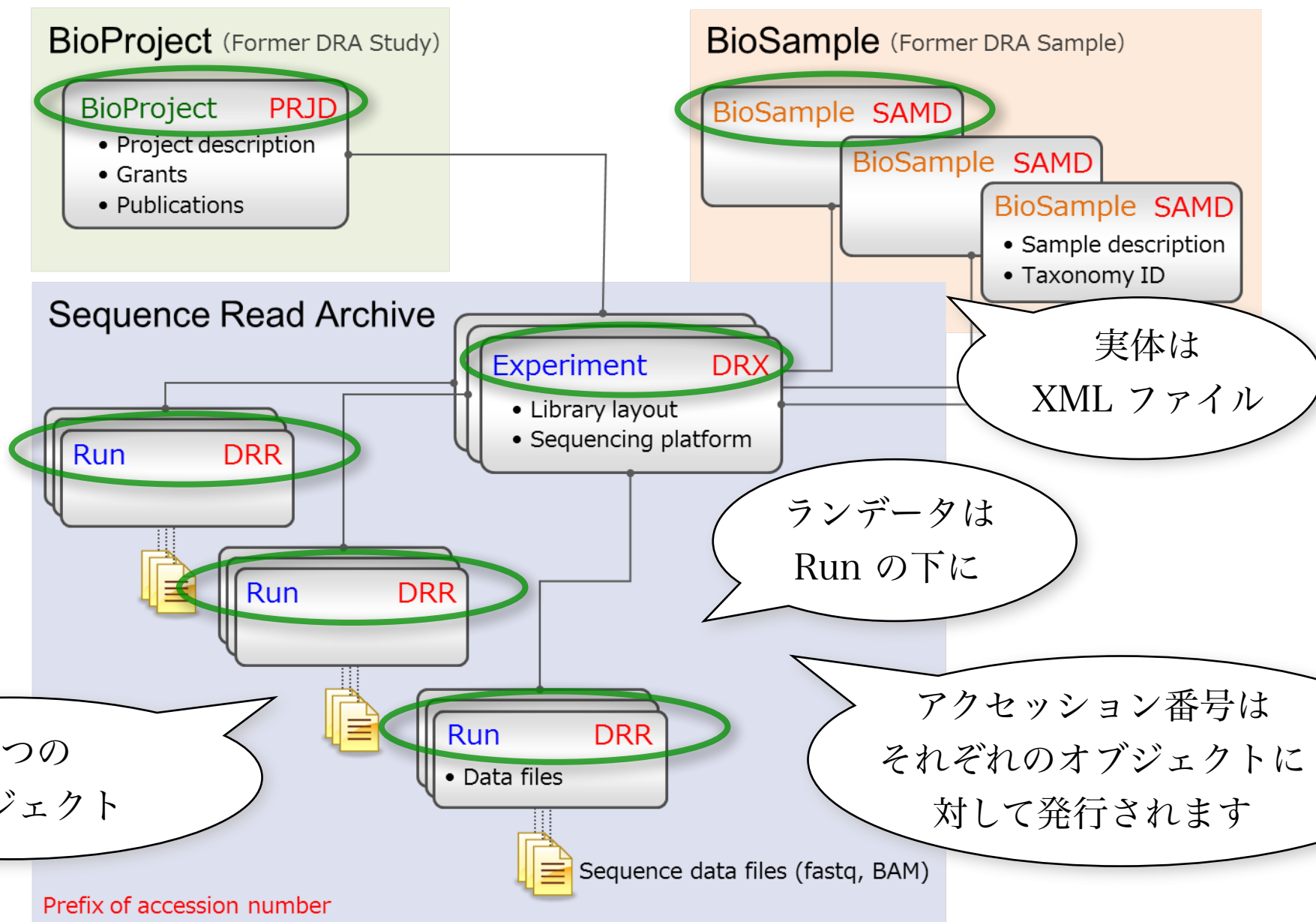
塩基配列 と
Quality Value

ランデータ

メタデータ

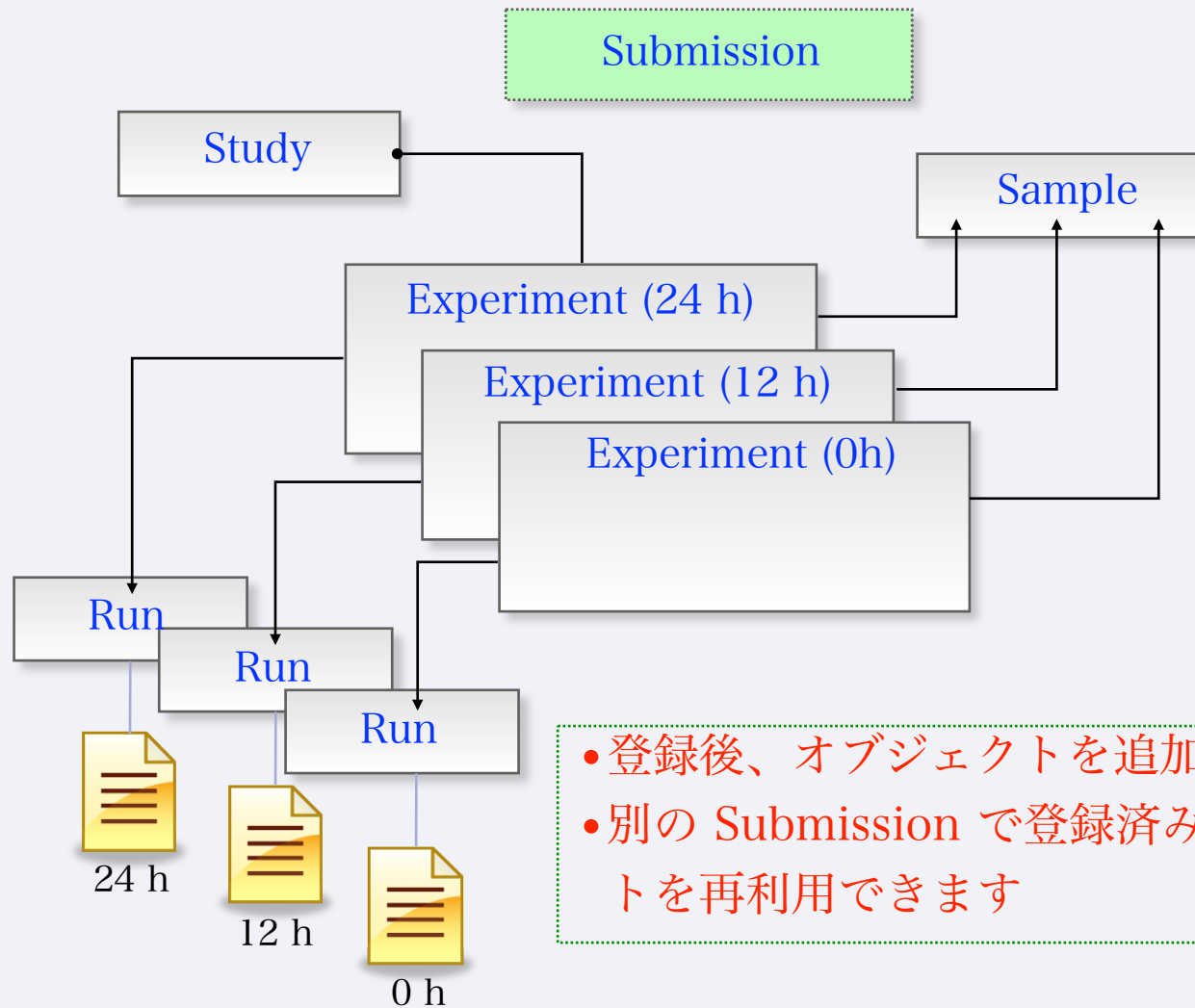
(データに関する情報：実験手法、解析方法 etc)

メタデータとランデータの構成



メタデータ構成の例

例) 培養細胞: 薬剤処理 0, 12, 24 h 後の転写プロファイル解析



- 登録後、オブジェクトを追加できます
- 別の Submission で登録済みのオブジェクトを再利用できます

【実習】 DRAsearch で検索してみよう

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検索



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DDBJ Sequence Read Archive のサイトを開く

DRAsearch: *A. thaliana* を選択

DRAsearch

[Search Home](#) [DRA Home](#)

Accession :

Organism : StudyType :

CenterName : m :

Keyword :

Show re

Arabidopsis thaliana x Arabidopsis halleri

Arabidopsis thaliana x Arabidopsis lyrata

Statistics

Data Last Update 2017-08-23

Released Entries

Type	Count
Submission	731969
Study	112803
Experiment	3187852
Sample	2855310
Run	3593768

Organism

#	Organism Name	Study
1	Homo sapiens	10517
2	Mus musculus	8290
3	soil metagenome	2886
4	Oryza sativa	1341
5	Drosophila melanogaster	1333
6	Arabidopsis thaliana	1312
7	marine metagenome	1294
8	Populus trichocarpa	1088
9	Neurospora crassa	984
10	Saccharomyces cerevisiae	950

Study Type

#	Study Type	Study
1	Whole Genome Sequencing	45282
2	Other	36478
3	Transcriptome Analysis	15382
4	Metagenomics	13570
5	Population Genomics	787
6	Epigenetics	703
7	Exome Sequencing	231
8	Transcriptome Sequencing	169
9	Cancer Genomics	115
10	Pooled Clone Sequencing	35

Center Name

#	Center Name	Study
1	BioProject	61272
2	GEO	18494
3	UMIGS	2557
4	DOE - JOINT GENOME INSTITUTE	2485
5	JGI	2365
6	WUGSC	1394
7	JCVI	1148
8	BI	962
9	SC	904
10	The Wellcome Trust Sanger Institute	689

DRAsearch: Transcriptome を選択

DRAsearch

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Accession :

Organism :

StudyType :

CenterName :

Platform :

Keyword :

Show records Sort by

Search Results (1312 studies)

#	STUDY	SUBMISSION	STUDY_TITLE	STUDY_TYPE	ORGANISM	BASES	SUBMITTED	CENTER_NAME
1	DRP000209	DRA000208	Arabidopsis Transcriptome	Transcriptome	Arabidopsis thaliana	11.2G	2010-08-02	NIG
2	DRP000347	DRA000344	Identification of EMS-induced Causal Mutations in Arabidopsis thaliana Accession by Whole Genome Sequencing	Transcriptome	Arabidopsis thaliana	11.6G	2011-02-18	NAIST_BS
3	DRP000422	DRA000414	Whole genome bisulfite sequencing analysis on tobacco (Nicotiana glauca) leaves	Transcriptome	Arabidopsis thaliana	15.1G	2011-07-05	UT_SCI
4	DRP000428	DRA000420	Re-sequencing of A. thaliana ddm1 genome 18A	Transcriptome	Arabidopsis thaliana	19.2G	2011-07-13	NIG
5	DRP000429	DRA000421	Re-sequencing of A. thaliana ddm1 genome 18C	Transcriptome	Arabidopsis thaliana	19.4G	2011-07-13	NIG
6	DRP000430	DRA000422	Re-sequencing of A. thaliana ddm1 genome 18H	Transcriptome	Arabidopsis thaliana	21.2G	2011-07-13	NIG
7	DRP000431	DRA000423	Re-sequencing of A. thaliana ddm1 genome 18J	Transcriptome	Arabidopsis thaliana	17G	2011-07-13	NIG
8	DRP000432	DRA000424	Re-sequencing of A. thaliana ddm1 genome 18L	Transcriptome	Arabidopsis thaliana	17.6G	2011-07-13	NIG
9	DRP000899	DRA000865	FE, a phloem-specific Myb protein, regulates the mobile floral signal FT	Transcriptome	Arabidopsis thaliana	5.9G	2012-12-10	NAIST_BS
10	DRP001015	DRA000976	Mechanism for full-length RNA processing over intron retention	Transcriptome	Arabidopsis thaliana	8.1G	2013-04-19	OIST
11	DRP001104	DRA001060	Whole genome bisulfite sequencing of A. thaliana empty vector.	Transcriptome	Arabidopsis thaliana	41.5G	2013-06-27	NIG
12	DRP001105	DRA001061	Whole genome bisulfite sequencing of A. thaliana, FT-203, transformed with full length VANDAL21, Hiun.	Transcriptome	Arabidopsis thaliana	44.3G	2013-06-28	NIG
13	DRP001134	DRA001087	Whole genome sequencing of a backcrossed F2 plant of EMS-mutagenized Arabidopsis thaliana	Transcriptome	Arabidopsis thaliana	4.5G	2013-07-18	IBRC
14	DRP001245	DRA001183	Small RNA sequences in transgenic Arabidopsis plants expressing a viral RNA silencing suppressor of plantago asiatica mosaic virus.	Transcriptome	Arabidopsis thaliana	703.4M	2013-10-17	UT-GALS
15	DRP001756	DRA001683	mRNA-seq analysis for Arabidopsis max1-1 mutant	Transcriptome	Arabidopsis thaliana	143.7G	2014-02-04	TUAGRI
16	DRP001761	DRA001688	RNA-seq of rps1dml2-3 triple mutant under ABA and osmotic stress treatment	Transcriptome	Arabidopsis thaliana	45.4G	2014-02-05	PS_SNU

- ✓ 16S pyrosequencing
- amplicon analysis
- Amplicon sequencing
- Cancer Genomics
- ChIP-seq
- CLIP-seq
- Epigenetics
- Exome Sequencing
- genome partial sequencing
- genome-wide SNP discovery
- MAP
- Metagenomics
- Metatranscriptomics
- multi-isolate
- Other
- pooled clone
- Pooled Clone Sequencing
- Population Genomics
- RAD-seq
- Random Shotgun Sequencing
- RRBS
- small RNA
- Synthetic Genomics
- Target sequencing
- Targeted sequencing
- Transcriptome Analysis
- Transcriptome Sequencing
- vector insertion site analysis
- Whole chromosome sequencing
- Whole genome bisulfite sequencing
- Whole Genome Sequencing
- Whole Genome Sequencing

DRAsearch: 検索結果リスト

DRAsearch

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Accession :

Organism :

StudyType :

CenterName :

Platform :

Keyword :

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Search Results (548 studies)

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#	STUDY	SUBMISSION	STUDY_TITLE	STUDY_TYPE	ORGANISM	BASES	SUBMITTED	CENTER_NAME
1	DRP000209	DRA000208	Arabidopsis Transcriptome	Transcriptome Analysis	Arabidopsis thaliana	11.2G	2010-08-02	NIG
2	DRP001800	DRA001727	Transcriptomic analysis of Arabidopsos rfl2 mutant	Transcriptome Analysis	Arabidopsis thaliana	6.5G	2014-02-21	NUGSS
3	ERP001018	ERA070277	Study of genome-wide alternative polyadenylation in A. thaliana	Transcriptome Analysis	Arabidopsis thaliana	326.9M		DUNDEE
4	ERP001616	ERA146059	CPL phosphatases as plant miRNA-processing regulators - mRNA reads	Transcriptome Analysis	Arabidopsis thaliana	18.2G		MPI-TUEBINGEN
5	ERP001622	ERA146132	CPL phosphatases as plant miRNA-processing regulators - sRNA reads	Transcriptome Analysis	Arabidopsis thaliana	7.7G		MPI-TUEBINGEN
6	ERP002233	ERA194802	Single-cell RNA-seq for pGL2 and QC cells from the Arabidopsis thaliana root	Transcriptome Analysis	Arabidopsis thaliana	89G		EMBL-EBI
7	ERP002617	ERA212631	Salt priming A. thaliana RNA-Seq	Transcriptome Analysis	Arabidopsis thaliana	10G		University of Glasgow
8	ERP004034	ERA256782	arabidopsis_thaliana_floral_meristem_atlas	Transcriptome Analysis	Arabidopsis thaliana	15.8G		University of Milan. Dept. of Biosciences
9	ERP005391	ERA295485	Transcriptome profiling of Arabidopsis embryogenesis in vitro	Transcriptome Analysis	Arabidopsis thaliana	21.3G		SCHOOL OF AGRICULTURE, POLICY AND DEVELOPMENT, THE UNIVERSITY OF READING, UK
10	ERP005565	ERA300733	Transcriptomic profiling of Arabidopsis DNA POLYMERASE EPSILON CATALYTIC SUBUNIT A (AtPOL2a) and B (AtPOL2b) mutants	Transcriptome Analysis	Arabidopsis thaliana	45.4G		SCHOOL OF AGRICULTURE, POLICY AND DEVELOPMENT, THE UNIVERSITY OF READING, UK
11	ERP006258	ERA326935	Arabidopsis thaliana RNase H2 deficiency counteracts the needs for the WEE1 checkpoint kinase but triggers genome instability	Transcriptome Analysis	Arabidopsis thaliana	11.7G		European Bioinformatics Institute
12	ERP006353	ERA330074	Extensive small RNAs sequestration in diverse eukaryotes	Transcriptome Analysis	Arabidopsis thaliana Caenorhabditis elegans Drosophila melanogaster Mus musculus Nicotiana glauca	11.9G		EBI

DRAsearch: フリーキーワードで検索

Accession :

Organism : StudyType :

CenterName : Platform :

Keyword :

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Search Results (6367 records)

<< < 1 / 319 Page > >>

Filtered by

document type:study(2812) sample(1858) experiment(1393) submission(177) run(122) analysis(5)
organism:Arabidopsis thaliana(4150) Homo sapiens(460) Mus musculus(289) rhizosphere metagenome(151) Brassica rapa(110)
Drosophila melanogaster(70)

#	META_FILE	ACCESSION	STUDY	STUDY_TITLE	STUDY_TYPE	ORGANISM	BASES	SUBMITTED	CENTER_NAME
1	SRA050132.study.xml <i>splicing</i> in <i>Arabidopsis thaliana</i> defense against the bacterial pathogen <i>Pseudomonas syringae</i> pv tomato (Pst)	SRP010938	SRP010938	Arabidopsis thaliana strain:Columbia (Col-0) Transcriptome or Gene expression	Transcriptome Analysis	Arabidopsis thaliana	85.2G	2012-02-15	NCSU
2	SRA009031.study.xml </SUBMITTER_ID> </IDENTIFIERS> <DESCRIPTOR> <STUDY_TITLE>Transcriptome-wide map of alternative <i>splicing</i> in <i>Arabidopsis</i>	SRP000935	SRP000935	Transcriptome-wide map of alternative splicing in Arabidopsis	Transcriptome Analysis	Arabidopsis thaliana	12.5G	2009-07-07	OSU-CGRB
3	SRA200829.submission.xml in <i>Arabidopsis thaliana</i> lab_name="Bioinformatics core" center_name="IPMB" accession="SRA200829	SRA200829	SRP049707	Arabidopsis thaliana Transcriptome or Gene expression	Transcriptome Analysis	Arabidopsis thaliana	67.1G		BioProject
4	SRA198305.submission.xml <i>splicing</i> -contributed proteome diversity in <i>Arabidopsis thaliana</i> center_name="Institute of Genetics	SRA198305	SRP049534	Transcriptome survey of alternative splicing-contributed proteome diversity in Arabidopsis thaliana	Transcriptome Analysis	Arabidopsis thaliana	84.3G		BioProject
5	SRA198305.study.xml <i>splicing</i> -contributed proteome diversity in <i>Arabidopsis thaliana</i> </STUDY_TITLE> <STUDY_TYPE existing	SRP049534	SRP049534	Transcriptome survey of alternative splicing-contributed proteome diversity in Arabidopsis thaliana	Transcriptome Analysis	Arabidopsis thaliana	84.3G		BioProject
6	SRA200829.study.xml , that influences pre-mRNA <i>splicing</i> and is essential for embryonic development in <i>Arabidopsis thaliana</i> . A genome	SRP049707	SRP049707	Arabidopsis thaliana Transcriptome or Gene expression	Transcriptome Analysis	Arabidopsis thaliana	67.1G		BioProject
7	SRA496773.study.xml </EXTERNAL_ID> </IDENTIFIERS> <DESCRIPTOR> <STUDY_TITLE> <i>Arabidopsis thaliana</i> strain:Col-0	SRP093582	SRP093582	Arabidopsis thaliana strain:Col-0 Transcriptome or Gene expression	Transcriptome Analysis	Arabidopsis thaliana	0		BioProject
8	SRA291694.study.xml </EXTERNAL_ID> </IDENTIFIERS> <DESCRIPTOR>	SRP062001	SRP062001	Arabidopsis thaliana strain:Columbia	Other	Arabidopsis	33.1G		BioProject

DRAsearch: Study Detail

SRP000935

Study Detail

Title	Transcriptome-wide map of alternative splicing in Arabidopsis
Study Type	Transcriptome Analysis
Abstract	placeholder
Description	Alternative splicing was profiled in Arabidopsis thaliana using Illumina-based RNA-seq. Five abiotic stress treatments and untreated controls were analyzed. All samples represented Col-0 wildtype plants.
Center Name	OSU-CGRB

Navigation

	Submission	SRA009831		FTP
	Experiment	SRX006191		FASTQ
		SRX006192		FASTQ
		SRX006193		FASTQ
		SRX006681		FASTQ
		SRX006682		FASTQ
		SRX006688		FASTQ
		SRX006690		FASTQ
		SRX006692		FASTQ
		SRX006704		FASTQ
		SRX179490		FASTQ
		SRX179491		FASTQ
		SRX179492		FASTQ
		SRX179493		FASTQ
		SRX179494		FASTQ
		SRX179495		FASTQ
	Sample	SRS004095		
		SRS004097		
		SRS004098		
		SRS004099		
		SRS004100		
		SRS004101		
		SRS004102		
		SRS004103		
		SRS004104		

DRAsearch: Experiment Detail

SRX006191  [FASTQ](#)  [SRA](#)

Experiment Detail

Title	FC14
Design Description	Total RNA was extracted using "The Plant RNA Reagent" (Invitrogen). RNA was treated for 10 min at 65C with RNaseqsecure reagent (Ambion). To eliminate genomic DNA amplification, all RNA preparations were treated for 15 min at 37C with RNase-free "Turbo DNase" (Ambion). Next, total RNA was further purified using the "RNAeasy Mini RNA kit" (Qiagen) according to the manufacturer's RNA clean up protocol. Isolation of mRNA essentially free of ribosomal and other non-polyadenylated RNAs was critical for generation of non-biased randomly primed (RP) libraries. For the RP libraries the poly(A) mRNA was isolated by two consecutive cycles of purification on oligo d(T) cellulose using the "Micro-PolyA-Purist" kit (Ambion). Concentration, integrity and extent of contamination by ribosomal RNA were monitored using a ND-1000 spectrophotometer (Thermo Fisher Scientific) and Bioanalyzer 2100 (Agilent Technologies). Full-length enriched (FL) cDNA libraries were generated using the SMART method (Zhu et al., 2001). cDNA (5-7 ug in a 50 µL volume) was mixed with 750 uL of Illumina nebulization buffer and fragmented for 7 min in a nebulizer (Invitrogen) using compressed nitrogen at 35 psi. The sheared cDNA was purified using "QIAquick PCR Purification Kit" (Qiagen) and eluted into 32 uL of water. For the randomly primed (RP) cDNA libraries the first cDNA strand was synthesized using 1 ug of poly(A) mRNA essentially free of rRNA, random hexamer primers (300 ng per each ug of RNA), and Superscript III reverse transcriptase (RT) (Invitrogen). The second strand of cDNA was synthesized using DNA polymerase I (Klenow fragment) by combining 20 uL of the 1st strand reaction, 8 uL of 10x Klenow Buffer (NEB), 1 unit of RNase H (Invitrogen), 68.8 uL of water and 30 units of DNA Polymerase I (NEB). The reaction was incubated for 90 min at 15C and cDNA was purified using "QIAquick PCR clean up" kit. To prepare cDNAs for sequencing on the Illumina Genome Analyzer, FL or RP cDNA (30 uL) was combined with 10 uL of 10 mM ATP in 5X T4 DNA ligase buffer (Invitrogen), 4 uL of 10 mM dNTPs mix, 2.5 uL of T4 DNA polymerase (3 U/uL), 1 uL of Klenow DNA Pol (5 U/uL) and 2.5 uL of T4 polynucleotide kinase (10 U/uL, NEB). After incubation for 30 min at 20C the DNA was purified using "QIAquick PCR Purification kit". To add dA to the termini, 32 uL DNA from the prior step was mixed with 5 uL of 10X Klenow buffer, 10 uL of 1 mM dATP, and 3 uL of Klenow exo-polymerase (3' to 5' exo minus, 5 U/uL, NEB) and incubated for 30 min at 37C. DNA was purified using a "QIAquick MinElute Reaction Clean-up" (Qiagen) kit and eluted into 12 uL of water. To ligate Illumina adapters, 10 uL of cDNA from the prior step was mixed with 5 uL of 5X T4 DNA ligase buffer, 6 uL of adapter oligo mix, 4 uL of T4 DNA ligase (NEB) and incubated for 15 min at 25C. DNA was purified using a "QIAquick MinElute PCR Purification Kit". cDNA was size-fractionated (typically with average fragment length of 170 base pairs) on 3.5% (w/v) "NuSieve GTG" agarose. The fractionated libraries were PCR amplified using "Phusion Hot Start High-Fidelity" DNA polymerase (NEB) and the following PCR protocol: 30 sec at 98C, then 10 sec at 98C, 30 sec. at 65C, and 30 sec. at 72C for 18 cycles, followed by a 10-min extension step at 72C. Prior to cluster generation, DNA was diluted to a final concentration of 5 to 10 pM to generate 25,000 to 40,000 clusters per tile of the flow cell.
Organism	Arabidopsis thaliana

Navigation

 Submission	SRA009031	 FTP
 Study	SRP000935	
 Sample	SRS004095	
 Run	SRR018346	 FASTQ  SRA

例: この SRA データを使った二次論文

SRP000935 pubmed



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4 件 (0.19 秒)

[Determinants of Exon-Level Evolutionary Rates in Ar](#)

[www.ncbi.nlm.nih.gov](#) > ... > v.8; 2012 ▼ このページを訳す
GCT Wu 著 - 2012 - 引用元 1 - 関連記事

2012/07/04 - We retrieved a series of raw data submitted by Filic and Schmidt's lab (SRP007763). These RNA-seq data cover several conditions, including abiotic stresses (cold, drought, heat, highlig

[Estimation of Gene Expression at Isoform Level from](#)

[www.ncbi.nlm.nih.gov](#) > ... > Front Genet > v.3; 2012 ▼ この
M Bhattacharjee 著 - 2012 - 関連記事

2012/11/27 - The dataset was downloaded from NCBI GEO webs **SRP000935**). Pooled data contains [PubMed]; Bhattacharjee Nelson P. S., Arjas E. (2004). Bayesian integrated functional an

[7075 - DNAnexus - SRA](#)

[sra.dnanexus.com/?page=7075&result_type...](#) ▼ このページ
SRR019209, Oregon St Univ - Center for Genome Research & B SRX006688 · Arabidopsis thaliana · **SRP000935**, SRA009031. 1 Oregon St Univ ... [pubmed\(21393572\)](#)» · SRR099327, Stanford

[Determinants of exon-level evolutionary rates in ... - F](#)

Evol Bioinform Online. 2012; 8: 389–415.

Published online 2012 July 4. doi: [10.4137/EBO.S9743](#)

PMCID: PMC3399485

Determinants of Exon-Level Evolutionary Rates in *Arabidopsis* Species

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Front Genet. 2012; 3: 239.

Published online 2012 November 27. doi: [10.3389/fgene.2012.00239](#)

PMCID: PMC3536024

Estimation of Gene Expression at Isoform Level from mRNA-Seq Data by Bayesian Hierarchical Modeling

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検索



登録

DDBJ pipeline: ソフトウェア

よく用いられる
解析用ソフトウェアを
用意。クリックだけで
実行可能



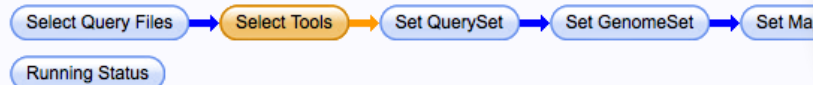
CINA Data Bank of Japan

ACCOUNT
 login ID [guest]
[Logout](#)

ANALYSIS
 Data setup
 DRA Start
 FTP upload
 HTTP upload
 DRA Import
 Preprocessing Start
 step-1
 Preprocessing
 Mapping /
de novo Assembly
 step-2
Workflow
 Genome (SNP/Short
 Indel)
 RNA-seq (Tag count)
 ChIP-seq
[☞](#)

JOB STATUS
 step1.
 Preprocessing
 step1.
 Mapping
 step1.
de novo Assembly
 step2-All status

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 DDBJ Read Annotation
 Pipeline.
 Development Team.



Selecting Tools for Basic Analysis of DDBJ ANNOTATION

Reference Genome Mapping

	Tool	Help	Version	Input data			Evaluation			Analysis		Output format			Comment
				Base space	Color space	Paired end	Depth	Coverage	Error rate	SNP	Indel	.gff	.bed	SAM	
☐	BLAT	☞	34	✓					✓						Single-end analysis only
☐	bwa	☞	0.6.1	✓		✓	✓	✓	✓					✓	
☐	Bowtie	☞	0.12.7	✓	✓	✓	✓	✓	✓	✓				✓	
☐	TopHat	☞	1.0.11	✓		✓	✓	✓	✓					✓	
☐	Bowtie2	☞	2.2.6	✓	✓	✓	✓	✓	✓	✓				✓	For reads longer than about 50 bp, Bowtie2 is generally faster, more sensitive, and uses less memory than Bowtie1.
☐	TopHat2	☞	2.1.0	✓		✓	✓	✓	✓					✓	

☐ *de novo* Assembly Total limit = 22 Gbp

	Tool	Help	Version	Base space	Color space	Paired-end	MSS(WGS)	Comment
☐	SOAPdenovo	☞	2.04-r240	✓		✓		
☐	ABYSS	☞	1.3.2	✓		✓		Maximum K-mer value is 64.
☐	Velvet	☞	1.2.10	✓		✓	✓	We severe recommend when performing Velvet, total length of those reads is up to 22G bp.Maximum K-mer value is 64.
☐	Trinity	☞	2.1.1	✓		✓		RNA-Seq De novo Assembly
☐	Platanus	☞	1.2.2	✓		✓		
☐	HGAP	☞	Protocol3 (v 2.2.0)					HGAP Pipeline for PacBio Sequence based on SMRT Analysis v2.2.0. For box.h5 file only. (Beta version)

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良く使われるソフトウェアの特徴

マッピング

BLAT	NGS以前からあるアライメントツール。発現データはイントロンを想定したギャップを考慮。
MAQ	NGS初期にショートリードに対応。リード長が長くなるに従い開発はBWAに引き継がれる。現在では DDBJ pipeline では提供していない。
BWA	MAQより速く、Titaniumのリードもオプションで対応。
SOAP	メモリ消費量少なく、高速。精度はBWAより弱冠落ちる。
Bowtie/Bowtie2	ギャップは考慮しないが処理は速い。BWA、SOAP2、Bowtieは Burrows-Wheeler変換というアルゴリズムでゲノムDNAにたいしてインデックスを作成、高速でマッピングする。Bowtie2は50bp以上に最適化。
TopHat/TopHat2	RNA-Seqのリードを内部でBowtieを利用してマッピング、スプライスジャンクションを特定する。

アセンブル

SOAPdenovo	ヒト、パンダ等大型ゲノムのアセンブリで使用された。比較的高速。
Abyss	初期に並列処理に対応したアセンブラ。
Velvet	NGS初期に開発された。メモリ消費多め。
Trinity	RNA-Seq配列用のアセンブラ。
Platanus	東工大で開発された国産アセンブラ。高速・メモリ消費少なめで、ヘテロなゲノムに強い。 おすすめ 。上記いずれも de bruijn graph というアルゴリズムを使用。
HGAP	PacBio データのための SMRT 法によるアセンブラ。

DDBJ pipeline: 比較対象

イネ、マウスなど
解析比較対象となる
配列を多数用意

DDBJ
DNA Data Bank of Japan

ACCOUNT
login ID [yaskaz]
Logout
Change password

ANALYSIS
Data setup
DRA Start
FTP upload

JOB STATUS
step1. Preprocessing
step1. Mapping
step1. de novo Assembly
step2-All status

HELP

Select Query Files → Select Tools → Set QuerySet → Running Status

Specifying Database of Reference

Major genome sets

Organisms: Arabidopsis thaliana
Genome sets: ☒ TAIR8, ☐ TAIR9, ☐ TAIR10

☒ all.fa
☐ chr01.fa
☐ chr02.fa
☐ chr03.fa
☐ chr04.fa
☐ chr05.fa
☐ chrC.fa
☐ chrM.fa

Major genome sets

Organisms: Oryza sativa japonica
Genome sets: ☒ IRGSP Releases Build 4.0, ☐ IRGSP Releases Build 5.0, ☐ IRGSP Releases Build 5.0 masked by RepeatMasker with tigr version5.0, ☐ tigr version6.0, ☐ tigr version6.1, ☐ tigr mitochondrion, ☐ tigr chloroplast

Major genome sets

Organisms: Homo sapiens
Genome sets: ☒ Homo sapiens Feb. 2009 (hg19), ☐ Mar.2006 (hg18), ☐ May.2004 (hg17), ☐ NCBI build 36.1_CRA, ☐ NCBI build 36.1_Celera, ☐ NCBI build 36.1_ref, ☐ NCBI build 36.2_CRA, ☐ NCBI build 36.2_Celera, ☐ NCBI build 36.2_ref, ☐ NCBI build 36.3_CRA, ☐ NCBI build 36.3_Celera, ☐ NCBI build 36.3_ref, ☐ NCBI build 36.3_HuRef, ☐ NCBI build 37.1_CRA, ☐ NCBI build 37.1_Celera, ☐ NCBI build 37.1_GRCh, ☐ NCBI build 37.1_HuRef

1. Mapping

2. Assembly

1. Mapping

2. Assembly

DRAウェブサイト ⇒ [DRA] で検索

<http://trace.ddbj.nig.ac.jp/dra/>

登録関係情報



Sequence Read Archive

Login & Submit | Databases ▾ | English | Contact

Google™ カスタム検索



Home

Submission ▾

Search

Download ▾

Pipeline

About

解析パイプライン

DDBJ Sequence Read Archive (DRA) は, the 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD® System などの次世代シーケンサからの出力データ (Raw Data) を, Nucleotide Sequence Database Collaboration (INSDC) のメンバーであり, DDBJ, EMBL, GenBank との国際協力ののもと, 運営されています。従来のキャピタシオンシーケンサからの出力データ (Raw Data) を DRA Archive にご登録ください。

データ検索

データ取得



検索

データをキーワード、生物名、シーケンサなどで検索する



登録

新型シーケンサからの生データやアライメントデータを登録する



動画マニュアル

DRA の利用方法や登録方法を解説している動画をみる

Mappingの例 (DRAsearch+pipeline)

Accession :

Organism :

CenterName :

Keyword :

シロイヌナズナ
alternative splicing

Show records Sort by

Search Results (3656 records)

/ 183

Filtered by

document type:study(1890) sample(1020) experiment(600) submission(103) run(41) analysis(2)
organism:Arabidopsis thaliana(1704) Homo sapiens(523) Mus musculus(462) Drosophila melanogaster(55) Saccharomyces cerevisiae(31)
Arabidopsis lyrata(30)

#	META_FILE	ACCESSION	STUDY	STUDY_TITLE	STUDY_TYPE	ORGANISM	BASES	SUBMITTED	CENTER_NAME
1	SRA050132.study.xml <?xml version="1.0" encoding="UTF-8"?> <STUDY center_name="NCSU" alias="Arabidopsis - Pseudomonas alternative splicing study" accession="SRP010938"> </STUDY>	SRP010938	SRP010938	Arabidopsis thaliana strain:Columbia (Col-0) Transcriptome or Gene expression	Transcriptome Analysis	Arabidopsis thaliana	85.2G	2012-02-15	NCSU
2	SRA009031.study.xml </SUBMITTER_ID> </IDENTIFIERS> <DESCRIPTOR> <STUDY_TITLE>Transcriptome-wide map of alternative splicing in Arabidopsis	SRP000935	SRP000935	Transcriptome-wide map of alternative splicing in Arabidopsis	Transcriptome Analysis	Arabidopsis thaliana	12.5G	2009-07-07	OSU-CGRB
3	SRA050132.submission.xml <?xml version="1.0" encoding="UTF-8"?> <SUBMISSION alias="Arabidopsis alternative splicing project">	SRA050132	SRP010938	Arabidopsis thaliana strain:Columbia (Col-0) Transcriptome or Gene expression	Transcriptome Analysis	Arabidopsis thaliana	85.2G	2012-02-15	NCSU
4	SRA198305.submission.xml splicing-contributed proteome diversity in Arabidopsis thaliana" center_name="Institute of Genetics	SRA198305	SRP049534	Transcriptome survey of alternative splicing-contributed proteome diversity in Arabidopsis thaliana	Transcriptome Analysis	Arabidopsis thaliana	84.3G		BioProject
5	SRA044892.study.xml <?xml version="1.0" encoding="UTF-8"?> <STUDY center_name="Institute of Plant and Microbial Biology, Academia" alias="Alternative Splicing">	SRP007763	SRP007763	Genome-wide detection of context-sensitive alternative splicing in Arabidopsis roots	Other	Arabidopsis thaliana	3.6G		Institute of Plant and Microbial Biology, Academia
6	DRA002223.run.xml <?xml version="1.0" encoding="UTF-8"?> <TITLE>Phytochrome controls alternative splicing to mediate light responses in Arabidopsis	DRR018422 DRR018423 DRR018425 DRR018424 DRR018428 DRR018427 DRR018426	DRP002301			Arabidopsis thaliana	202.4G	2014-04-15	

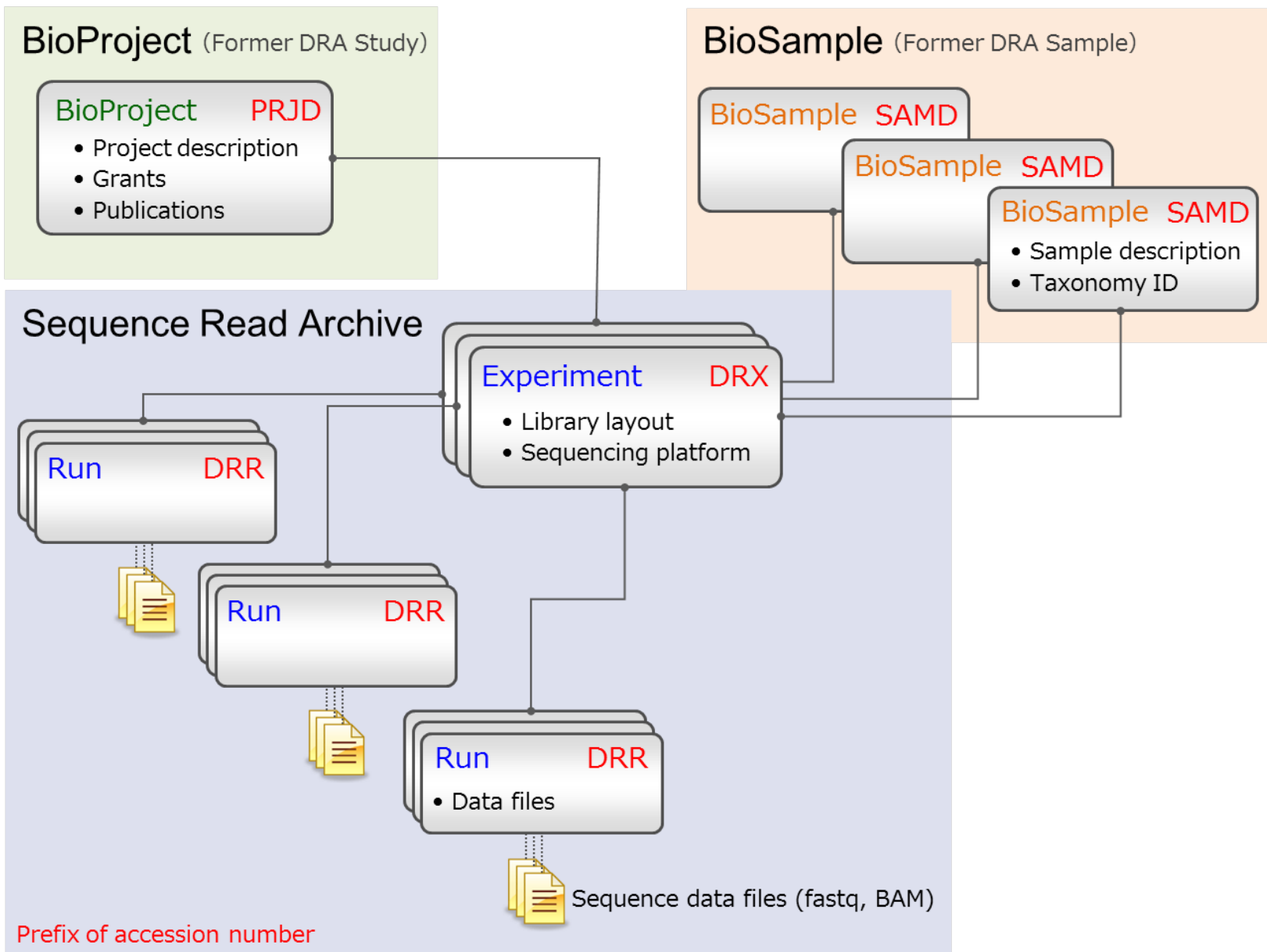
データのIDはこちら

SRP007763

Study Detail	
Title	Genome-wide detection of context-sensitive alternative splicing in Arabidopsis roots
Study Type	Other
Abstract	To analyze context-sensitive changes in pre-mRNA splicing pattern and gene expression, we mapped the transcriptome of iron-deficient and iron-sufficient Arabidopsis roots using the RNA-seq technology. RNA-seq data were analyzed with a newly developed software package, RACKJ (Read Analysis & Comparis .. [more]
Description	
Center Name	Institute of Plant and Microbial Biology, Academia

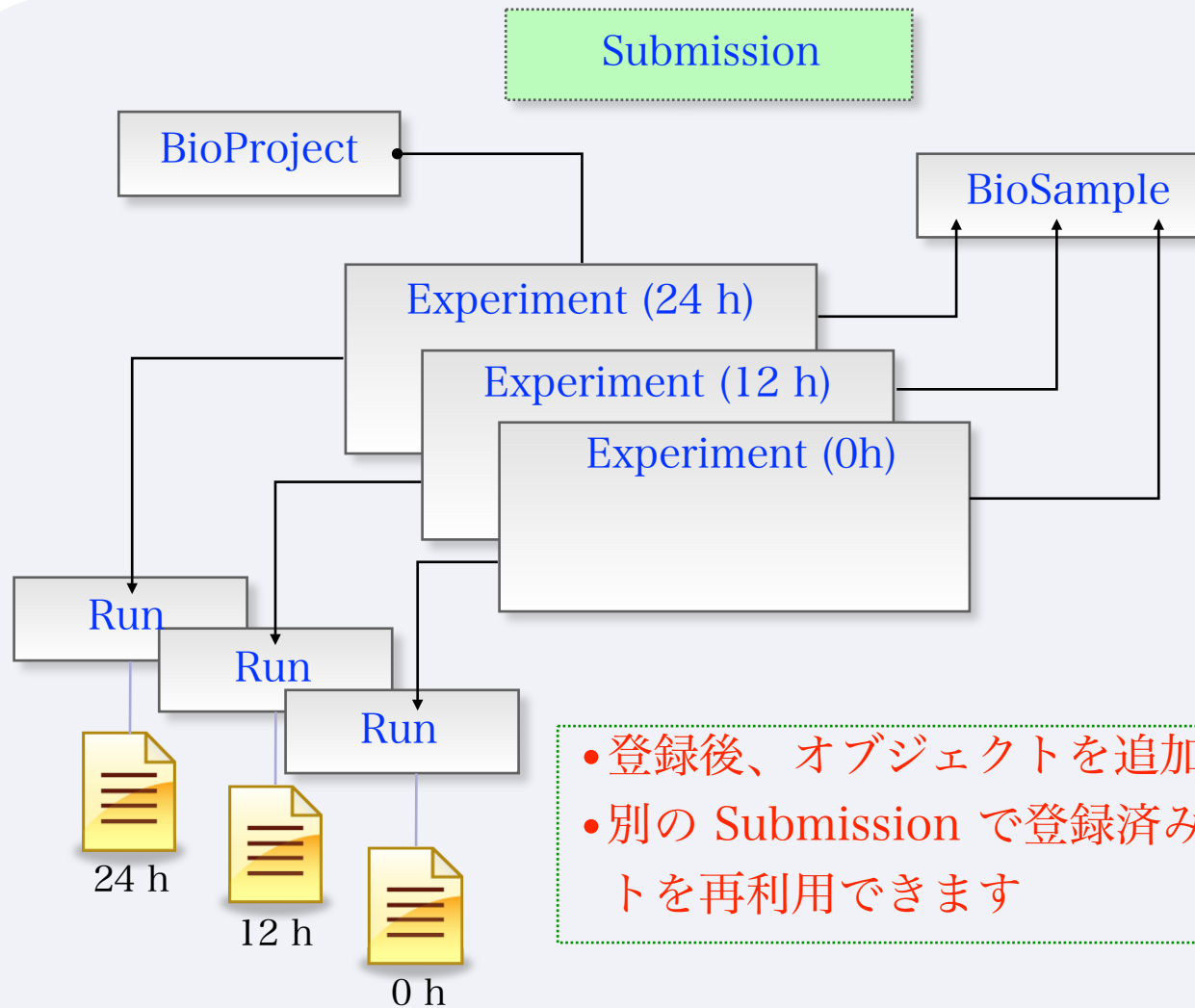
Navigation		
Submission	SRA044892	 FTP
	SRA045009	 FTP
Experiment	SRX092047	 FASTQ  SRA
	SRX092048	 FASTQ  SRA
	SRX092049	 FASTQ  SRA
	SRX092050	 FASTQ  SRA
Sample	SRS256250	
	SRS257585	
	SRS257586	
	SRS257587	

SRA の Metadata <https://trace.ddbj.nig.ac.jp/dra/submission.html>



メタデータ構成の例

例) 培養細胞: 薬剤処理 0, 12, 24 h 後の転写プロファイル解析



- 登録後、オブジェクトを追加できます
- 別の Submission で登録済みのオブジェクトを再利用できます

DDBJ パイプライン、体験してみましょう

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



DDBJ Read Annotation Pipeline

English

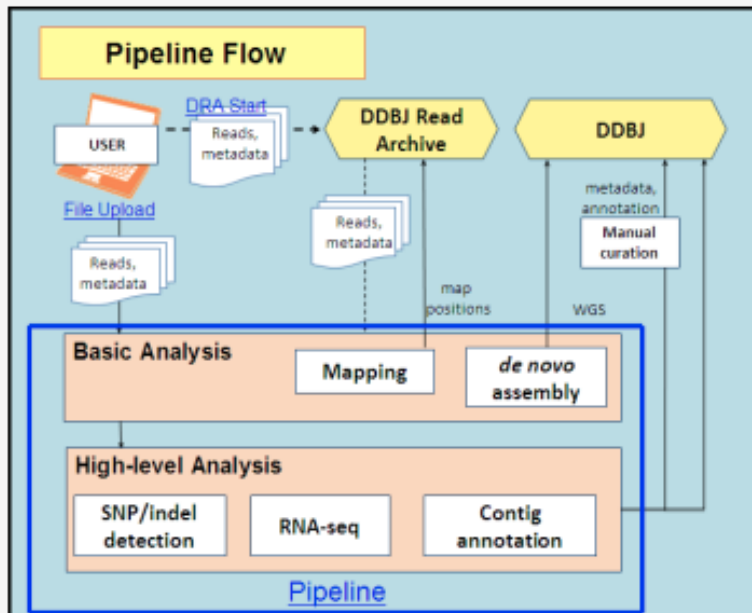
Japanese

DDBJ Read Annotation Pipeline is a cloud-computing based analytical platform for next-generation sequencing data.

LOGIN

New account

Login as "guest"



ゲストとして
ログイン

User ID:

Check current jobs

* by the guest account.

Manual & tutorial

- [Japanese Tutorial](#)
- [English manual](#)
- [DBCLS togotv Tutorial video 1 \(JP\) - Reference Genome Mapping](#)
- [DBCLS togotv Tutorial video 2 \(JP\) - De novo Assembly](#)
- [FAQ : How to upload and register query files to DDBJ Pipeline \(JP\)](#)
- [Tutorial : How to run HGAP for PacBio sequence read on DDBJ Pipeline \(JP\)](#)

Tweets

Follow

pipeline

11 Jun

処理に使うNGSの配列ファイルの用意



Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation

Running Status

Selecting Query Files

NEXT

FTP upload Private DRA entry Import public DRA Preprocessing HTTP upload

Metadata of the DRA entry.

Select a metadata : DRA000001

TYPE	ACCESSION	ALIAS	FILENAME	DL	VIEW
Submission	DRA000001	DRA000001	DRA000001.submission.xml	Download	View
Sample	DRS000001	DRS000001	DRA000001.sample.xml	Download	View
Study	DRP000001	DRP000001	DRA000001.study.xml	Download	View
Experiment	DRX000001	DRX000001	DRA000001.experiment.xml	Download	View
Run	DRR000001	DRR000001	DRA000001.run.xml	Download	View

STUDY TITLE Whole genome sequencing of *Baillus subtilis* subsp. natto BEST195

STUDY TYPE Whole Genome Sequencing

Select your registered query files.

Queries with different Instrument models can't be selected together.

single paired all clear

	No.	Experiment ACCESSION	Sample ACCESSION	Run ACCESSION	STRAIN	Run_date	Read #	Read length	Instrument model	Layout
☐	1	DRX000001	DRS000001	DRR000001	strain BEST195	2008-09-13	9,977,388	36	ILLUMINA	paired

☐ : from metadata ☒ : Counted from query file (Read length is calculated from the first entry.)

DELETE NEXT

アップロード
されている配列

ACCOUNT

login ID [guest]

Logout

ANALYSIS

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HTTP upload

DRA Import

Preprocessing Start

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Preprocessing

Mapping /
de novo Assembly

step-2

Workflow

Genome (SNP/Short
Indel)
RNA-seq (Tag count)
ChIP-seq

JOB STATUS

step1.

Preprocessing

step1.

Mapping

step1.

de novo Assembly

step2-All status

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処理に使うNGSの配列ファイルの用意

FTP で手元から
アップロード可能

Select Query Files → Set Map Options → Confirmation →

Running Status

Selecting

NEXT

FTP upload Private DRA entry Import public DRA Preprocessing HTTP upload

List of your uploaded files by FTP client. [\[Add new files\]](#)

	Filename	Description	Layout	Instrument model	File size
☐	demo.fastq	demo study	single	ILLUMINA	340.9 KB
☐	coli_allmands_5runs.fastq	coliAll	single	LS454	139.9 MB
☐	56-Rb1_S6_L001_R1_001.fastq.gz.0 (more 1 files)	150220 Rb1	paired	ILLUMINA	304.2 MB
☐	56-Rb1_S6_L001_R1_001.fastq.gz.0 (more 1 files)	150220 Rb1	paired	ILLUMINA	304.2 MB
☐	demo.fastq.6	DEMO	single	ILLUMINA	340.9 KB
☐	1.fas	lab	single	ILLUMINA	0 byte
☐	1.fas	RNR	single	ILLUMINA	0 byte
☐	RRRRR.fna	RNR-LAB	single	ABI_SOLID	12.3 MB
☐	AC_R1.fastq (more 1 files)	Assembly of Honey Bee Mitogenome	paired	ILLUMINA	188.2 MB
☐	C668HACXX_PG0614_98A0501_H1_L007_R1-50bp_QV10.fastq	test_1	single	ILLUMINA	337.6 MB
☐	demo.fastq	ddbj pipeline demo	single	ILLUMINA	340.9 KB
☐	demo.fastq	ddbj pipeline demo	single	ILLUMINA	340.9 KB

DELETE NEXT



ACCOUNT

login ID [guest]

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Indel)
RNA-seq (Tag count)
ChIP-seq

JOB STATUS

step1.

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HELP

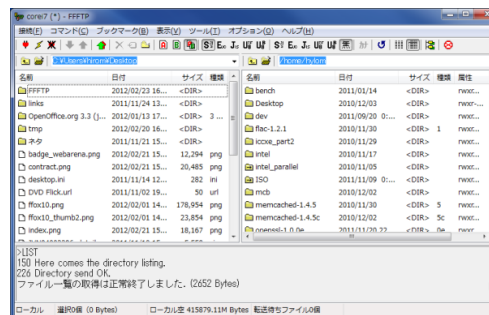
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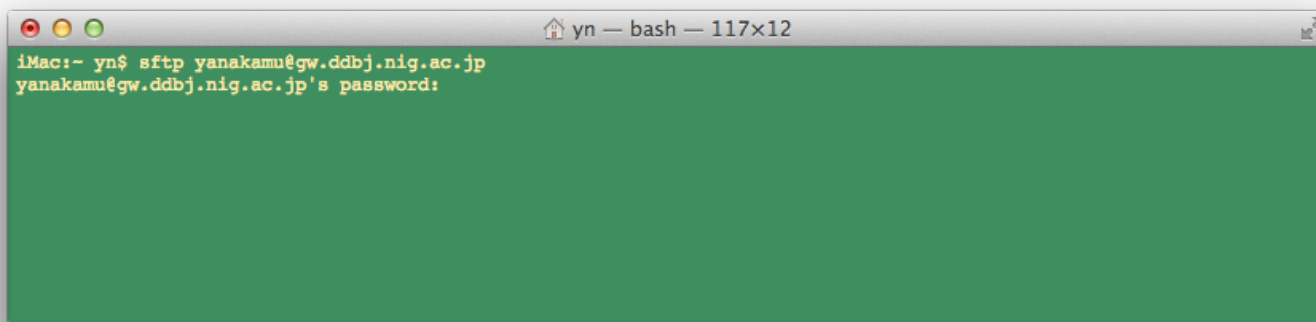
FTP (file transfer protocol) クライアント



Cyberduck



FFFTP



Cyberduck のような専用クライアントを使えば
ドラッグ&ドロップでファイル転送可能。コマン
ドでの送受信もたいして難しくありませんが。

処理に使うNGSの配列ファイルの用意



ACCOUNT

login ID [guest]

Logout

ANALYSIS

Data setup

DRA Start

FTP upload

HTTP upload

DRA Import

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Mapping /
de novo Assembly

step-2

Workflow

Genome (SNP/Short
Indel)
RNA-seq (Tag count)
ChIP-seq

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HELP

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Select Query Files

Select Tools

Set QuerySet

Set GenomeSet

Set Map Options

Confirmation

Running Status

Selecting Query Files

FTP upload

Private DRA entry

Import public DRA

Preprocessing

Import public FASTQ files from DRA database.

Here is do the section of automatic download of public DRA/ERA/SRA entries.

Please input DRA/ERA/SRA accession number. Then the pipeline system import metadata and FASTQ files from DRA database.

Input DRA/ERA/SRA Accession Number

Add my DRA entry

Accession Number can find here.
[DRA Search](#)

Your request. (Here is display only. can not select.)

To select your downloaded entries. See Private DRA entry tab.
When the status makes "done", your requested entry is added in "Private DRA entry" tabs.
When the status makes "failed" or "preparing", please retry it.

queued : waiting or during download, **done** : file is ready, **failed** : please retry it, **preparing** : file is not yet in
DRA **unchecked** : download is ok, but md5 was not check.

Status	Submission	Request date
✓ done	SRA045657	2015-11-18 15:55:10.735
✗ preparing	SRA221099	2015-10-28 17:33:00.955
✓ done	SRA073646	2015-10-22 15:34:33.954
✓ done	ERA000035	2015-10-21 16:43:31.226
✗ preparing	SRA176628	2015-10-18 23:11:12.59
✓ done	SRA012701	2015-09-28 12:37:52.009
✗ preparing	SRA245648	2015-07-29 14:52:11.178
✓ done	SRA010042	2015-07-24 11:39:14.19
✓ done	ERA209804	2015-07-24 10:56:30.546
✓ done	SRA009815	2015-07-20 20:51:21.762

公開データを
インポート可能

p.ddbj.nig.ac.jp を開き、さっきのIDを入力



ACCOUNT

login ID [guest]

Logout

ANALYSIS

Data setup

DRA Start

FTP upload

DRA Import

Workflow

Genome (SNP/Short Indel)

RNA-seq (Tag count)

ChIP-seq

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Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation

Running Status

Selecting Query Files

FTP upload Private DRA entry **Import public DRA** Preprocessing HTTP upload

Import public FASTQ files from DRA database.

Here is do the section of automatic download of public DRA/ERA/SRA entries.
Please input DRA/ERA/SRA accession number. Then the pipeline system import metadata and FASTQ files from DRA database.

Input DRA/ERA/SRA Accession Number

SRA044892 Add my DRA entry

でも今は押さないで！

When the status makes "failed" or "preparing", please retry it.

queued : waiting or during download, done : file is ready, failed : please retry it, preparing : file is not yet in DRA unchecked : download is ok, but md5 was not check.

Status	Submission	Request date
✓ done	SRA045657	2015-11-18 15:55:10.735
✗ preparing	SRA221099	2015-10-28 17:33:00.955
✓ done	SRA073646	2015-10-22 15:34:33.954
✓ done	ERA000035	2015-10-21 16:43:31.226
✗ preparing	SRA176628	2015-10-18 23:11:12.59
✓ done	SRA012701	2015-09-28 12:37:52.009
✗ preparing	SRA245648	2015-07-29 14:52:11.178
✓ done	SRA010042	2015-07-24 11:39:14.19
✓ done	ERA209804	2015-07-24 10:56:30.546
✓ done	SRA009815	2015-07-20 20:51:21.762

SRA044892 をロードしておきました



Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation

Running Status

Selecting Query Files

NEXT

FTP upload **Private DRA entry** Import public DRA Preprocessing HTTP upload

Metadata of the DRA entry.

Select a metadata: SRA044892

TYPE	ACCESSION	ALIAS	FILENAME	DL	
Submission	SRA044892	AraEsFeP	SRA044892.submission.xml	Download	View
Sample	SRS256250 SRS256251 SRS256252	Control Iron Phosphate	SRA044892.sample.xml	Download	View
Study	SRP007763	Alternative Splicing	SRA044892.study.xml	Download	View
Experiment	SRX092046	control	SRA044892.experiment.xml	Download	View
Run	SRR331219 SRR331224	control iron	SRA044892.run.xml	Download	View

STUDY TITLE Genome-wide detection of context-sensitive alternative splicing in Arabidopsis roots
STUDY TYPE Other

Select your registered query files.

Queries with different Instrument models can't be selected together.

single paired all clear

	No.	Experiment ACCESSION	Sample ACCESSION	Run ACCESSION	STRAIN	Run_date	Read #	Read length	Instrument model	Layout
☐	1	SRX092046	SRS256250	SRR331219					ILLUMINA	single
☐	2	SRX092046	SRS256250	SRR331224					ILLUMINA	single

☐ : from metadata ☒ : Counted from query file (Read length is calculated from the first entry.)

DELETE NEXT

Tophat2 を選んで NEXT



Select Query Files → **Select Tools** → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation

Running Status

Selecting Tools for Basic Analysis of DDBJ ANNOTATION PIPELINE

BACK **NEXT**

Reference Genome Mapping

	Tool	Help	Version	Input data			Evaluation			Analysis		Output format			Comment
				Base space	Color space	Paired end	Depth	Coverage	Error rate	SNP	Indel	.gff	.bed	SAM	
☐	BLAT		34	✓					✓						Single-end analysis only
☐	bwa		0.6.1	✓		✓	✓	✓	✓					✓	
☐	Bowtie		0.12.7	✓	✓	✓	✓	✓	✓	✓				✓	
☐	TopHat		1.0.11	✓		✓	✓	✓	✓					✓	
☒	Bowtie2		2.0.0	✓	✓	✓	✓	✓	✓	✓				✓	For reads longer than about 50 bp, Bowtie2 is generally faster, more sensitive, and uses less memory than Bowtie1.
☐	Bowtie2		2.0.9	✓		✓	✓	✓	✓	✓				✓	

☐ de novo Assembly

Total limit = 22 Gbp

	Tool	Help	Version	Base space	Color space	Paired-end	MSS(WGS)	Comment
☐	SOAPdenovo		1.05	✓		✓		
☐	ABYSS		1.3.2	✓		✓		Maximum K-mer value is 64.
☐	Velvet		1.2.10	✓		✓	✓	We severe recommend when performing Velvet, total length of those reads is up to 22G bp.Maximum K-mer value is 64.
☐	Trinity		r2013-02-25	✓		✓		RNA-Seq De novo Assembly
☐	Platanus		1.2.2	✓		✓		
☐	HGAP		Protocol3 (v 2.2.0)					HGAP Pipeline for PacBio Sequence based on SMRT Analysis v2.2.0. For bax.h5 file only. (Beta version)

☐ Mapping Contigs by de novo Assemble to Reference Sequences

配列を選んで confirm, NEXT



Select Query Files → Select Tools → **Set QuerySet** → Set GenomeSet → Set Map Options → Confirmation →

Running Status

Generating Query Sets from Query Read Files

RESET BACK NEXT

Single analysis

Layout of single sequence.

5' 3'
Linker(1) Target Linker(2)

	Run ID/SESSION	Read length	Quality Score
☒	SRR331219 ->	bp	
☒	SRR331224 ->	bp	

confirm

QUERY SET

RESET BACK NEXT

ACCOUNT

login ID [guest]

Logout

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Genome (SNP/Short
Indel)
RNA-seq (Tag count)
ChIP-seq

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リファレンスに TAIR10 を選んでNEXT



ACCOUNT

login ID [guest]

Logout

ANALYSIS

Data setup

DRA Start

FTP upload

HTTP upload

DRA Import

Preprocessing Start

step-1

Preprocessing

Mapping /
de novo Assembly

step-2

Workflow

Genome (SNP/Short
Indel)
RNA-seq (Tag count)
ChIP-seq

JOB STATUS

step1.

Preprocessing

step1.

Mapping

step1.

***de novo* Assembly**

step2-All status

HELP

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Select Query Files

Select Tools

Set QuerySet

Set GenomeSet

Set Map Options

Confirmation

Running Status

Specifying Database of Reference Genome

RESET

BACK

NEXT

Major genome sets

Organisms

Arabidopsis thaliana

Genome sets

TAIR10

all check

all clear

☒ all.fa

☐ chr01.fa

☐ chr02.fa

☐ chr03.fa

☐ chr04.fa

☐ chr05.fa

☐ chrC.fa

☐ chrM.fa

User original sets

Download or upload reference

RESET

BACK

NEXT

option 変更なければそのままNEXT



Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → **Set Map Options** → Confirmation

Running Status

Setting for Reference Genome Mapping

BACK

NEXT

bowtie2

Set optional parameters of the single-end analysis

Step1) Convert reference sequence

bowtie2-build -f refgenome.fasta bt2-idx

Step2) Map

bowtie2 -q -p 4 -x bt2-idx -U query1.fastq(.fasta) -S out.sam -u out.unmapped

Step3) Convert the read alignment to .BAM format

samtools view -bS -o out.bam out.sam

Step4) Detect DNA polymorphism

Please choose one of the following.

☐	samtools pileup -c	-c -f refgenome.fasta out.bam bcftools view
☒	samtools mpileup -u -C50 -BQ0 -d10000000	-f refgenome.fasta out.bam bcftools view -bvcg - > out.var.raw.bcf
	bcftools view out.var.raw.bcf vcftools.pl varFilter -D10000	> out.var.flt.vcf

Step5) Analysis for Depth, Coverage

samtools sort -o out.bam out_sorted.bam

samtools pileup -c -f reference.fa out_sorted.bam > out.pileup

perl pileup_for_CoverageDepth.pl out.pileup reference.fa

* This command does not appear in the list.

Step6) Create assembled sequences in FASTA file from pileupped reads to [submit WGS division of DDBJ](#).

☐ perl getConsGeno_4pipeline.pl pileupFile Not to include insertion of pileupped reads. out_WGS.txt

* Threshold of insertion of pileupped reads: the quality threshold for indels <= 50 and allele constitutes 80% of pileupped reads.

BACK

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終了したらメールが来ます



Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation →

Running Status

Run Confirmation

BACK

Destination of mail

When the request is completed, the system sends an email to this address.

* Required

Resources will be deleted 60 days after submission.

Reference Genome Map [bowtie2]

Query sets

Query set1

PairedOrientation	RunAccession	RunAlias	RowLength	QualityScore1	QualityScore2
single	SRR331219	control			
single	SRR331224	iron			

genome sets

TAIR10

- all.fa

Command Options

bowtie2

Set optional parameters of the single-end analysis

Step1) Convert reference sequence

bowtie2-build -f refgenome.fasta bt2-idx

Step2) Map

bowtie2 -q -p 4 -x bt2-idx -U query1.fastq(.fasta) -S out.sam

Step3) Convert the read alignment to .BAM format

samtools view -bS -o out.bam out.sam

Step4) Detect DNA polymorphism

Please choose one of the following.

☐ samtools pileup -c -c -f refgenome.fasta out.bam | bcftools view

☐ samtools mpileup -u -C50 -BQ0 -d100000000 -f refgenome.fasta out.bam | bcftools view -bvc

☐ out var raw bcf

連絡先いれたら
RUN可能

guest は
run できません

pipeline_team@g.nig.ac.jp

Job finished : DDBJ Read Annotation Pipeline

宛先: 中村保一 <yn@nig.ac.jp>, CC: pipeline_report@g.nig.ac.jp

Message-Id: <599d04f7.4507630a.708a1.2bb9@mx.google.com>

Dear yaskaz,

Your request to DDBJ pipeline service has finished.
Please visit the web site to obtain analytical results.

Request ID: 27833

URL: <https://p.ddbj.nig.ac.jp/>

If you have troubles in this service, please write to

ACCOUNT

login ID [guest]

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「RUN を押した」と思ってください



Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation →

Running Status

Status - Mapping

Mapping Job

de novo Assembly Job

Preprocessing Job

Order

Sort by : ID Descending

☒ Show Only Your Own Job

Reload

Delete *

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	ID	UserID	Submission accession	P/S	Status	Tool	Read #	Read length	Genome size	Detail	Start time End time	Elapsed time
☐	5499	guest	DRA000001 DRR000001	P	complete	SOAP	9,977,388	36	121 M	View	2013-04-26 15:38:54	00:18:45
☐	5267	guest	DRA000001 DRR000001	P	complete	Bowtie2	9,977,388	36	121 M	View	2013-04-08 10:30:52	01:30:24
☐	5235	guest	---	S	error	BLAT	---	---	3,197 M	View	---	---
☐	5167	guest	DRA000001 DRR000001	P	complete	Maq	9,977,388	36	3,197 M	View	2013-03-14 11:31:11	00:31:26
☐	5137	guest	DRA000001 DRR000001	P	complete	TopHat	9,977,388	36	253 M	View	2013-03-05 09:53:55	00:46:30
☐	5050	guest	ERA000095 ID49_020708_2	S	complete	Bowtie	5,925,048	---	121 M	View	2013-02-15 12:26:14	00:47:03
☐	5050	guest	ERA000095 ID49_020708_2	P	complete	bwa	3,543,021	36	6 M	View	2013-02-07 22:21:37	00:26:48
☐	5055	guest	ERA000095 ID49_020708_2	P	complete	bwa	3,543,021	36	12 M	View	2013-02-07 20:33:31	00:47:42
☐	5050	guest	ERA000095	P	complete	bwa	3,543,021	36	6 M		2013-02-07 21:21:14	00:39:30

処理状況は
こちらから

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Detail view
[BACK](#)
Job info

ID
27833
Tool (Version)
TopHat2 (2.1.0)

RunAccession or Filename	Download	Read length	Alias
SRR331219	SRR331219.fastq.bz2	N.A. bp	control
SRR331224	SRR331224.fastq.bz2	N.A. bp	iron

Genome set
TAIR10

Chromosome
all.fa

Download modified queries
mergedout.fastq.gz (Original size 4.6 GB)

Download merged pileup file
Uniq.sam files have been merged if you specified 'uniq' option.
merged.var.ftt.vcf.gz (Original size 923.6 KB) merged.sam.gz (Original size 4.3 GB)

Download wgs file
out_WGS.fasta.gz (Original size 138.4 KB)

Position errors	Map ratio	Depth, Coverage
PDF download	total query # : 17,352,005 mapped query # : 15,596,984 map ratio : 89.886 %	coverage : 53774974 / 119482012 * 100 = 45.007 depth : 2452979062 / 53774974 = 45.616

Time

Wait time	Start time	End time
0: 3:35	2017-08-23 11:28:12	2017-08-23 13:30:44

all.fa	Command	Start time	End time	Log1	Log2	Result	MD5
Create Bowtie Index File	bowtie2-build -f all.fa refgenome	2017-08-23 11:28:13	2017-08-23 11:30:58	View	View		
Map reads with TopHat	tophat2 -p 4 -o result_directory refgenome mergedout.fastq	2017-08-23 11:30:58	2017-08-23 12:30:26		View	Download(992.0 MB)	MD5
Convert BAM to SAM	samtools view -h accepted_hits.bam > out.sam	2017-08-23 12:31:18	2017-08-23 12:32:00			Download(1488.0 MB)	MD5
Sort BAM File	samtools sort accepted_hits.bam out2	2017-08-23 12:35:16	2017-08-23 12:39:24	View		Download(891.3 MB)	MD5
Create BAM Index File	samtools index out2.bam	2017-08-23 12:40:05	2017-08-23 12:40:26			Download(110.4 KB)	MD5
Mpileup and Create BCF File	samtools mpileup -u -C50 -BQ0 -d10000000 -f all.fa out2.bam bcftools view -bvog - > non-uniq.var.bcf	2017-08-23 12:40:37	2017-08-23 12:59:42	View			
Filter BCF and Convert to VCF File	bcftools view non-uniq.var.bcf perl vcftools.pl varFilter -D10000 > out.var.ftt.vcf	2017-08-23 12:59:42	2017-08-23 12:59:53			Download(187.2 KB)	MD5
PileUp from Sorted BAM File For DepthCoverage	samtools pileup -c -f all.fa out2.bam > out.pileup	2017-08-23 13:00:04	2017-08-23 13:14:50				
Sort BAM File For MapRatio	samtools sort -n accepted_hits.bam out_sorted_by_name	2017-08-23 13:14:51	2017-08-23 13:21:54	View			
Convert BAM to SAMX For MapRatio	samtools view -hX out_sorted_by_name.bam > out_sorted_by_name.samX	2017-08-23 13:21:54	2017-08-23 13:22:46				
Convert BAM to SAMX For ErrorRate	samtools view -hX accepted_hits.bam > out.samX	2017-08-23 13:22:46	2017-08-23 13:23:27				

out2.bam
out2.bam.bai

マッピング結果を眺めるビューワ

IGV (<http://www.broadinstitute.org/igv/>)



Integrative
Genomics
Viewer

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 - File Formats
 - Release Notes
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- Contact

Search website

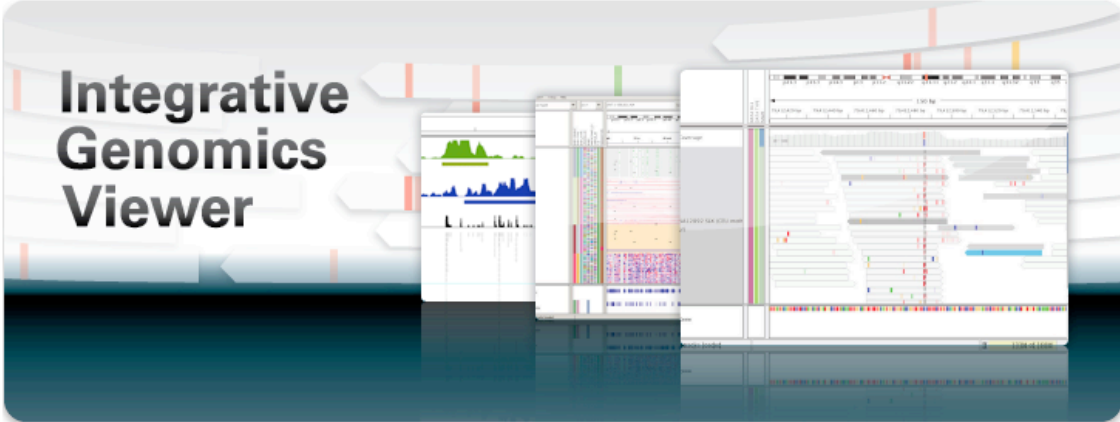
search

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[Cancer Program](#)



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Home



Integrative Genomics Viewer

What's New

December 18, 2012. IGV 2.2 has been released. See the [release notes](#) for more details.

April 20, 2012. IGV 2.1 has been released. See the [release notes](#) for more details.

April 19, 2012. See our new [IGV paper](#) in Briefings in Bioinformatics.

Overview



The **Integrative Genomics Viewer (IGV)** is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.

Citing IGV

To cite your use of IGV in your publication:

Helga Thorvaldsdóttir, James T. Robinson, Jill P. Mesirov. [Integrative Genomics Viewer \(IGV\): high-performance genomics data visualization and exploration](#). *Briefings in Bioinformatics* 2012.

James T. Robinson, Helga Thorvaldsdóttir, Wendy Winckler, Mitchell Guttman, Eric S. Lander, Gad Getz, Jill P. Mesirov. [Integrative Genomics Viewer](#). *Nature Biotechnology* 29, 24–26 (2011)

Funding

Development of IGV is made possible by funding from the [National Cancer Institute](#), the [National Institute of General Medical Sciences](#) of the [National Institutes of Health](#), and the [Howard Hughes Medical Institute](#).

1. Mapping

2. Assembly

インポート済のエントリから



Select Query Files → Select Tools → Set QuerySet → Set GenomeSet → Set Map Options → Confirmation

Running Status

Selecting Query Files

NEXT

FTP upload **Private DRA entry** Import public DRA Preprocessing HTTP upload

Metadata of the DRA entry.

Select a metadata : DRA000001

TYPE	ACCESSION	ALIAS	FILENAME	DL	VIEW
Submission	DRA000001	DRA000001	DRA000001.submission.xml	Download	View
Sample	DRS000001	DRS000001	DRA000001.sample.xml	Download	View
Study	DRP000001	DRP000001	DRA000001.study.xml	Download	View
Experiment	DRX000001	DRX000001	DRA000001.experiment.xml	Download	View
Run	DRR000001	DRR000001	DRA000001.run.xml	Download	View

STUDY TITLE Whole genome sequencing of Baillus subtilis subsp. natto BEST195

STUDY TYPE Whole Genome Sequencing

Select your registered query files.

Queries with different Instrument models can't be selected together.

single paired all clear

No.	Experiment ACCESSION	Sample ACCESSION	Run ACCESSION	STRAIN	Run_date	Read #	Read length	Instrument model	Layout
☐	DRX000001	DRS000001	DRR000001	strain BEST195	2008-09-13	9,977,388	36	ILLUMINA	paired

☐ : from metadata ☒ : Counted from query file (Read length is calculated from the first entry.)

DELETE

NEXT

納豆菌の
公開データが
インポート済

checkして

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login ID [guest]

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Indel)
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ChIP-seq

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Selecting Tools for Basic Analysis of DDBJ ANNOTATION PIPELINE

BACK NEXT

☐ Reference Genome Mapping

	Tool	Help	Version	Input data			Evaluation			Analysis		Output format			Comment
				Base space	Color space	Paired end	Depth	Coverage	Error rate	SNP	Indel	.gff	.bed	SAM	
☐	BLAT		34	✓					✓						Single-end analysis only
☐	bwa		0.6.1	✓		✓	✓	✓	✓					✓	
☐	Bowtie		0.12.7	✓	✓	✓	✓	✓	✓	✓				✓	
☐	TopHat		1.0.11	✓		✓	✓	✓	✓					✓	
☐	Bowtie2		2.0.0	✓	✓	✓	✓	✓	✓	✓				✓	For reads longer than about 50 bp, Bowtie2 is generally faster, more sensitive, and uses less memory than Bowtie1.
☐	TopHat2		2.0.9	✓		✓	✓	✓	✓					✓	

☒ de novo Assembly Total limit = 22 Gbp

	Tool	Help	Version	Base space	Color space	Paired-end	MSS(WGS)	Comment
☐	SOAPdenovo		1.05	✓		✓		
☐	ABYSS		1.3.2	✓		✓		Maximum K-mer value is 64.
☒	Velvet		1.2.10	✓		✓	✓	We severe recommend when performing Velvet, total length of those reads is up to 22G bp.Maximum K-mer value is 64.
☐	Trinity		r2013-02-25	✓		✓		RNA-Seq De novo Assembly
☐	Platanus		1.2.2	✓		✓		
☐	HGAP		Protocol3 (v 2.2.0)					HGAP Pipeline for PacBio Sequence based on SMRT Analysis v2.2.0. For bax.h5 file only. (Beta version)

☐ Mapping Contigs by de novo Assemble to Reference Sequences. The contigs will be aligned to reference genome.

	Tool	Comment
☒	BLAT	Single-end analysis only

BACK NEXT

velvet で
アセンブル
しましょう

配列とペア形式のセットを選択



Select Query Files → Select Tools → **Set QuerySet** → Set Ass. Options → Confirmation → Running Status

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ChIP-seq

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***de novo* Assembly**

step2-All status

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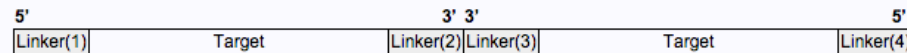
Contact Us.
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Generating Query Sets from Query Read Files

RESET BACK NEXT

Paired-end analysis

Layout of paired sequence. 5'-3' 3'-5'



Run	ACCESSION	Read length	Quality Score
☒	DRA0000001 -><-	36 bp	Read1 Read2

Set as Mate-P

Set as Pair-End

QUERY SET

RESET BACK NEXT

配列のセットの形式を選んで次へ



Select Query Files → Select Tools → **Set QuerySet** → Set Ass. Options → Confirmation → Running Status

ACCOUNT

login ID [guest]

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DRA Start

FTP upload

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DRA Import

Preprocessing Start

step-1

Preprocessing

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Workflow

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Indel)
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ChIP-seq

JOB STATUS

step1.

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***de novo* Assembly**

step2-All status

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TUTORIAL

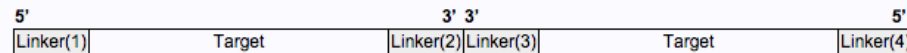
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Generating Query Sets from Query Read Files

RESET BACK NEXT

Paired-end analysis

Layout of paired sequence. 5'-3' 3'-5'



Run ACCESSION Read length Quality Score

Set as Mate-Pair Set as Pair-End

QUERY SET

Query set1

PairedOrientation	RunAccession	RunAlias	RowLength	QualityScore1	QualityScore2
paired	DRR000001	DRR000001	36		

RESET BACK **NEXT**

オプションのパラメータを選びます



Select Query Files → Select Tools → Set QuerySet → **Set Ass. Options** → Confirmation → Running Status

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Setting for De Novo Assembly

BACK NEXT

velvet

Set optional parameters of the paired-end analysis

Step1) Convert sequences

Shuffle the sequence.

perl shuffleSequences_fastq.pl query_1.fastq query_2.fastq shuffle_query_pe.fastq

Running velveth.

Velveth output_directory/ 23 -fastq -shortPaired shuffle_query_pe.fastq

Step2) Assembly

Velvetg output_directory/ -ins_length 300 -exp_cov auto

Step3) Set parameters of the CONFIG mapping tool

Step4) Create assembled sequences in FASTA file from pileupped reads to [submit WGS division of DDBJ.](#)

Set filtered length for contigs

☐ perl lengthfilter.pl pileupFile 100 out_WGS.txt

BACK **NEXT**

特になければ
そのまま次へ

連絡先をいれたら、RUN ボタン押すだけ！



Select Query Files → Select Tools → Set QuerySet → Set Ass. Options → **Confirmation** → Running Status

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Run Confirmation

BACK

Destination of mail

When the request is completed, the system sends an email to this address.

yn@nig.ac.jp

* Required

Resources will be deleted 60 days after submission.

Assembly [velvet]

Query sets

Query set1

PairedOrientation	RunAccession	RunAlias	RowLength	QualityScore1	QualityScore2
paired	DRR000001	DRR000001	36		

Assembly commands

velvet

Set optional parameters of the paired-end analysis

Step1) Convert sequences

Shuffle the sequence.

perl shuffleSequences_fastq.pl query_1.fastq query_2.fastq shuffle_query_pe.fastq

Running velvet.

Velvet output_directory/ 23 -fastq -shortPaired shuffle_query_pe.fastq

Step2) Assembly

Velvetg output_directory/ -ins_length 300 -exp_cov auto

Step3) Set parameters of the CONFIG mapping tool

Step4) Create assembled sequences in FASTA file from pileupped reads to [submit WGS division of DDBJ.](#)

Set filtered length for contigs

☐ perl lengthfilter.pl pileupFile 100 out_WGS.txt

BACK

連絡先いれたら
RUN可能

guest は
run できません

「RUN を押した」と思ってください



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Status - de novo Assembly

Mapping Job

de novo Assembly Job

Preprocessing Job

Order

Sort by : ID Descending

☐ Show Only Your Own Job

Reload

Delete *

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	ID	UserID	Submission accession	P/S	Status	Tool	Read #	Read length	Assembly detail	Mapping detail	Start time End time	Elapsed time
☐	20023	---	SRA020075 CGA1a	S	complete	SOAPdenovo	866,837	---			2015-11-18 18:49:44 2015-11-18 18:59:58	00:10:14
☐	20014	---	SK1_R1 by Pre	P	complete	SOAPdenovo	3,744,114	---			2015-11-18 10:36:14 2015-11-18 11:54:48	01:18:34
☐	20010	---	SK1_R1 by Pre	P	complete	Velvet	3,744,114	---			2015-11-18 08:39:52 2015-11-18 09:15:58	00:36:06
☐	20008	---	Aster-s1 Aster-s2	P	running	Trinity	100,829,136	---			2015-11-17 23:18:12 ---	
☐	20007	---	Aster-r1 Aster-r2	P	running	Trinity	91,276,607	---			2015-11-17 23:09:00 ---	
☐	20004	---	As-IS	P	complete	Trinity	46,700,225	---			2015-11-17 21:07:32 2015-11-18 17:46:39	20:39:07
☐	20004	---	As-IS	P	complete	Trinity	28,101,597	---			2015-11-17 21:03:17 2015-11-18 07:46:04	10:42:47
☐	20003	---	As-IR	P	complete	Trinity	18,598,628	---			2015-11-17 21:00:52 2015-11-18	06:57:37

処理状況は
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Detail view

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Job info

ID

4914

Tool (Version)

SOAPdenovo (1.05)

RunAccession or Filename	Download	Read length	Alias
DRR000001	DRR000001.fastq.gz DRR000001_1.fastq.gz DRR000001_2.fastq.bz2	36 bp	DRR000001

Download modified queries

- [DRR000001_1.fastq.gz](#) (Original size 1.7 GB)
- [DRR000001_2.fastq.gz](#) (Original size 1.7 GB)

Download wgs file

- [out_WGS.fasta.gz](#) (Original size 3.9 MB)

Assembly statistics

Contig # : 5,300
Total contig size : 4,138,179
Maximum contig size : 49,938
Minimum contig size : 24
N50 contig size : 13,255

アセンブル結果の
基本情報

Time

Wait time	Start time	End time
0: 1:22	2013-01-11 22:06:40	2013-01-11 22:13:40

Command	Start time	End time	Log1	Log2	Result	MD5
SOAPdenovo127mer all -s soapdenovo.conf -o output	2013-01-11 22:06:40	2013-01-11 22:12:28	View	View	Download(174.7 MB)	MD5

結果ファイル

BACK

パイプライン利用申請はこちら

<http://p.ddbj.nig.ac.jp> [DDBJ pipeline] で検索



DDBJ Read Annotation Pipeline

English

Japanese

DDBJ Read Annotation Pipelineは、次世代シーケンサ配列のクラウド型データ解析プラットフォームです。

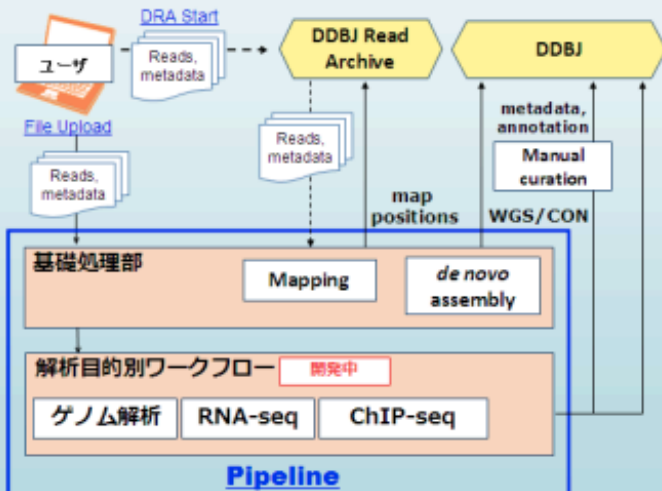
LOGIN

新規アカウント作成

ゲストとしてログイン

スパコンの
利用申請後に

Pipelineフローチャート



User ID:

Password:

Login

動作中JOBの確認

PipelineのIDをお持ちでない場合、[ゲストとしてログインすることができます。](#)

マニュアルおよびチュートリアル

- [日本語チュートリアル](#)
- [英語マニュアル](#)
- [DBCLS 統合TV チュートリアル 1 - 今日からはじめるDDBJ Read Annotation Pipeline](#)
- [DBCLS 統合TV チュートリアル 2 - DDBJ Read Annotation Pipelineによるde novo Assembly解析](#)

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29 Jul