



URGI Plant and Fungi Platform: Distributed Resources through GMOD Tools

PAG XXII – GMOD session

January 10 - 15, 2014





❖ Research Unit

- INRA unit (French National Institute for Agricultural Research)
- Plant breeding and Genetics Department
- Strong connexions with other plant INRA departments
- URGI Quality Management System (QMS) certified iso 9001:2008 since 2012

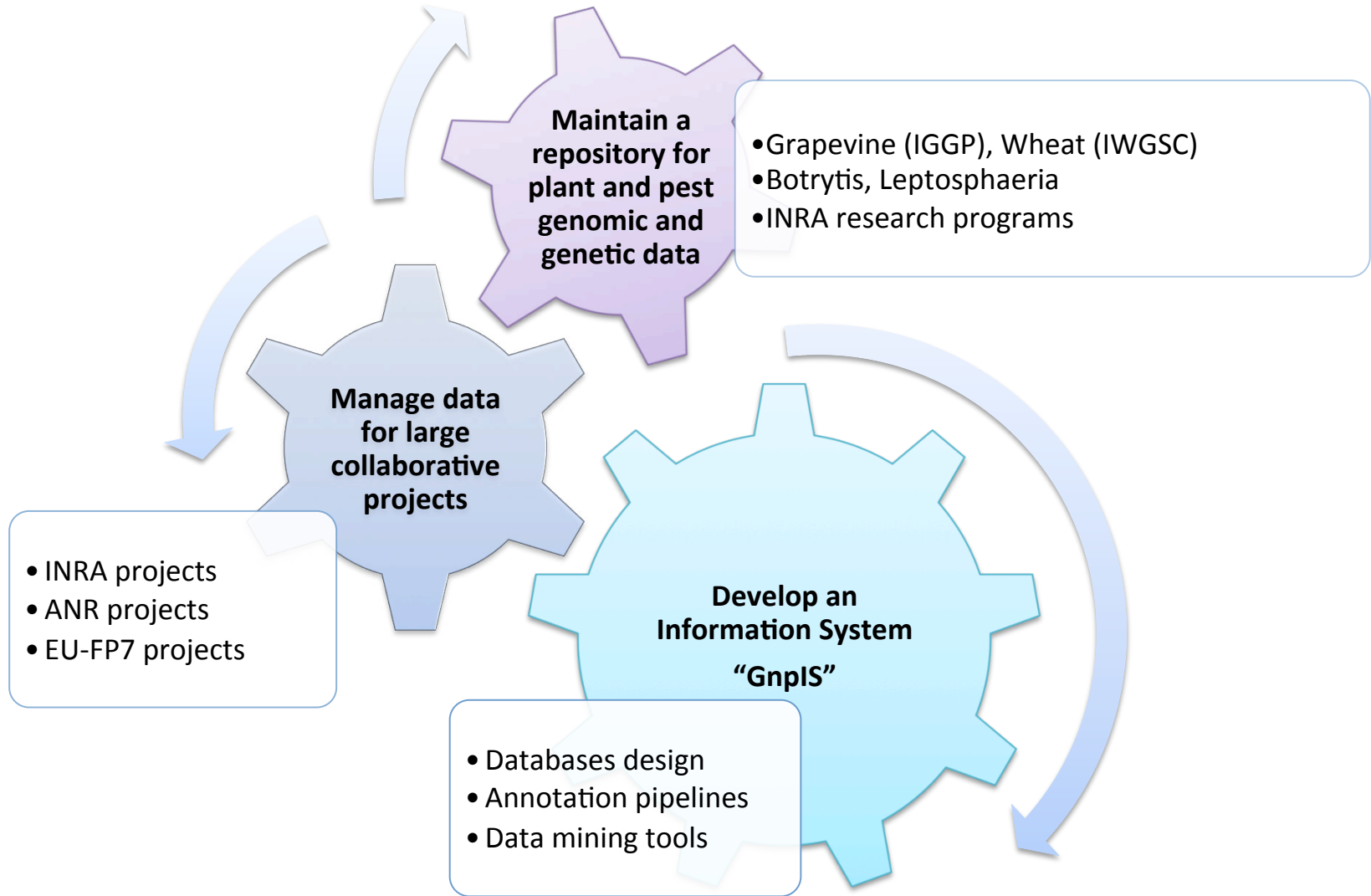


❖ Bioinformatic platform

- Member of the French National Network of Bioinformatic Platforms
- Member of the French Bioinformatic Infrastructure (IBF)

❖ Research

- Data integration
- Genome structure and dynamics



<https://urgi.versailles.inra.fr/gnpis>

Database tool

GnpIS: an information system to integrate genetic and genomic data from plants and fungi

Delphine Steinbach, Michael Alaux, Joelle Amselem, Nathalie Choisne, Sophie Durand, Raphaël Flores, Aminah-Olivia Keliet, Erik Kimmel, Nicolas Lapalu, Isabelle Luyten, Célia Michotey, Nacer Mohellibi, Cyril Pommier, Sébastien Reboux, Dorothee Valdenaire, Daphné Verdelet and Hadi Quesneville*

INRA, UR1164 URGI - Research Unit in Genomics-Info, INRA de Versailles, Route de Saint-Cyr, Versailles, 78026, France

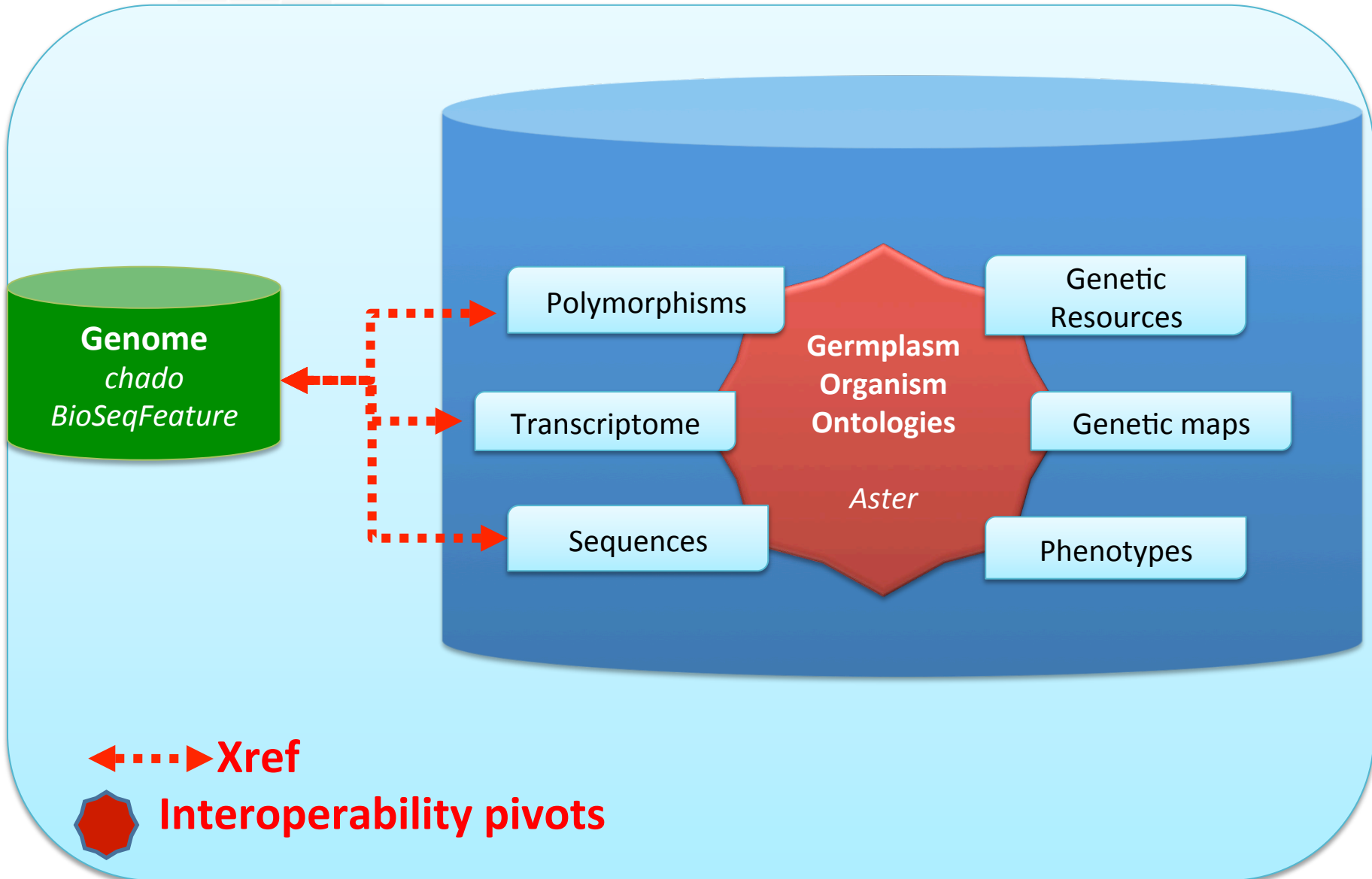
*Corresponding author: Tel: +33 1 30 83 30 08; Fax: +33 1 30 83 38 99; Email: hadi.quesneville@versailles.inra.fr

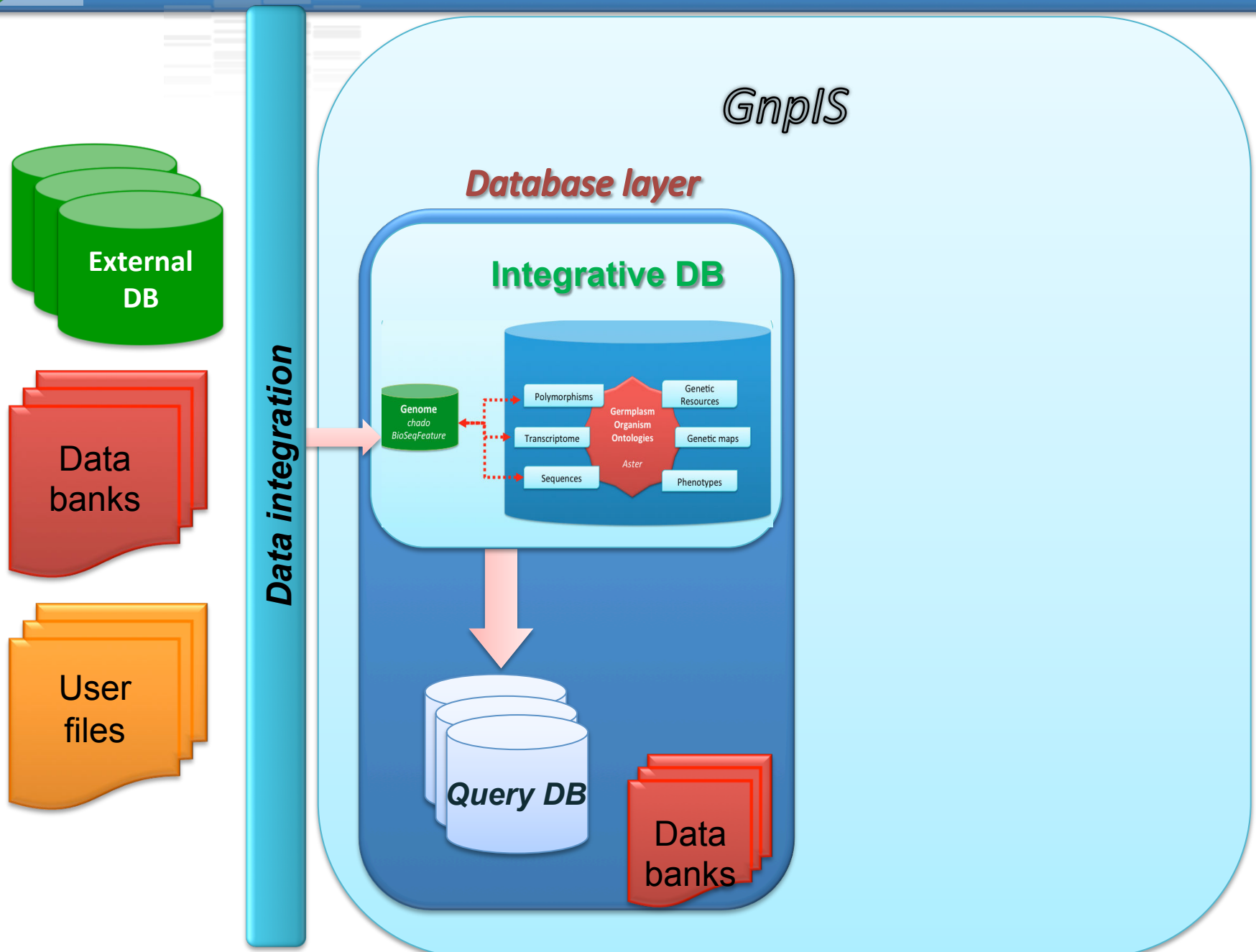
Submitted 5 March 2013; Revised 11 June 2013; Accepted 11 July 2013

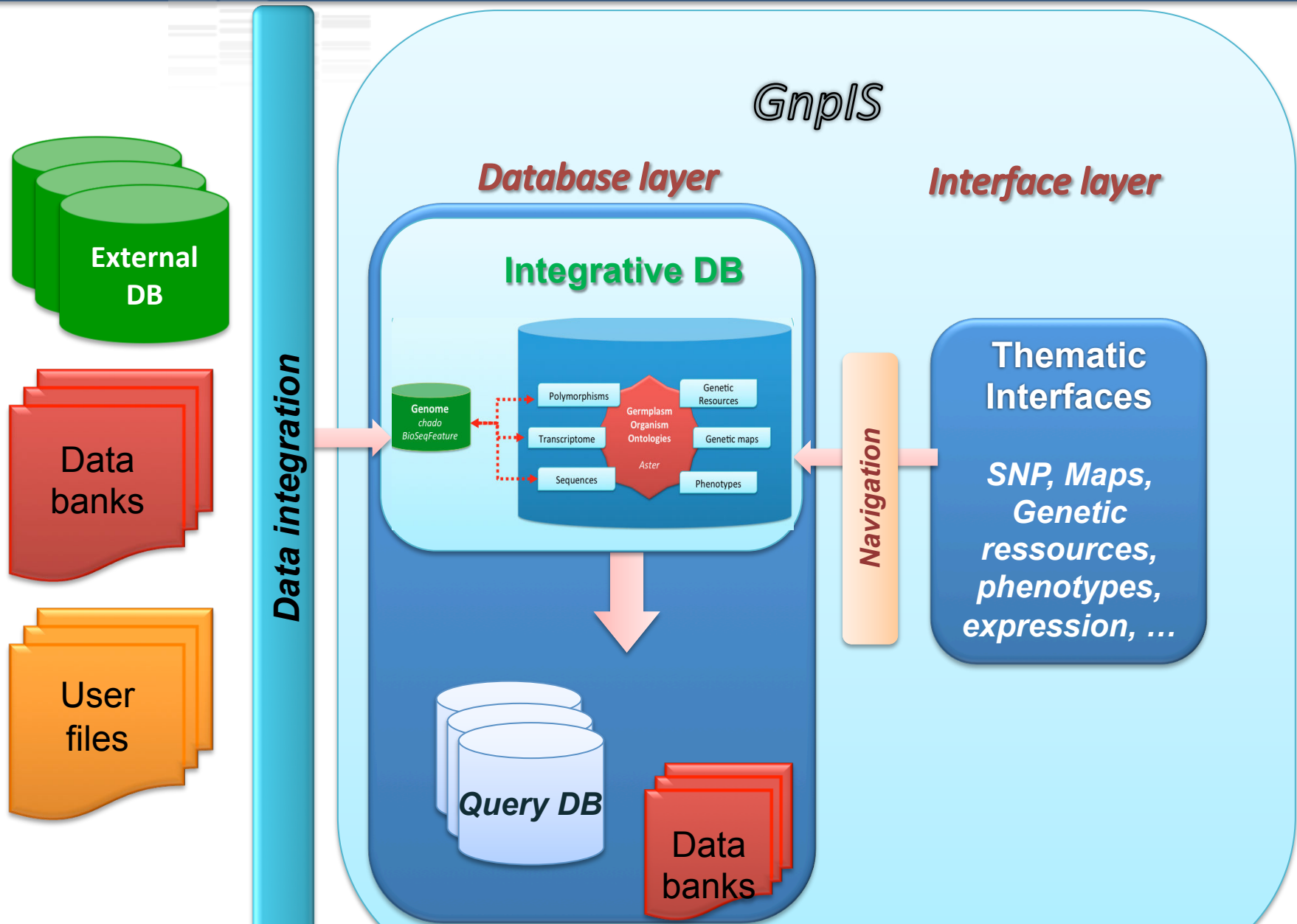
Citation details: Steinbach D, Alaux M, Amselem J, et al. GnpIS: an information system to integrate genetic and genomic data from plants and fungi. *Database*, Vol. 2013, Article ID bat058, doi:10.1093/database/bat058

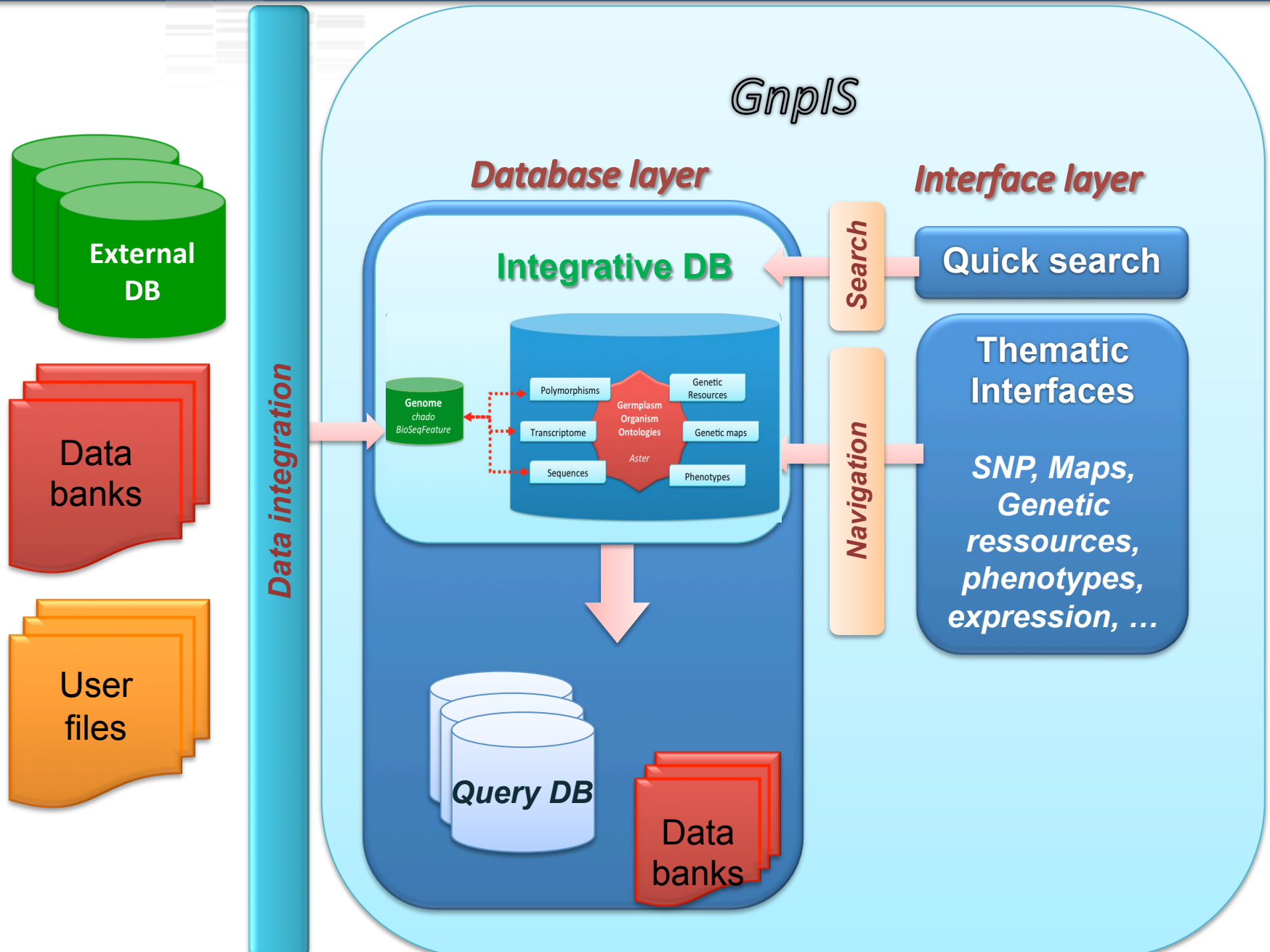
Data integration is a key challenge for modern bioinformatics. It aims to provide biologists with tools to explore relevant data produced by different studies. Large-scale international projects can generate lots of heterogeneous and unrelated data. The challenge is to integrate this information with other publicly available data. Nucleotide sequencing throughput has been improved with new technologies; this increases the need for powerful information systems able to store, manage and explore data. GnpIS is a multispecies integrative information system dedicated to plant and fungi pests. It bridges genetic and genomic data, allowing researchers access to both genetic information (e.g. genetic maps, quantitative trait loci, markers, single nucleotide polymorphisms, gemplasms and genotypes) and genomic data (e.g. genomic sequences, physical maps, genome annotation and expression data) for species of agronomical interest. GnpIS is used by both large international projects and plant science departments at the French National Institute for Agricultural Research. Here, we illustrate its use.

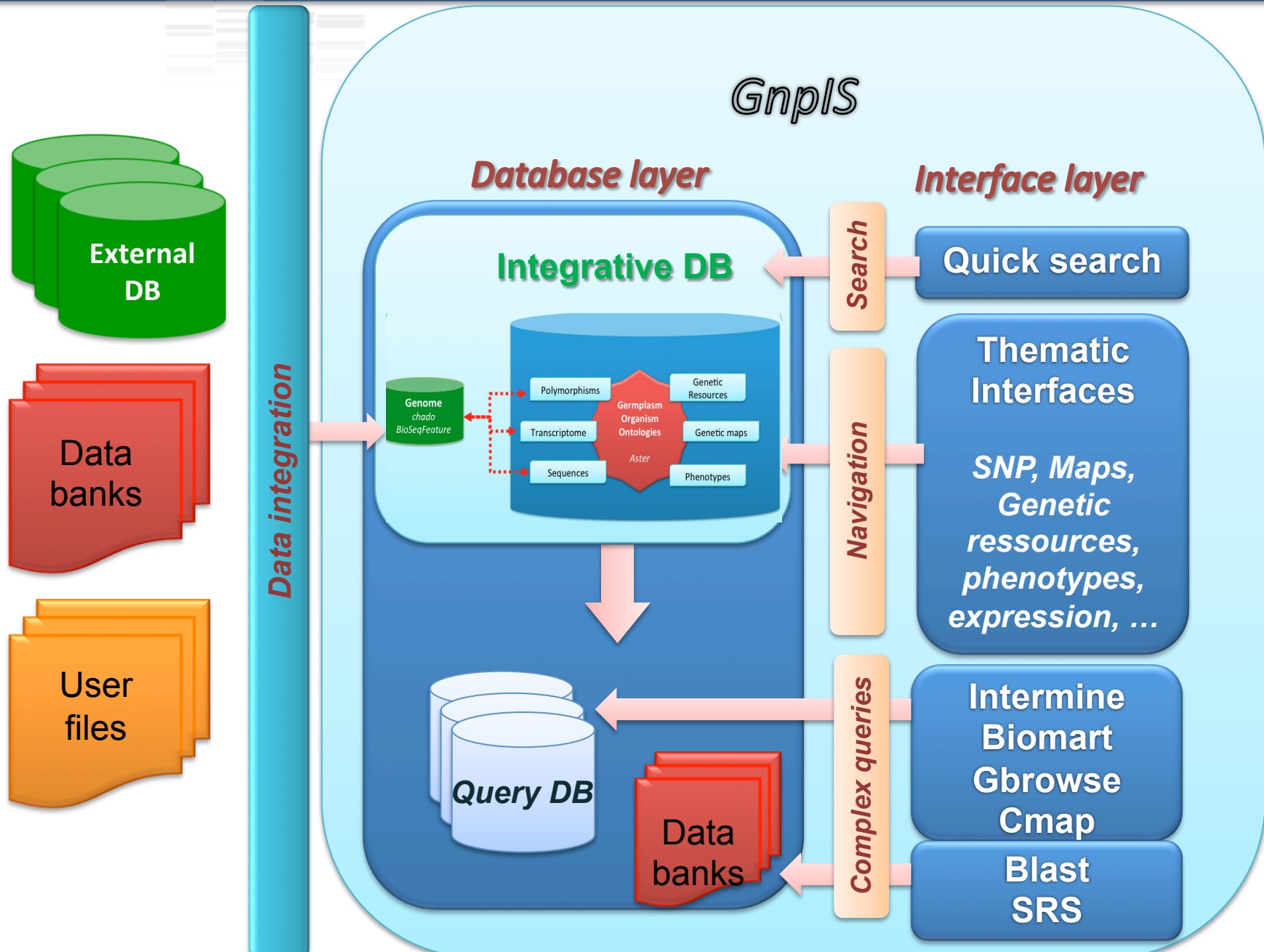
Database URL: <http://urgi.versailles.inra.fr/gnpis>











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Searches

- QUICK SEARCH
- ADVANCED TOOLS

Documentation

- USER GUIDE
- NEWS
- RELEASE NOTES

Data

- DATA SUBMISSION
- ARRAYS
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- TAXONS
- GENETIC MAPS
- SEQUENCES
- POLYMORPHISMS
- PHENOTYPES
- GENETIC RESOURCES
- PLANT SYNTENY

QUICK SEARCH

All species

SUBMIT

You can find the indexed data list [here](#).

Examples: [VVI](#), [VVIF52](#), [gene](#), [arabidopsis](#),
[AY109603](#), [Xwmc430](#)

ADVANCED TOOLS

[BIOMART](#)

[GALAXY](#)

[INTERMINE](#)

Genomes

Genome annotation data. GnpGenome.

Taxons

Taxonomic data.

Sequences

NGS projects description. GnpSeq.

Genetic maps

Genetic maps and QTLs. GnpMap.

Polymorphisms

Molecular polymorphism. GnpSNP.

Phenotypes

Phenotypic and environmental experiments. Ephesis.

Genetic resources

Plant genetic resources data. Siregal.

Arrays

Expression data. GnpArray.

Hybridization results

Information

Display results per page
 34 items found, displaying 1 to 10

Results

Address	Result number	Hybridization date	Description	Experiments	Array name	Design name	Bio materials	Protocol	Image	Raw acquisition data
	1	30/10/2003	T4_MM3_H301003	STUDY OF BOTRYTIS	BC2002_286/BCARRAY_MAI02	T4_MM3_M301003		HYBRIDPROTOCOL_BC_TH1		Access to Images
	2	10/07/2003	T4_MM3_H100703	STUDY OF BOTRYTIS	BC2002_46/BCARRAY_MAI02	T4_MM3_M100703		HYBRIDPROTOCOL_BC_TH1		Access to Images
	3	21/07/2003	T4_MM3_H210703	STUDY OF BOTRYTIS	BC2002_3C/BCARRAY_MAI02	T4_MM3_M210703		HYBRIDPROTOCOL_BC_TH1		Access to Images
	4	27/10/2003	T4_MM3_H271003	STUDY OF BOTRYTIS	BC2002_24C/BCARRAY_MAI02	T4_MM3_M271003		HYBRIDPROTOCOL_BC_TH1		Access to Images
	5	10/10/2003	T4_MM3_H101003	STUDY OF BOTRYTIS	BC2002_256/BCARRAY_MAI02	T4_MM3_M101003		HYBRIDPROTOCOL_BC_TH1		Access to Images
	6	07/10/2003	T4_MM3_H071003	STUDY OF B						Access to Images
	7	30/10/2003	T4_Sider3_H301003	STUDY OF B						Access to Images
	8	10/10/2003	T4_Sider3_H101003	STUDY OF B						Access to Images

Transcriptome

Searches

- QUICK
- ADVANCED

Documents



INFORMATIO

Landmark or Region: Reports & Analysis:

Data Source: ScrollZoom: Show 10 kbp Flip

Overview

Details

- Contigs: boFu4_2030
- Gene (Manual curation): boFu4_1977_rgw47549
- CDS (Eugene prediction): boFu4_T146290.1, boFu4_T146270.1, boFu4_T146270.1, boFu4_T146290.1
- Gene (Eugene prediction): boFu4_T146290.1, boFu4_T146270.1
- Feature (BT4 param): boFu4_T146290.1, boFu4_T146270.1
- IRNA prediction
- B. cinerea ESTs (Sim4): boFu4_T146290.1, boFu4_T146270.1
- B. cinerea EST contigs (Sim4)
- S. sclerotiorum ESTs
- Nimblegen oligos
- Fungal proteins 10 heat hits (Blastx)
- Swissprot

Genome Annotation

Vegetables

Large crops

Model plants

Fruits

Genetic resources

SUBMIT

Genetic resources

GALAXY

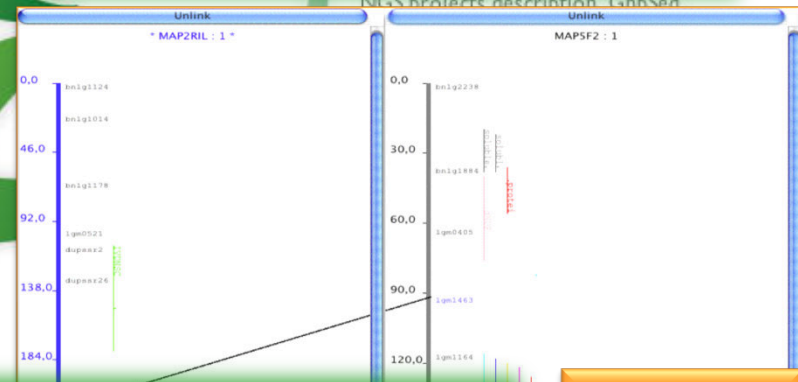
Lot

Add all lots from the collections:

Add lots from accession

Lot id	Lot number	Taxon
123	P0038-E13	Prunus domestica L.
124	P0062-D1	Prunus domestica L.
125	P0068-O11	Prunus domestica L.
126	P0072-E8	Prunus insititia L.
127	P0107-I5	Prunus domestica L.

Phenotypes



Genetic Maps

SNP card

IRSA

SNP details

Name: rs2228729

Ref. Sequences:

Source: dbSNP

Internal references

Database	Reference name	Reference value
Rice and Arabidopsis Genome Browser	SNP name	rs2228729
TAIR v7 G. Browser with SNPs data	SNP name	rs2228729

External references

Database	Reference name	Reference value
dbSNP	accession number	rs2228729

SNP complements

SNP type: SNP

Variation: A/G

SNP sequences

5' flanker on ref.seq.: >r2228729 chr22:100000000-100000000

3' flanker on ref.seq.: >r2228729 chr22:100000000-100000000

Polymorphisms



CHADO

Bio::DB





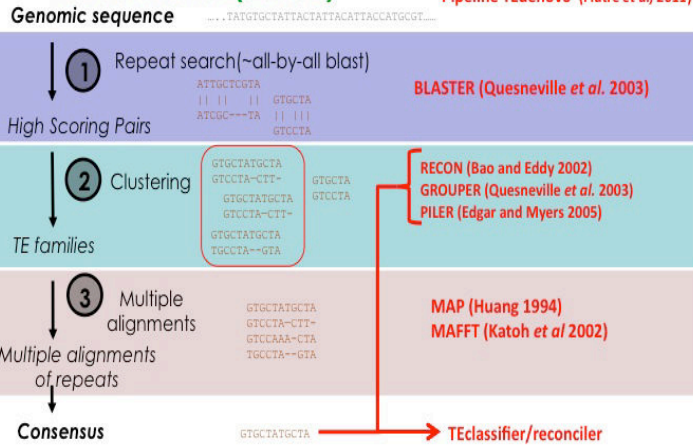
Genome annotation pipelines and data workflows

Transposable Elements (TEs) Detection & Annotation Pipelines REPET package

<http://urgi.versailles.inra.fr/Tools/REPET>

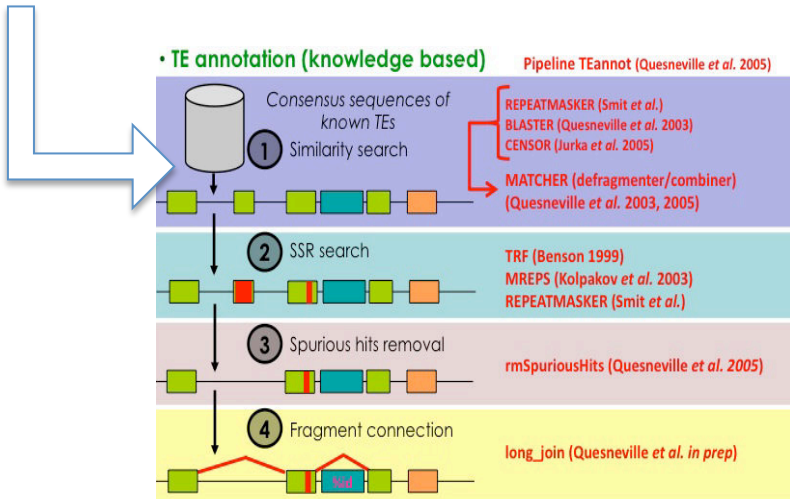
TE identification (de novo)

Pipeline TEde novo (Flutre et al, 2011)



TE annotation (knowledge based)

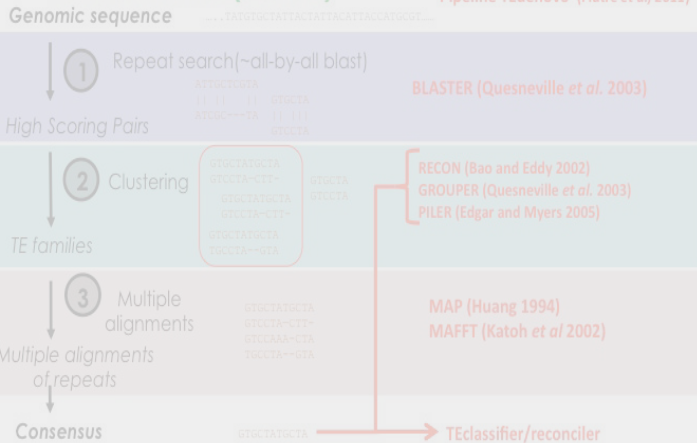
Pipeline TEannot (Quesneville et al. 2005)



Transposable Elements (TEs)
 Detection & Annotation Pipelines
 REPET package
<http://urgi.versailles.inra.fr/Tools/REPET>

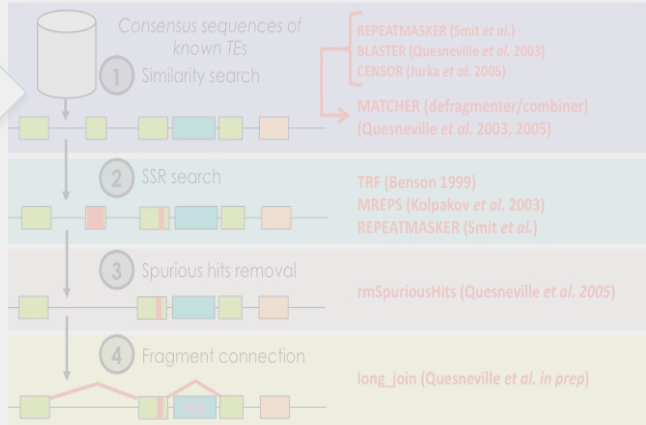
• TE identification (de novo)

Pipeline TEde novo (Flutre et al., 2011)

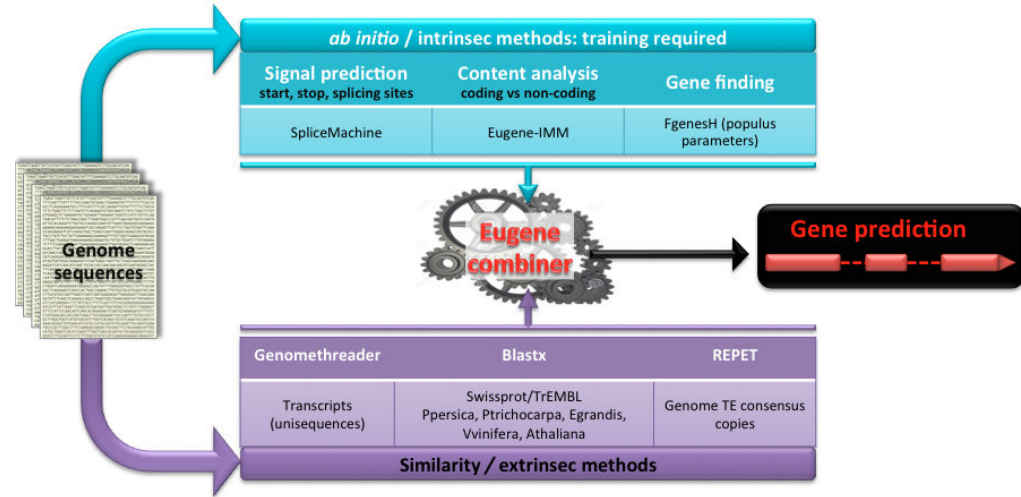


• TE annotation (knowledge based)

Pipeline TEannot (Quesneville et al. 2005)



Gene prediction
 Eugene (Species training @ URGI)
<http://eugene.toulouse.inra.fr/>

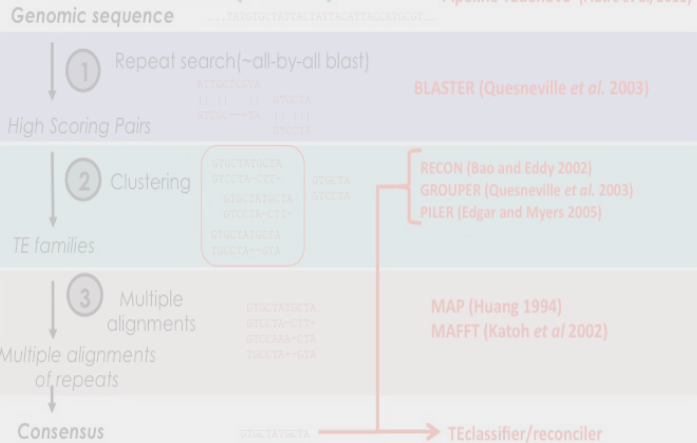


Transposable Elements (TEs) Detection & Annotation Pipelines REPET package

<http://urgi.versailles.inra.fr/Tools/REPET>

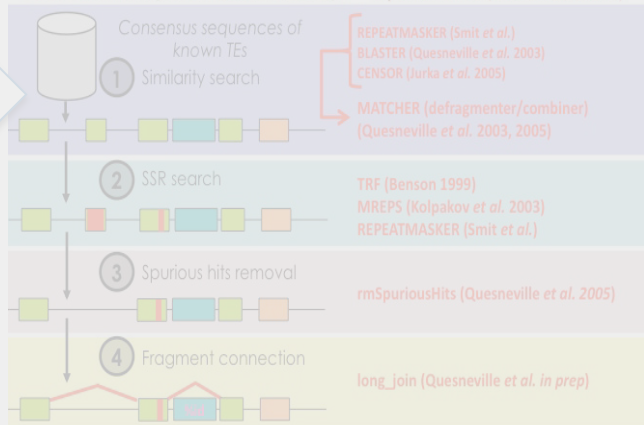
TE identification (de novo)

Pipeline TEde novo (Flutre et al, 2011)

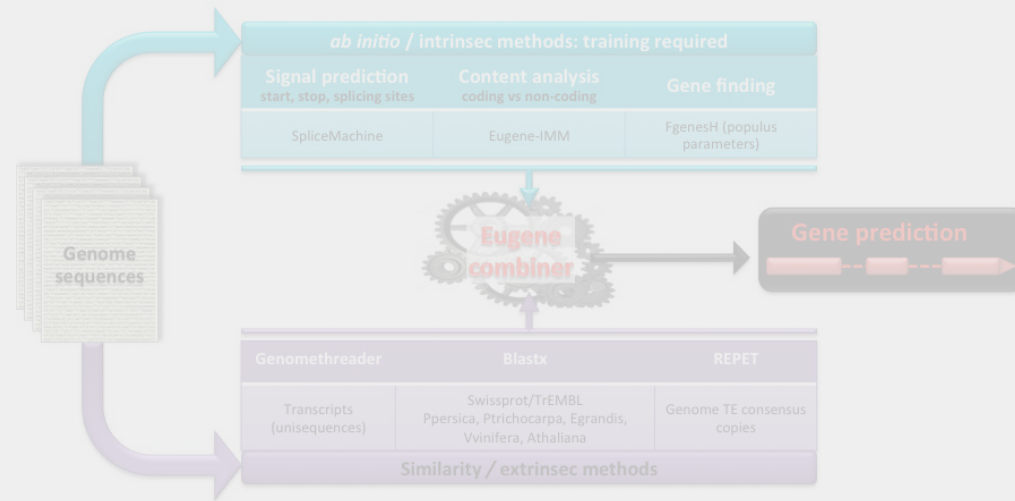


TE annotation (knowledge based)

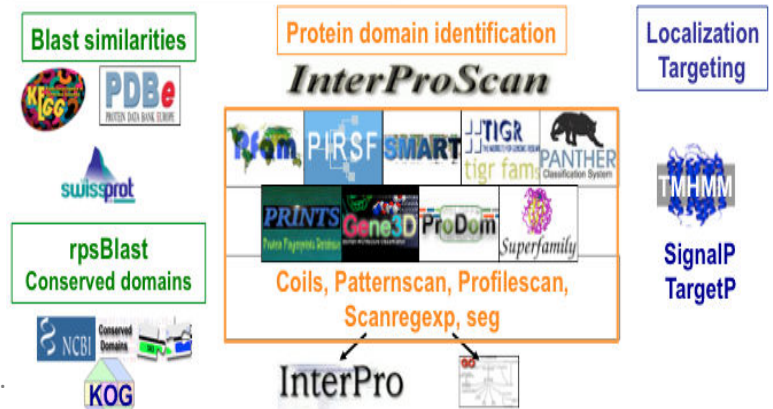
Pipeline TEannot (Quesneville et al. 2005)

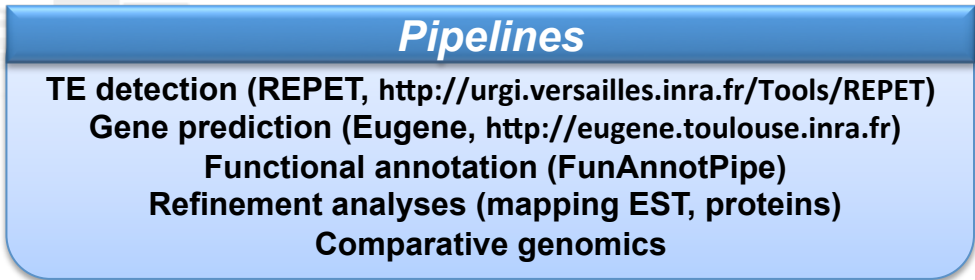


Gene prediction Eugene (Species training @ URGI) <http://eugene.toulouse.inra.fr/>



Gene functional annotation





Annotation pipelines :

- TE detection
- Gene prediction
- Functional annotation
- Refinement analyses

Ref = scaffold

~50 GGB

Ref = Predicted protein

Botrytis cinerea T4 automated functional gene annotation: Vue de 752 bp depuis BotuT4_P000020.1, positions 1 à 753

Synteny between genomes

Synteny between Botrytis cinerea T4/B05.10 and Sclerotinia sclerotiorum

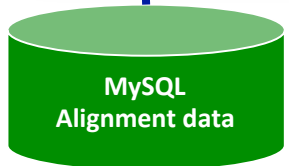
MERCATOR/MAVID based Clustering and alignments

4 GGB_syn



GBrowse

Gbrowse_Syn



Annotation pipelines :

- TE detection
- Gene prediction
- Functional annotation
- Refinement analyses

Ref = supercontig

Botrytis cinerea T4 genome annotation: Vue de 23

Ref = Predicted protein

Botrytis cinerea T4 automated functional gene annotation: Vue de 752 bp depuis BofuT4_P000020.1, positions 1 à 753

Synteny between genomes

Synteny between Botrytis cinerea TA/B05.10 and Sclerotinia sclerotiorum

MERCATOR/MAVID based Clustering and alignments



GRS
Genome Report System

Homepage GnpGenome FunAnnot Browser Blast Downloads

Botrytis cinerea T4 GRS

Functional annotation

BofuT4P143000035001

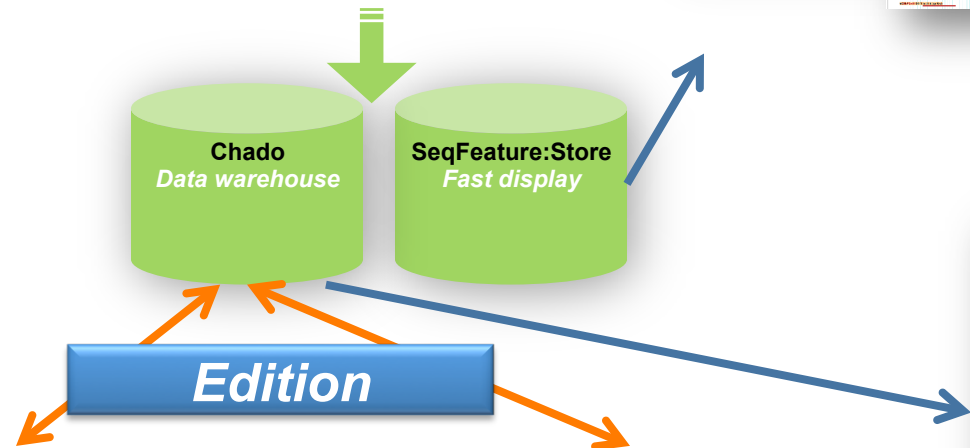
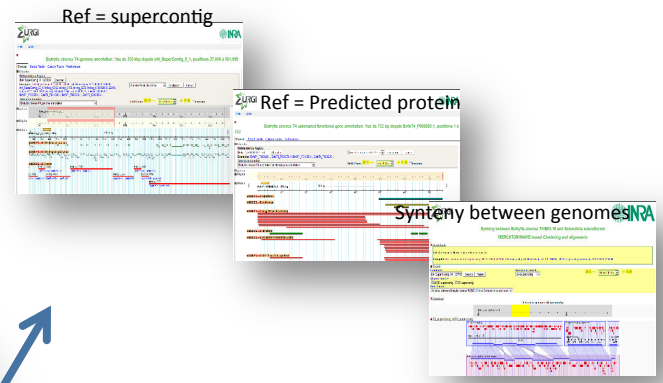
- + Gene Identifier
- + DlxKrefs
- + Domain/Motif (Interproscan results)
- + Localization / Targeting
- + Predicted function
- + Blast based analysis
- + Other analysis
- + Functional Gbrowse
- + Structural Gbrowse
- + Genome Mapping at gene locus
- + Current manual annotation
- + Ortholog

[Link to edition](#)

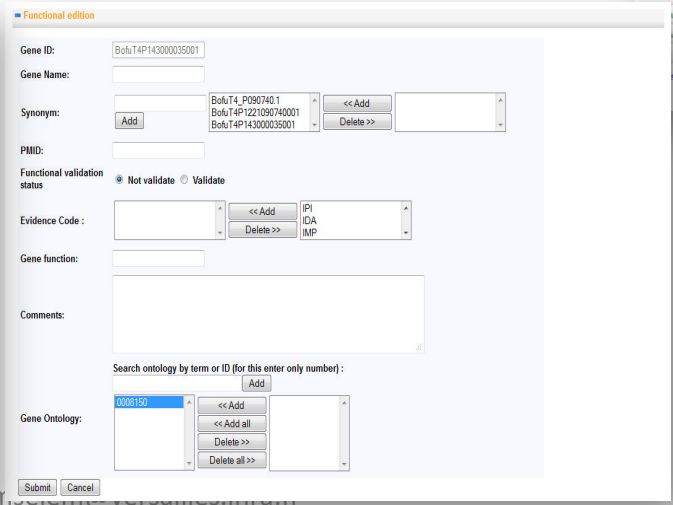
ZURGI GNPannot Genome Report System - copyright INRA 2012

Annotation pipelines :

- TE detection
- Gene prediction
- Functional annotation
- Refinement analyses



Apollo : manual structural edition **GRE : manual functional edition**



Annotation pipelines :

- TE detection
- Gene prediction
- Functional annotation
- Refinement analyses

All species: kinase

General information Botrytis (B0510) functional Botrytis (T4) functional Botrytis (T4) genome
Leptosphaeria genome Leptosphaeria functional Poplar genome Sclerotinia functional

Vitis (12X) genome Wheat 3B genome

EST libraries (1150) **EST samples (1145)**

AB014801	*****	AB012854	*****
AB014802	*****	AB012855	*****
AB042270	*****	AF122888	*****
AF122888	*****	AF122889	*****
AF122889	*****	AF042272	*****
AF042272	*****	AF122890	*****
AF122890	*****	AF122891	*****
AF122891	*****	AF122892	*****
AF122892	*****	AF122893	*****
AF122893	*****	AF122894	*****
AF122894	*****	AF122895	*****
AF122895	*****		

All species:

Quick search
Lucene™ based

ZURGI (Biolinformatics)

Database: Please restrict your query using criteria below

Species: Botrytis cinerea
Feature:

Reference Feature:

Feature Type:

Program:

Accession:

Analysis source name:

DB Name:

DB Ref Accession:

Category Term:

Advanced search
Biomart

Galaxy / ZURGI

Analysis tool:

History:

Tools:

Galaxy features:

Galaxy tools:

Galaxy workflows:

Galaxy datasets:

Galaxy history:

Galaxy preferences:

Galaxy help:

Galaxy
Data mining
and analysis



Ref = supercontig

ZURGI Ref = Predicted protein

Synergy between genomes

ZURGI

GRS : Genome Report System

Botrytis cinerea T4 GRS

Functional annotation

Gene Identifier

DBKeys

Domain/KEGG (preprocess results)

Localization / Targeting

Predicted function

Rise based analysis

Other analysis

Structural Genome

Genome Mapping at gene locus

Current manual annotation

Apollo : manual structural edition

GRE : manual functional edition

Zoom: x10 x2 x5 x1

Type	Name	Range	Score
TE	TE1	21815-16697	0.0
TE	TE2	21820-19763	0.0
TE	TE3	21812-19763	0.0
TE	TE4	21796-19763	0.0
TE	TE5	21813-19763	0.0
TE	TE6	21813-19763	0.0

Intermine
Data
integration

Botrytis cinerea T4 genome annotation: 13 kbp from

bt4_SupSuperContig_110r_56_1:216,500..229,499

Browser [Select Tracks](#) [Custom Tracks](#) [Preferences](#)

Search

Landmark or Region:

Examples: bt4_SuperContig_0_1:40000..60000,
 bt4_SuperContig_0_1:380000..390000, bt4_SuperContig_63_1, bt4ctg_0012,
 bt4ctg_0198, bt4ctg_0200, BofuT4_T004650,
 BofuT4_P001590.

Data Source

Overview
 bt4_SupSuperContig_110r_56_1

Region
 120k 130k

Details
 216k 217k

BofuT4_T146250.1

Feature Infos :

Length 1566

Ref: start..end bt4_SupSuperContig_110r_56_1:
215944..217509

cds_length 1566

quality regular

[GnpArray](#)

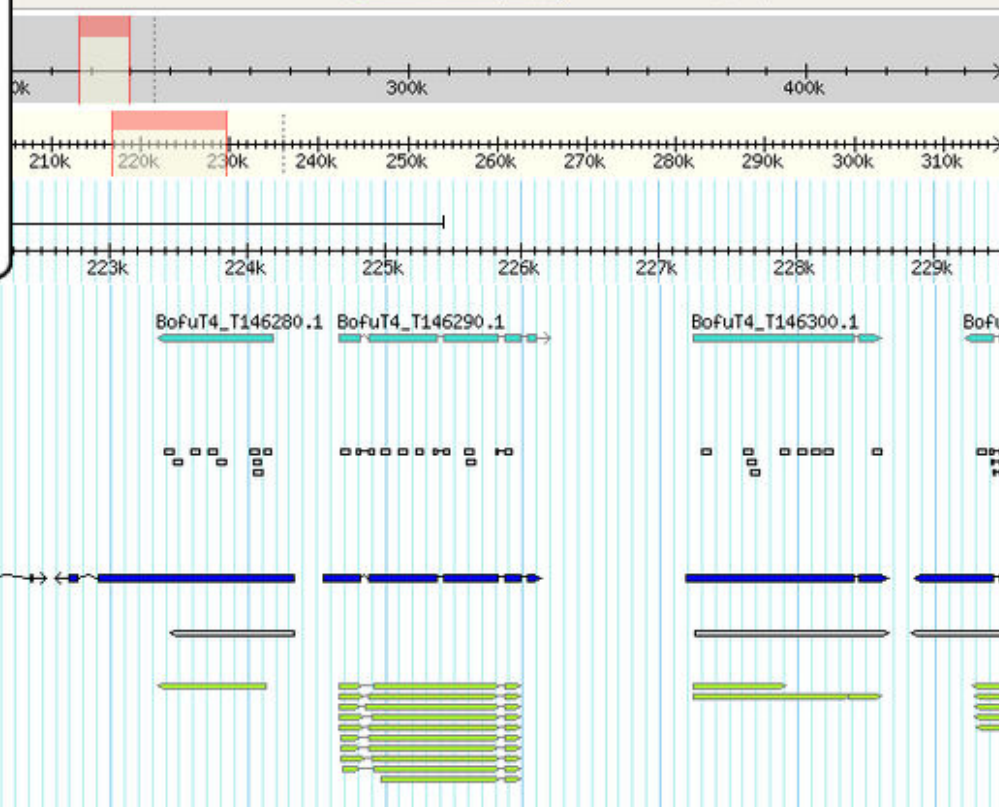
[Gene Report](#)

[Gene Domain Browser](#)

[Zoom to this feature](#)

[Detailed Report](#)

Scroll/Zoom:



The genomic map displays several tracks aligned to a 13 kbp region of the Botrytis cinerea T4 genome. The top track shows CDS (Eugene prediction) with genes BofuT4_T146250.1, BofuT4_T146260.1, BofuT4_T146270.1, BofuT4_T146280.1, BofuT4_T146290.1, BofuT4_T146300.1, and BofuT4_T146310.1. Below this are tracks for Nimblegen oligos (represented by small squares), Gene (Eugene prediction) (represented by blue arrows), B. cinerea EST contigs (Sim4) (represented by grey bars), and Fungal protein 10 best hits (Blastx) (represented by green bars). The x-axis at the bottom is labeled with genomic coordinates from 216k to 229k.

BofuT4_T146250.1

Feature Infos :
Length 1566
Ref: start..end bt4_SupSuperContig_110r_56_1: 215944..217509
cds_length 1566
quality regular

[GnpArray](#)
[Gene Report](#)
[Gene Domain Browser](#)
[Zoom to this feature](#)
[Detailed Report](#)

Botrytis cinerea T4 automated functional gene annotation: 520 bp from BofuT4_P146250.1:1..521

Browser [Select Tracks](#) [Custom Tracks](#) [Preferences](#)

Search
Landmark or Region:
BofuT4_P146250.1:1..5 Search
Download Decorated FASTA File Configure... Go
Examples: BofuT4_P000020.1, BofuT4_P000570.1, BofuT4_P015510.1, BofuT4_P000200.1.
Data Source Botrytis cinerea T4 automated functional gene annotation
Scroll/Zoom: << < - Show 521 bp + > >> Flip

Overview
Region
Details
BofuT4_P146250.1: 521 bp
200 bp

coils
FPRINTScan
gene3d
HMMPanther
HMMPfam
CDD 10 best hits (rpsBlast)
Swissprot 10 best hits (Blastp)

Select Tracks Clear highlighting

Gbrowse: functional domains, Motifs

BofuT4_T146250.1

Feature Infos :
 Length 1566
 Ref: start..end bt4_SupSuperContig_110r_56_1:
 215944..217509
 cds_length 1566
 quality regular

- GnpArray
- Gene Report
- Gene Domain Browser
- Zoom to this feature
- Detailed Report

Genome Report System

BofuT4_P146250.1

- [+ Gene Identifier](#)
- [+ DbXrefs](#)
- [- Domain/Motif \(Interproscan results\)](#)

Analysis	Domains	Begin	End	Length	Gene Ontology	Cross Ref	InterPro
HMMPFam	PF07690	38	432	395	GO:0055085 transmembrane transport	---	IPR011701
HMMSmart					no results		
HMMTigr					no results		
HMMPanther	PTHR10074:SF57	490	520	31			none
	PTHR10074:SF57	275	443	169			none
	PTHR10074:SF57	32	228	197			none
	PTHR10074	490	520	31			none
	PTHR10074	275	443	169			none
superfamily	SSF103473	21	512	492			none
	coils				no results		
gene3d					no results		
seg					no results		
profiles	PS50850	34	517	484			none
PRODOM					no results		
FPRINTScan	PR01036	157	181	25	GO:0015520 tetracycline:hydrogen antiporter activity	---	IPR001411
					GO:0015904 tetracycline transport	---	
					GO:0016021 integral to membrane	---	
					GO:0046677 response to antibiotic	---	
FPRINTScan	PR01036	127	147	21	GO:0046677 response to antibiotic	---	IPR001411
					GO:0015520 tetracycline:hydrogen antiporter activity	---	
					GO:0015904 tetracycline transport	---	
					GO:0016021 integral to membrane	---	
					GO:0015904 tetracycline transport	---	
					GO:0016021 integral to membrane	---	

BofuT4_T146250.1

Feature Infos :

Length 1566
 Ref: start..end bt4_SupSuperContig_110r_5
 215944..217509
 cds_length 1566
 quality regular

[Log in](#)

My basket 0 item(s)

Preferences

All species

Main

● HOME

Global queries

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Queries

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 ● ARRAY DESIGNS
 ● PROTOCOLS
 ● PROCESS
 ● GENE LISTS

Documentation

● USER GUIDE
 ● FAQ
 ● GNPARRAY NEWS
 ● RELEASE NOTES

Data

● DATA SUBMISSION

- [GnpArray](#)
- [Gene Report](#)
- [Gene Domain Browser](#)
- [Zoom to this feature](#)
- [Detailed Report](#)

GnpArray / Gene - BofuT4_P146250.1

GENE DETAILS

Name : BofuT4_P146250.1
Associated sequences : BofuT4_P146250.1

ASSOCIATED GENE LISTS

- [Bc1 - In planta Unchanged \(Botrytis-B0510 : in vitro vs in planta\[sunflower\] 48h\)](#)
- [Bc2 - deltaBcYOH1 Unchanged \(Botrytis B0510 : WT vs deltaBcYOH1 on solid grape juice\)](#)
- [Bc3 - deltaBcVEL1 Down \(Botrytis B0510 : WT vs deltaBcVEL1 in planta \[French bean\] 48h\)](#)
- [Bc4 - deltaBcLTF1 Unchanged \[in darkness condition\] \(Botrytis B0510 : WT vs deltaBcLTF1, on solid CM in darkness\)](#)
- [Bc5 - deltaBcLTF1 Unchanged \[in light stimulus condition\] \(Botrytis B0510 : WT vs deltaBcLTF1, on solid CM with a light stimulus\)](#)
- [Bc6 - Light Unchanged \[in WT background\] \(Botrytis B0510 WT : dark vs light stimulus, on solid CM\)](#)
- [Bc7 - Light Unchanged \[in deltaBcLTF1 background\] \(Botrytis B0510 deltaBcLTF1 : dark vs light stimulus, on solid CM\)](#)

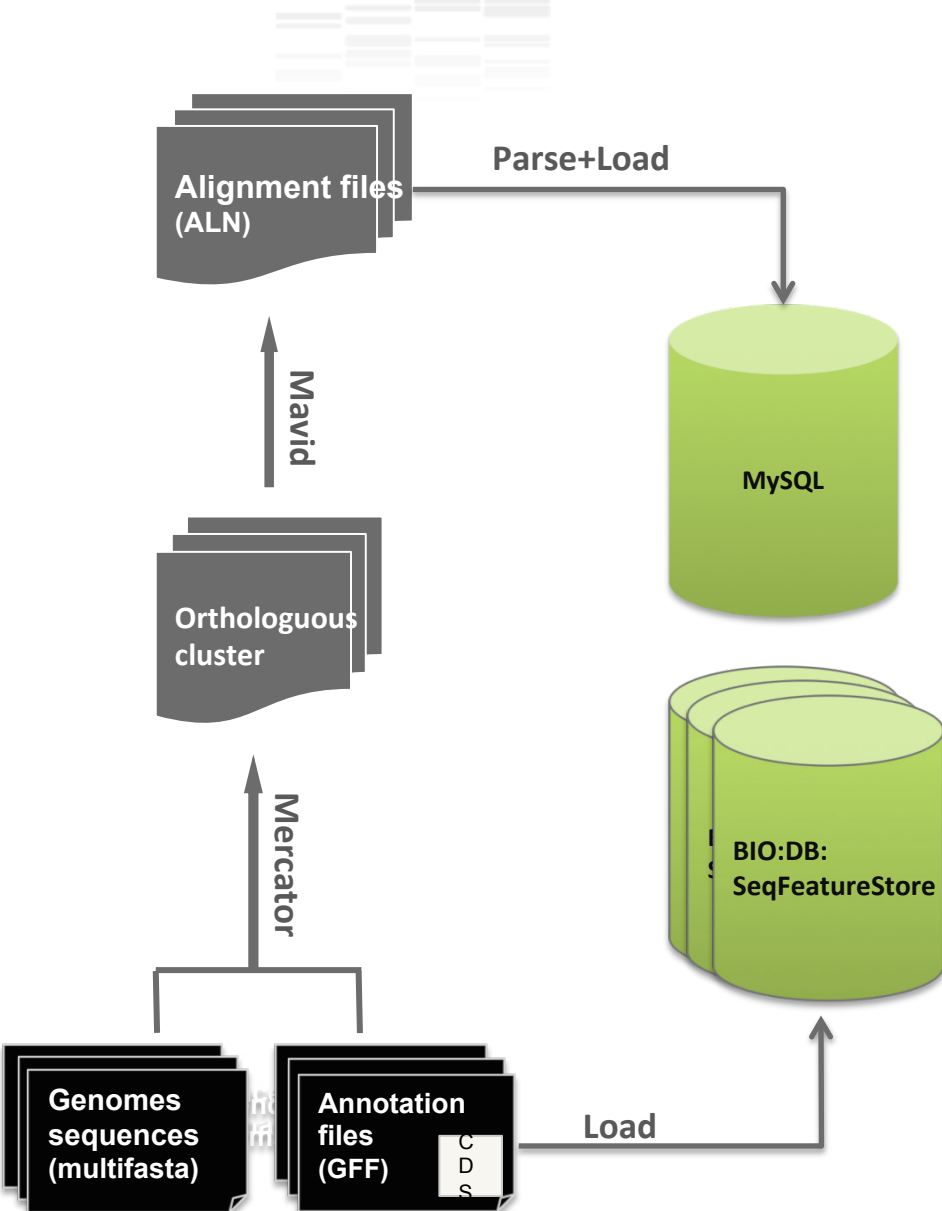
ASSOCIATED REPORTERS

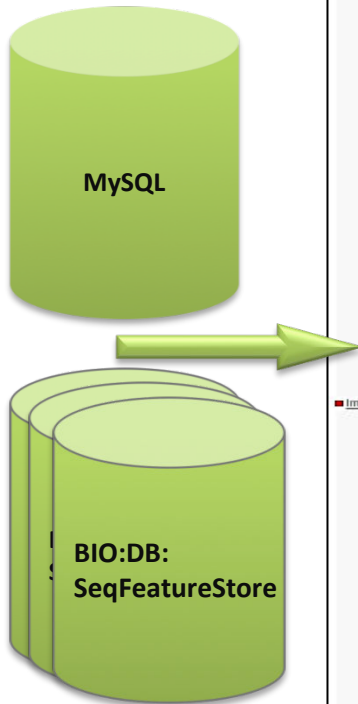
- [botrytisP00148361](#)
- [botrytisP00148362](#)
- [botrytisP00148363](#)
- [botrytisP00148365](#)
- [botrytisP00148366](#)
- [botrytisP00148367](#)
- [botrytisP00148368](#)
- [botrytisP00148369](#)
- [botrytisP00148370](#)

NORMALIZED DATA

Gene list	FOLD CHANGE	Normalized_Variance	pVALUE
Bc1 - In planta Unchanged (Botrytis-B0510 : in vitro vs in planta[sunflower] 48h)	1.3000	0.6000	0.0024
Bc2 - deltaBcYOH1 Unchanged (Botrytis B0510 : WT vs deltaBcYOH1 on solid grape juice)	1.9307	-	0.1604
Bc3 - deltaBcVEL1 Down (Botrytis B0510 : WT vs deltaBcVEL1 in planta [French bean] 48h)	-4.0699	-	0.0288
Bc4 - deltaBcLTF1 Unchanged [in darkness condition] (Botrytis B0510 : WT vs deltaBcLTF1, on solid CM in darkness)	1.1200	-	0.6710

GnpArray:Gene card





Leptosphaeria complex synteny

MERCATOR/MAVID based Clustering and alignments

Leptosphaeria species complex synteny

Instructions

Search

Landmark: Search Genome to Search:

Aligned Species:
Imaculans_omr19 Imbiglobosa_ibcn65 Imaculans_wa74 Imbiglobosa_b3.5 Imaculans_ibcn84 Imaculans_nz14

Data Source: Synteny between Leptosphaeria complex genomes Display Mode: Three species/panel Click to show all species in one panel

Overview
Imbiglobosa_b3.5, Imbiglobosa_ibcn65

Imbiglobosa_b3.5
Leb1_B3-5_scaffol00019
400k 500k 600k

Imaculans_jn3 (reference)
Im_SuperContig_0_v2
0k 100k 200k 300k 400k

Imbiglobosa_ibcn65 (reference)
Leb1_IBCN65_scaffol00016
0k 100k 200k 300k

Imaculans_ibcn84, Imaculans_nz14

Imaculans_ibcn84
Lem1_IBCN84_scaffol00008
0k 100k 200k 300k

Imaculans_jn3 (reference)
Im_SuperContig_0_v2
0k 100k 200k 300k 400k

Imaculans_nz14 (reference)
Lem1_NZ14_scaffol00015
0k 100k 200k 300k 400k

Imaculans_omr19, Imaculans_wa74

Imaculans_omr19
Lem1_OMR19_scaffol00005
0k 100k 200k

Imaculans_wa74
Lem1_WA74_scaffol00002
0k 100k 200k

Imaculans_jn3 (reference)
Im_SuperContig_0_v2
0k 100k 200k 300k 400k



Data querying and browsing system

Quick search: whole GnpIS indexed

Hibernate search + Lucene™ full-featured text search engine library

Genomes DBs: Chado: 8; MySeqFeature: 5; BioDbGFF: 5

[Log in](#)

Searches

- QUICK SEARCH
- ADVANCED TOOLS

Documentation

- USER GUIDE
- NEWS
- RELEASE NOTES

Data

- DATA SUBMISSION
- ARRAYS
- GENOMES
- TAXONS
- GENETIC MAPS
- SEQUENCES
- POLYMORPHISMS
- PHENOTYPES
- GENETIC RESOURCES
- PLANT SYNTENY

QUICK SEARCH All species

VVIF52

You can find the indexed data list [here](#).

Examples: [VVI](#), [VVIF52](#), [gene](#), [arabidopsis](#), [AY109603](#), [Xwmc430](#)

ADVANCED TOOLS

[BIOMART](#)

[GALAXY](#)

Taxons

Taxonomic data.

Sequences

NGS projects description. GnpSeq.

Genetic maps

Genetic maps and QTLs. GnpMap.

Polymorphisms

Molecular polymorphism. GnpSNP.

Phenotypes

Phenotypic and environmental experiments. Ephesis.

Genetic resources

Plant genetic resources data. Siregal.

Arrays

Expression data. GnpArray.

All species

General information | Botrytis (B0510) functional | Botrytis (T4) functional | **Botrytis (T4) genome**

Leptosphaeria genome | Leptosphaeria functional | Poplar genome | Sclerotinia functional

Vitis (12X) genome | Wheat 3B genome

Features (777)

- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SupSuperContig 1... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★
- bt4 SuperContig 0 1 ... ★★★★★

1 2 3 4 5 6 7 8 9 10 | 777 items found, dis

File - Help

Botrytis cinerea T4 genome annotation: 1.91 kbp from bt4_SuperContig_0_1:283,677..285,587

Browser

Search

Landmark or Region:

Examples: bt4_SuperContig_0_1:40000..60000, bt4_SuperContig_0_1:380000..390000, bt4_SuperContig_63_1, bt4ctg_0012, bt4ctg_0198, bt4ctg_0253, bt4ctg_0106:12010..22010, bt4ctg_0111:3858..6529, BofuT4_T004650.1, BofuT4_P000020.1, BofuT4_P000570.1, BofuT4_T005350.1, BofuT4_G005380.1.

Annotate Restriction Sites

Feature Infos:

Length	1911
Ref.start.end	bt4_SuperContig_0_1:283677..285587
cds_length	1815
quality	regular

[GnpArray](#)
[Gene Report](#)
[Gene Domain Browser](#)
[Zoom to this feature](#)
[Detailed Report](#)

Overview

Region

Details

CDS (Eugene prediction)
 Gene (Eugene prediction)
 B. cinerea EST contigs (Sim4)
 Fungal protein 10 best hits (Blastx)

Show 1.911 kbp

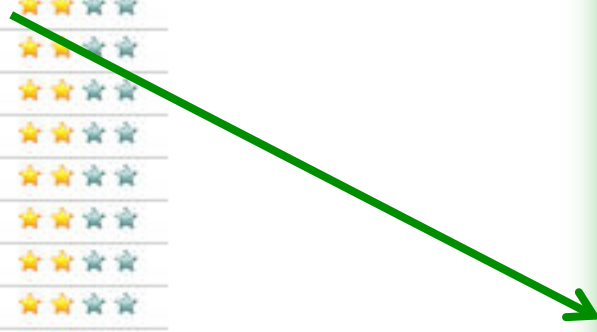
All species

- General information
- Botrytis (B0510) functional
- Botrytis (T4) functional**
- Botrytis (T4) genome
- Leptosphaeria genome
- Leptosphaeria functional
- Poplar genome
- Sclerotinia functional
- Vitis (12X) genome
- Wheat 3B genome

Features (748)

- [BofuT4_P021730.1](#) ★★☆☆
- [BofuT4_P001150.1](#) ★★☆☆
- [BofuT4_P121170.1](#) ★★☆☆
- [BofuT4_P101510.1](#) ★★☆☆
- [BofuT4_P064960.1](#) ★★☆☆
- [BofuT4_P066270.1](#) ★★☆☆
- [BofuT4_P045740.1](#) ★★☆☆
- [BofuT4_P140650.1](#) ★★☆☆
- [BofuT4_P132610.1](#) ★★☆☆
- [BofuT4_P035290.1](#) ★★☆☆

1 2 3 4 5 6 7 8 9 10 | 748 items found, displaying 1 to 10 | Display



Homepage GnpGenome FunAnnot Browser Blast Downloads

Botrytis cinerea T4 GRS

Functional annotation

BofuT4_P021730.1

- + Gene Identifier
- + DbXrefs
- Domain/Motif (Interproscan results)

Analysis	Domains	Begin	End	Length	Gene Ontology	Cross Ref	InterPro
HMMPFam	PF05224	175	338	164			none
HMMSmart					no results		
HMMTigr					no results		
HMMPanther					no results		
superfamily	SSF49417	90	340	251	GO:0003700 transcription factor activity GO:0045449 regulation of transcription	---	IPR008967
coils					no results		
gene3d					no results		
seg					no results		
profilescan					no results		
PRODOM					no results		
FPRINTScan					no results		
patternscan					no results		


---> : Genes sharing the same GOID

- + Localization / Targeting
- + Predicted function
- + Blast based analysis

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Searches 

- QUICK SEARCH
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- NEWS
- RELEASE NOTES

Data 

- DATA SUBMISSION
- ARRAYS
- GENOMES
- TAXONS
- GENETIC MAPS
- SEQUENCES
- POLYMORPHISMS
- PHENOTYPES
- GENETIC RESOURCES
- PLANT SYNTENY

Genomes

Genome annotation data. GnpGenome.

Taxons

Taxonomic data.

Sequences

NGS projects description. GnpSeq.

Genetic maps

Genetic maps and QTLs. GnpMap.

Polymorphisms

Molecular polymorphism. GnpSNP.

Phenotypes

Phenotypic and environmental experiments. Ephasis.

Genetic resources

Plant genetic resources data. Siregal.

QUICK SEARCH

All species

VVIF52

SUBMIT

You can find the indexed data list [here](#).

Examples: [VVI](#), [VVIF52](#), [gene](#), [arabidopsis](#),
[AY109603](#), [Xwmc430](#)

ADVANCED TOOLS

BIOMART

GALAXY



for advanced and filtered queries

ZURGI

New Count Results URL XML Perl Help

Dataset

[None selected]

✓ - CHOOSE DATABASE -

- Genetic maps (markers, Qtls), Polymorphisms (snps, genes), Genetic and Phenotype resources with Genes annotations
- Grapevine 8x, structural annotation with Genetic maps (genetic markers..)
- Grapevine 12x, structural and functional annotation with Genetic maps (genetic markers..)
- Wheat, structural annotation with Genetic maps (genetic markers..) and Polymorphisms (snps)
- Arabidopsis Thaliana TAIRV10, genes functional annotation
- Zea mays ZmB73, genes functional annotation
- Populus trichocarpa, genes functional annotation
- Populus trichocarpa, genes functional annotation V2.0
- Botrytis cinerea T4, genes functional annotation**
- Botrytis cinerea B05
- Sclerotinia sclerotiorum
- Leptosphaeria maculans

New Count Results

Dataset 2137 / 366639 Entries

Botrytis_functional_annotation

Filters

Feature Type : signal_peptide

Start > : 30

Program : signalp

Start < : 1

End < : 30

Analysis source name : polypeptide_iprscan_annotation

Attributes

Reference Feature

Feature Type

Start (-1)

End

Program

Library

HIT

Description

Analysis source name

DB Xref DB

DB Xref Accession

Ontology Term

Please restrict your query using criteria below

URL XML Perl Help

Feature

Reference Feature (% for Wildcard). Example: BofuT4_P0001%

Feature Type

match

polypeptide

polypeptide_domain

signal_peptide

Feature Name (% for wildcard). Example: BofuT4_P009%

Feature Location

Start <

1

Start >

30

End <

End >

HIT (% for wildcard). Example: 3b95_%

Description (% for wildcard). Example: %Euchromatic%

Ontology Term (% for wildcard). Example: %kinase%

Program

signalp

Analysis source name

polypeptide_iprscan_annotation

polypeptide_vs_Cdd_profiles

polypeptide_vs_Kog_profiles

polypeptide_vs_kegg

polypeptide_vs_pdb

DB Xref DB

DB:PFAM

DB:PIR

DB:PRINTS

DB:PRODOM

DB:PROFILE

DB Xref Accession (% for wildcard)

Signal_peptide

Start<2

End<30

signalp

ZURGI

New Count Results URL XML Perl Help

Dataset [None selected] - CHOOSE DATABASE -
 Genetic maps (markers, Qtls), Polymorphisms (snps, genes), Genetic and Phenotype resources with Genes annotations
 Grapevine 8x, structural annotation with Genetic maps (genetic markers..)

Dataset 2137 / 366639 Entries
 Botrytis_functional_annotation

Filters

Feature Type : signal_peptide
 Start > : 30
 Program : signalp
 Start < : 1
 End < : 30
 Analysis source name : polypeptide_iprscan_annotation

Attributes

Reference Feature
 Feature Type
 Start (-1)
 End
 Program
 Library
 HIT
 Description
 Analysis source name
 DB Xref DB
 DB Xref Accession
 Ontology Term

Export all results to Unique results only

Email notification to

View rows as Unique results only

Reference Feature	Feature Type	Start (-1)	End	Program	Library	HIT	Description	Analysis source name	DB Xref DB	DB Xref Accession
BofuT4_P000030.1	signal_peptide	0	25	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000070.1	signal_peptide	0	18	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000200.1	signal_peptide	0	18	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000210.1	signal_peptide	0	19	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000260.1	signal_peptide	0	19	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000270.1	signal_peptide	0	19	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000290.1	signal_peptide	0	17	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000390.1	signal_peptide	0	17	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000440.1	signal_peptide	0	19	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
BofuT4_P000590.1	signal_peptide	0	3	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp

Results

iprscan_annotation

DB Xref DB

DB Xref Accession (% for wildcard)

DB:PFAM
 DB:PIR
 DB:PRINTS
 DB:PRODOM
 DB:PROFILE

Dataset 2137 / 366639 Entries
 Botrytis_functional_annotation

Filters

Feature Type : signal_peptide
 Start > : 30
 Program : signalp
 Start < : 1
 End < : 30
 Analysis source name : polypeptide_iprscan_annotation

Attributes

Reference Feature
 Feature Type
 Start (-1)
 End
 Program
 Library
 HIT
 Description
 Analysis source name
 DB Xref DB
 DB Xref Accession
 Ontology Term

Export all results to Unique results only

Email notification to

View rows as Unique results only

Reference Feature
BofuT4_P000030.1
BofuT4_P000070.1
BofuT4_P000200.1
BofuT4_P000210.1
BofuT4_P000390.1
BofuT4_P000440.1
BofuT4_P000590.1

Link to GRS

Botrytis cinerea T4 GRS

Functional annotation

BofuT4_P000210.1

- [+ Gene Identifier](#)
- [+ Domain/Motif \(Interproscan results\)](#)
- [+ Localization / Targeting](#)

Analysis	Start	End	Length	Location	Reliability class	Signal Peptide CutOff	Mitochondrion CutOff
targetp	1	19	19	Secretory pathway 3		0.820	0.301

Analysis	Start	End	Length
signalp	1	19	18
tmhmm	Not result		

- [+ Blast based analysis](#)
- [+ Other analysis](#)
- [+ Functional Gbrowse](#)
- [+ Structural Gbrowse](#)
- [+ Genome Mapping at gene locus](#)
- [+ Current manual annotation](#)

The screenshot shows the ZURGI bio:mart web interface. At the top left is the ZURGI logo. Below it is a navigation bar with buttons for 'New', 'Count', and 'Results'. On the right side of the navigation bar are icons for 'URL', 'XML', 'Perl', and 'Help'. The main content area is divided into two sections. On the left, under the heading 'Dataset', it says '[None selected]'. On the right, a dropdown menu is open, titled '- CHOOSE DATABASE -'. The menu lists several databases, with 'Grapevine 12x, stuctural and functional annotation with Genetic maps (genetic markers..)' highlighted by an orange box. The other databases listed are: Genetic maps (markers, Qtls), Polymorphisms (snps, genes), Genetic and Phenotype resources with Genes annotations; Grapevine 8x, stuctural annotation with Genetic maps (genetic markers..); wheat, stuctural annotation with Genetic maps (genetic markers..) and Polymorphisms (snps); Arabidopsis Thaliana TAIRV10, genes functional annotation; Zea mays ZmB73, genes functional annotation; Populus trichocarpa, genes functional annotation; Populus trichocarpa, genes functional annotation V2.0; Botrytis cinerea T4, genes functional annotation; Botrytis cinerea B0510, genes functional annotation; Sclerotinia sclerotiorum, genes functional annotation; and Leptosphaeria maculans, genes functional annotation.

Grapevine 12x, structural and functional annotation with Genetic maps (genetic markers..) ▾
vitis12x ▾

[Genetic maps (markers, Qtls), Polymorphisms (snps, genes), Genetic and Phenotype resources with Genes annotations] Genetic maps VITIS ▾

New Count Results ★ URL XML Perl Help

Dataset
vitis12x

Filters
Feature Type : Program :
microsatellite:Markers

Attributes
Feature Type : Program
Qualifiers Value
Start
End
Chromosome Name
Feature Name

Dataset
Genetic maps VITIS

Filters
[None selected]

Attributes
Map name (in GnpMap)
Link Map URGI (in GnpMap)

Export all results to TSV Unique results only

Email notification to

View 20 rows as HTML Unique results only

Feature Type : Program	Qualifiers Value	Start	End	Chromosome Name	Feature Name	Map name (in GnpMap)	Link Map URGI (in GnpMap)
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_F_Chardonnay	69
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_C_ChXBi	71
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_M_Bianca	70
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	Integrated	79
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	A1_C_SG	67
microsatellite:Markers	Markers SSR	13067657	13067837	chr12	VMC4F3-1	DG_F_Chardonnay	69
microsatellite:Markers	Markers SSR	13067657	13067837	chr12	VMC4F3-1	DG_C_ChXBi	71
microsatellite:Markers	Markers SSR	13067657	13067837	chr12	VMC4F3-1	DG_M_Bianca	70
microsatellite:Markers	Markers SSR	13067657	13067837	chr12	VMC4F3-1	Integrated	79
microsatellite:Markers	Markers SSR	13067657	13067837	chr12	VMC4F3-1	A1_C_SG	67
microsatellite:Markers	GT183H07	83697	83948	chr13	GT183H07	Integrated_fw	78
microsatellite:Markers	GT183H07	83697	83948	chr13	GT183H07	Integrated	79
microsatellite:Markers	Markers SSR	83697	83948	chr13	GT183H07	Integrated_fw	78
microsatellite:Markers	Markers SSR	83697	83948	chr13	GT183H07	Integrated	79
microsatellite:Markers	UDV-009	9994586	9994885	chr16	UDV-009	ChBi_080717	100
microsatellite:Markers	UDV-009	9994586	9994885	chr16	UDV-009	Chardonnay_080717	102
microsatellite:Markers	Markers SSR	9994586	9994885	chr16	UDV-009	ChBi_080717	100
microsatellite:Markers	Markers SSR	9994586	9994885	chr16	UDV-009	Chardonnay_080717	102
microsatellite:Markers	VVCS1H027C23F1-				VVCS1H027C23F1-		

Dataset
vitis12x

Filters
Feature Type : Program :
microsatellite:Markers

Attributes
Feature Type : Program
Qualifiers Value
Start
End

Export all results to Unique results only

Email notification to

View rows as Unique results only

Feature Type : Program	Qualifiers Value	Start	End	Chromosome Name	Feature Name	Map name (In GnpMap)	Link Map URGI (In GnpMap)
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_F_Chardonnay	69
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_C_ChXBI	71
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_M_Bianca	70
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	Integrated	79
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	A1_C_SG	67

Vitis vinifera (12x) Genome Browser: 180 bp from chr12:13,067,657..13,067,837

To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.
To switch to another organism, use the Data Source menu.

New names of gene in 12X version according to the genome release at EMBL : GSVIVG00 to GSVIVG01
New tracks available : Gene prediction (named V1) produced by CRIBI on the 12X sequence assembly. This V1 annotates V1_R (repetitive sequences)

Browser [Select Tracks](#) [Custom Tracks](#) [Preferences](#)

Search

Landmark or Region:


Examples: chr15:5282664..5322663, GSVIVG01032605001, EGT00018252001, SNAPVvG00016689001, GWSUNIT02500482001, VVii52, VV40024H100E01, Vv_10003495, Vv10s0116g00040, GSVIVG01001153001, NEW20, VVTP565, SNP_Vv_1272338, Indel_Vv_1272543, SNP_Vv_1273469, PN40024_heterozygous_SNPs_chr1_4012677, PN40024_seqErr_SNPs_chr1_1252920, SNP_ENSVVVI00100380.

Data Source
Vitis vinifera (12x) Genome Browser


Download Decorated FASTA File

Scroll/Zoom: Show 181 bp Flip

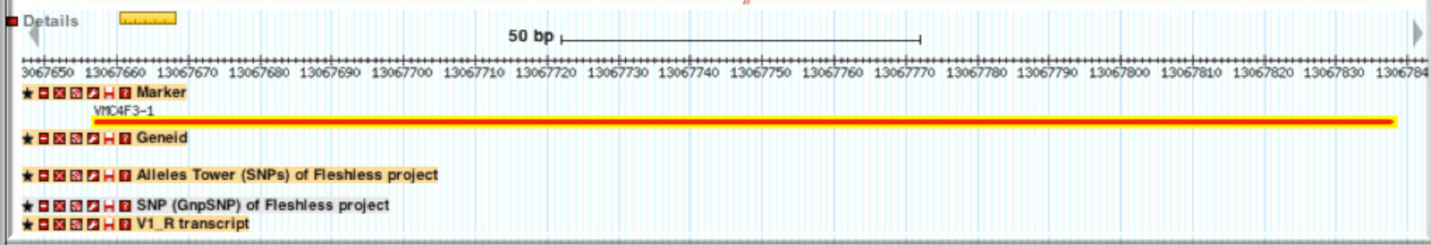
Overview



Region



Details



50 bp

3067650 3067660 3067670 3067680 3067690 3067700 3067710 3067720 3067730 3067740 3067750 3067760 3067770 3067780 3067790 3067800 3067810 3067820 3067830 3067840

Marker
 Gened
 Alleles Tower (SNPs) of Fleshless project
 SNP (GnpSNP) of Fleshless project
 V1_R transcript

G_F_Chardonnay	69
G_C_ChXBI	71
G_M_Bianca	70
egrated	79
I_C_SG	67
G_F_Chardonnay	69
G_C_ChXBI	71
G_M_Bianca	70
egrated	79
I_C_SG	67
egrated_fw	78
egrated	79
egrated_fw	78
egrated	79
hBI_080717	100
hardonnay_080717	102
hBI_080717	100
hardonnay_080717	102



Dataset
vitis12x

Filters
Feature Type : Program :
microsatellite:Markers

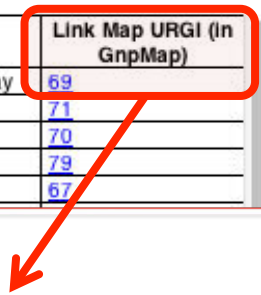
Attributes
Feature Type : Program
Qualifiers Value
Start
End
Chromosome Name
Feature Name

Export all results to Unique results only

Email notification to

View rows as Unique results only

Feature Type : Program	Qualifiers Value	Start	End	Chromosome Name	Feature Name	Map name (In GnpMap)	Link Map URGI (In GnpMap)
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_F_Chardonnay	69
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_C_ChXBI	71
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	DG_M_Bianca	70
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	Integrated	79
microsatellite:Markers	VMC4F3-1	13067657	13067837	chr12	VMC4F3-1	A1_C_SG	67



Dataset
Genetic maps VITIS

Filters
[None selected]

Attributes
Map name (in GnpMap)
Link Map URGI (in GnpMap)

[Log in](#)

Preferences

Main

- TEXTUAL INTERFACE
- MAPCOMPARATOR
- BIOMERCATOR

Global queries

- TAXONS
- PUBLICATIONS

Queries

- MAP
- LOCI
- QTL
- METAQTL
- MARKER
- POOL
- XREF
- TRAIT

Documentation

- USER GUIDE
- FAQ

GnpMap / Map card

MAP DETAILS

Map name :	DG_F_Chardonnay		
Map type :	genetic		
Map date :	2005/12/19		
Taxon :	Vitis vinifera L.		
Population :	DG		
Submitted by :	ADAM-BLONDON Anne-Francoise		
Genotype file :	rawdata_DG191205.csv		
Image file :			
Linkage group number :	19		
Loci number :	373		
Framework loci number :	373		
QTL number :	-		

BioMercator V4.0

File Analyses View Help Erase all

Panel 1

9		
10		
11		
12		
12		
13		
14		
15		
16		
17		
18		

Qtl's Genome version
General Expert Locus

Display loci
 Display loci's name
 Display loci's position

Type		
PCR	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
SSR	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

0,00	VMC2H4
0,00	VMC4H2
4,40	VMC4A9
13,20	VMC1G3-2
13,20	VMCNG2D11-DG-A
15,40	UDV518-CH-B
15,40	VMCNG2D11-CH
17,60	VVIM11
22,00	UDV024
28,60	VMC4F3-1
30,80	VMC4C10-DG-A
30,80	VMCNG2H7-DG-A
35,10	rgVripl15-CH-A
35,20	VMC4C10-DG-B
37,30	VMCNG2H7-CH
37,30	rgVripl15-CH-B
39,50	GLP6-1-CH
39,50	rgVripl16-CH
44,00	VMC8G9
46,10	VMC4C10-CH

Unique results only Go

Unique results only

Chromosome Name	Feature Name	Map name (In GnpMap)	Link Map URGI (In GnpMap)
2	VMC4F3-1	DG_F_Chardonnay	69
rd			
DG_F_Chardonnay			
genetic			
2005/12/19			
Vitis vinifera L.			
DG			
ADAM-BLONDON Anne-Francoise			
rawdata_DG191205.csv			
19			
373			
373			
-			

[Log in](#)

Searches

- QUICK SEARCH
- ADVANCED TOOLS

Documentation

- USER GUIDE
- NEWS
- RELEASE NOTES

Data

- DATA SUBMISSION
- ARRAYS
- GENOMES
- TAXONS
- GENETIC MAPS
- SEQUENCES
- POLYMORPHISMS
- PHENOTYPES
- GENETIC RESOURCES
- PLANT SYNTENY

QUICK SEARCH All species

You can find the indexed data list [here](#).
Examples: [VVI](#), [VVIF52](#), [gene](#), [arabidopsis](#),
[AY109603](#), [Xwmc430](#)

ADVANCED TOOLS

[BIOMART](#) [GALAXY](#)

INTERMINE

Genomes

Genome annotation data. GnpGenome.

Taxons

Taxonomic data.

Sequences

NGS projects description. GnpSeq.

Genetic maps

Genetic maps and QTLs. GnpMap.

Polymorphisms

Molecular polymorphism. GnpSNP.

Phenotypes

Phenotypic and environmental experiments. Ephasis.

Genetic resources

Plant genetic resources data. Siregal.

Arrays

Expression data. GnpArray.



Multiple sources data integration



GrapeMine v1.0

- Home
- Templates
- Lists
- QueryBuilder
- Regions
- Data Sources
- API
- MyMine

Contact Us | Log in

Search:

Search

Search GrapeMine. Enter **names, identifiers or keywords** for genes, markers, snp, ontology terms, accessions, etc. (e.g. Vv10s0116g01550, VMC4F8, Vv_1272649, membrane, Syrah).

Analyse

Enter a list of identifiers.

Gene

e.g. Vv10s0092g00620, Vv10s0116g00170, Vv10s0116g00240, Vv10s0116g00300

[advanced](#)

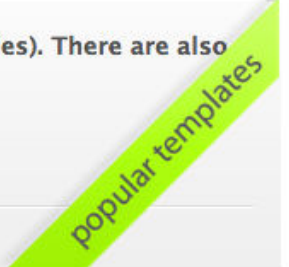
Welcome Back!

GrapeMine integrates many types of data for *Grape vine*. You can run flexible queries, export results and analyse lists of data. All data are from **GnpIS**.

GRAPEMINE CONTENT

Our Mine provides access to many kind of data types like genomic annotation data (genes, mRNAs, exons, polypeptides). There are also snp, markers and phenotyping data (accessions, phenotyping experiments). [Read more](#)

» [Queries](#)





GrapeMine v1.0

- Home
- Templates
- Lists
- QueryBuilder
- Regions
- Data Sources
- API
- MyMine

Search:

Marker : VMC4F3-1 *V. vinifera*

DB identifier	VMC4F3-1	Organism . Name	Vitis vinifera
Absdistance	36.5	Affiliation	INRA
Locus Name	VMC4F3-1	Mapname	Bianca080717
Marker Id	19575	Nextdistance	5.3
Scientificname	Vitis vinifera	Start	13067657
Stop	13067837	Taxon	Vitis vinifera L.

SHARE

Genome feature

Length:	181	FASTA...
Location:	chr12:13067657-13067837	

Overlapping Features

Genome features that overlap coordinates of this marker.
 No overlapping features

Lists

This Marker isn't in any lists. [Upload a list.](#)

External Links

- [Link to GnpMap](#)
- [Search for VMC4F3-1 and his associated genes in URGI Vitis12X Mart](#)
- [GBrowse URGI VITIS12X](#)

1 Organism

Name	Taxon Id
Vitis vinifera	29760



Search our database by keyword

[Back to index](#)



Examples

- Search this entire website. Enter **identifiers, names** or **keywords** for genes, markers, accessions, ontology terms, etc. (e.g. *Vv10s0116g00040*, *VMC4F8*, *Syrah*, *GO:0005794*)
- Use **OR** to search for either of two terms (e.g. *membrane OR protein*) or quotation marks to search for phrases (e.g. "tyrosine kinase").
- Boolean search syntax is supported: e.g. *GO** for partial matches or *gene AND NOT *orf* to exclude a term

Search results 1 to 6 out of 6 for "tyrosine kinase"

1.247s

Categories

Hits by Category

- OntologyTerm: 3
- Prosite: 2
- Pfam: 1

Type	Details	Score
Prosite	PS00007 Tyrosine kinase phosphorylation site	● ● ● ● ●
Ontology Term	GO:0004713 protein tyrosine kinase activity	● ● ● ● ●
Ontology Term	GO:0004715 non-membrane spanning protein tyrosine kinase activity	● ● ● ● ●
Pfam	PF07714 Protein tyrosine kinase	● ● ● ● ●
Prosite	PS00109 Tyrosine protein kinases specific active-site signature	● ● ● ● ●
Ontology Term	GO:0004714 transmembrane receptor protein tyrosine kinase activity	● ● ● ● ●

Pfam : PF07714

Description **Protein tyrosine kinase**

[SHARE](#)

1131 Mrnas

DB identifier	Length	FASTA...	Chromosome Location
Vv10s0116g00150.t01	2698	FASTA...	chr10: 72329-75026
Vv10s0116g00170.t01	2492	FASTA...	chr10: 77195-79686
Vv10s0116g00480.t01	1758	FASTA...	chr10: 222831-224588
Vv10s0116g00850.t01	2071	FASTA...	chr10: 394011-396081
Vv10s0116g00910.t01	7756	FASTA...	chr10: 414417-422172
Vv10s0116g00920.t01	4996	FASTA...	chr10: 422173-427168
Vv10s0116g01230.t01	1312	FASTA...	chr10: 641931-643242
Vv10s0116g01240.t01	3755	FASTA...	chr10: 645136-648890
Vv10s0116g01800.t01	8362	FASTA...	chr10: 1067284-1075645
Vv10s0003g00330.t01	3686	FASTA...	chr10: 1617819-1621504

▼ Show more rows

Lists

This Pfam isn't in any lists. Upload a list.

External Links

Pfam: [PF07714](#)

Categories

Hits by Category

- OntologyTerm: 3
- Prosite: 2
- Pfam: 1

1.247s

Type	Details	Score
Prosite	PS00007 Tyrosine kinase phosphorylation site	● ● ● ● ●
Ontology Term	GO:0004713 protein tyrosine kinase activity	● ● ● ● ●
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Ontology Term	GO:0004714 transmembrane receptor protein tyrosine kinase activity	● ● ● ● ●

Pfam : PF07714

Description

Protein tyrosine kinase

[SHARE](#)

1131 Mrnas

DB identifier

Vv10s0116g00150.t01

Vv10s0116g00170.t01

Vv10s0116g00480.t01

Vv10s0116g00850.t01

Vv10s0116g00910.t01

Vv10s0116g00920.t01

Vv10s0116g01230.t01

Vv10s0116g01240.t01

Vv10s0116g01800.t01

Vv10s0003g00330.t01

mRNA : Vv10s0116g00150.t01 *V. vinifera*

DB identifier	Vv10s0116g00150.t01	Hmmcoord	NULL
Hmmnh	0	Hmmtype	OUT
Tmhmmcoord	276-298	Tmhmmnh	1
Tmhmmtype	IN	Tplen	29
Tploc	S		

[SHARE](#)

Genome feature

Region:	mRNA	Length:	2698	FASTA...
Location:	chr10:72329-75026 reverse strand			

Overlapping Features

Genome features that overlap coordinates of this MRNA
 Exons: 14, Genes: 2, mRNA: 1, Polypeptides: 2

[Show all in a table »](#)

1 Organism

Name	Taxon Id
Vitis vinifera	29760

1 Data Sets

Name
vitis vinifera L.

7 Exons

Lists

This MRNA isn't in any lists. Upload a list.

External Links

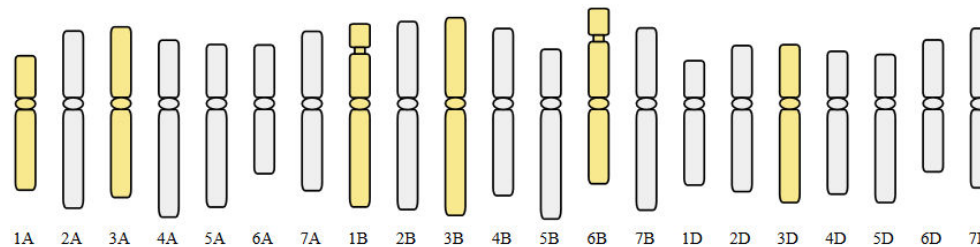
[GBrowse URGI](#)
[VITIS12X[®]](#)

Categories

Hits by Category

- OntologyTerm: 3
- Prosite: 2
- Pfam: 1





Browser [Select Tracks](#) [Custom Tracks](#) [Preferences](#)

Search

Landmark or Region:

ctg6:1..373,201

Data Source

Wheat physical map viewer: 3B v2

Scroll/Zoom: Show 373.2 kbp Flip

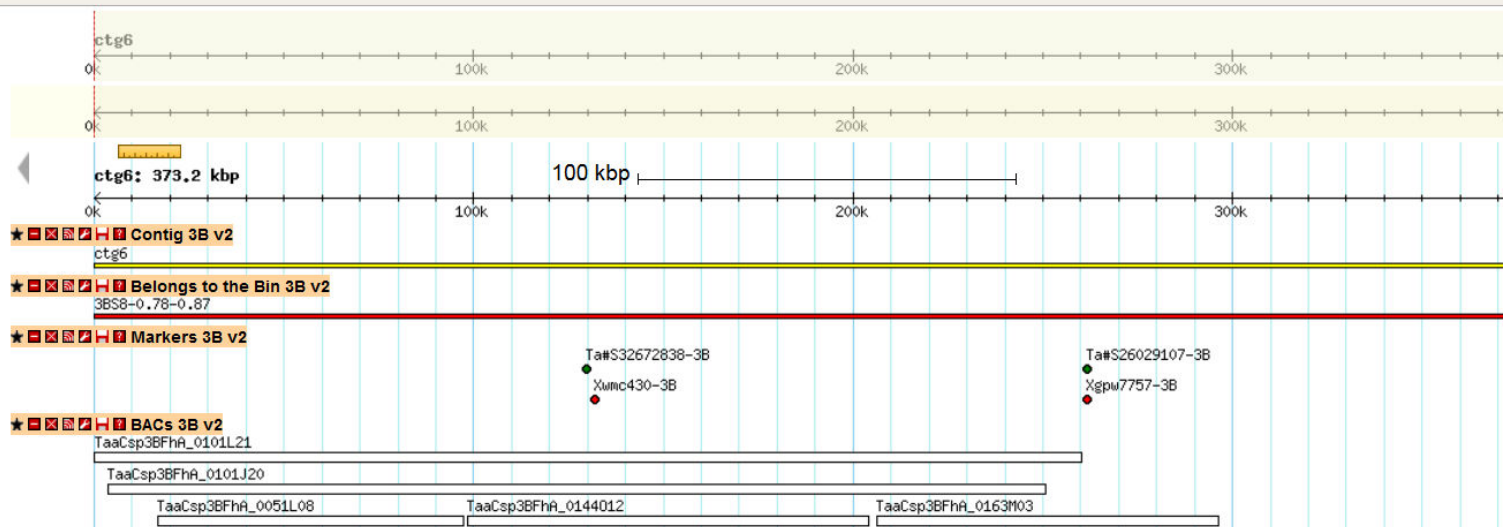
Examples :

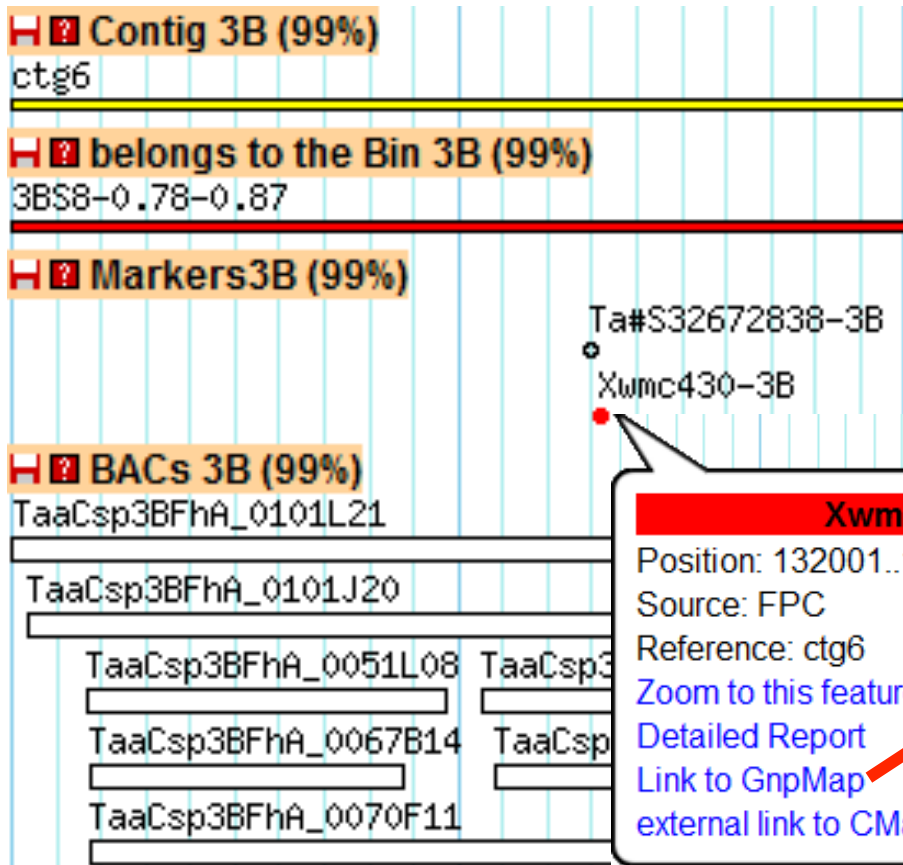
3B v2:	ctg6	ctg111	TaaCsp3BFhA_0100L17	Xgwm264-3B	ctg344
3B v1:	ctg1	ctg954	Xgwm264-3B	3B_039_H02	
1BL v2:	ctg45	wmc719			

Overview

Region

Details





MARKER DETAILS

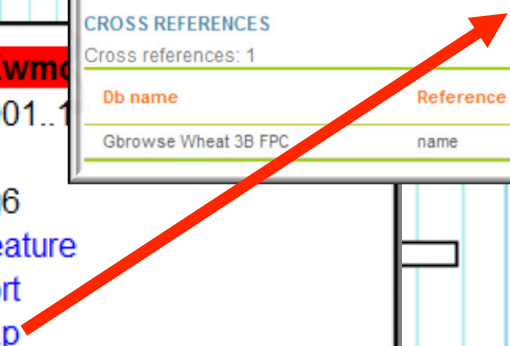
Marker name : WMC430
 Taxon : Triticum aestivum
 Marker type : SSR
 Marker origin : amplicon
 Target : WMC
 Origin laboratory : ITCF
 Reverse primer : TAGGGACCCCTTGACAAAAA
 Forward primer : TAGGGACCCCTTGACAAAAA

MAPPED LOCI
Mapped loci: 4

Locus name	Map name	Taxon	Linkage group	Distance	Reliability / (source map name)
Xwmc430-5B	TaVirtualPop01_071219	Triticum aestivum	5B	154.0	non_framework
Xwmc430-5B	RLAc_071219	Triticum aestivum	5B	162.6	non_framework
Xwmc430-3B	SupBW_071212	Triticum aestivum	3B	3.1	non_framework
Xwmc430-3B	TaVirtualPop01_071219	Triticum aestivum	3B	3.0	non_framework

CROSS REFERENCES
Cross references: 1

Db name	Reference name	Reference value	Evidence
Gbrowse Wheat 3B FPC	name	Xwmc430-3B	-



Contig 3B (99%)
ctg6

belongs to the Bin 3B (99%)
3BS8-0.78-0.87

Markers3B (99%)

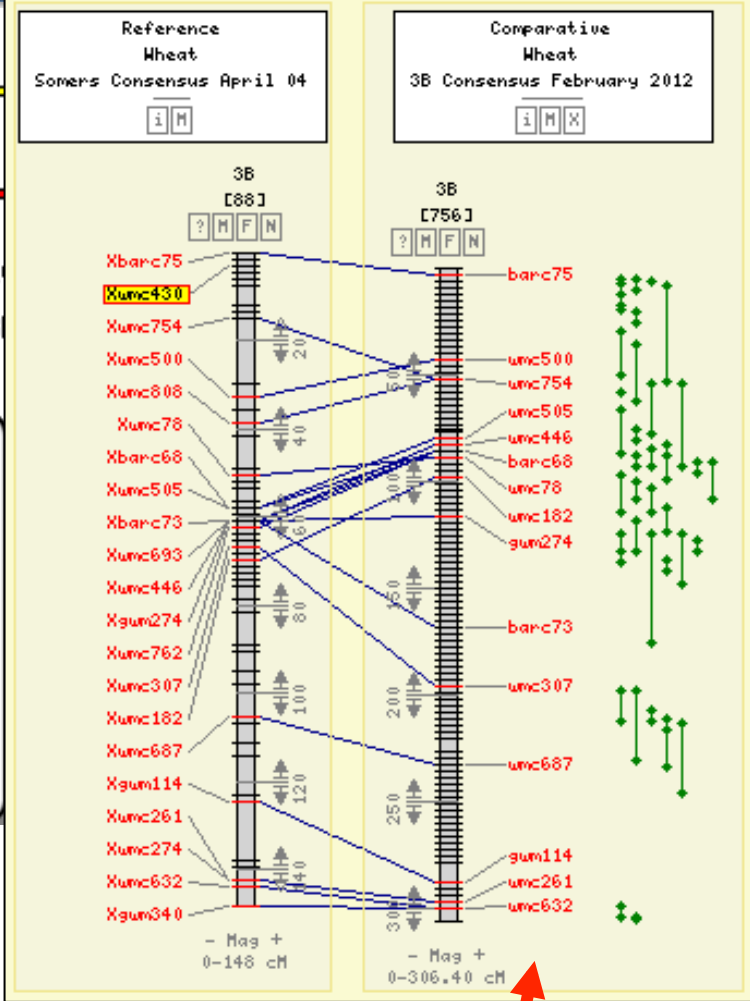
BACs 3B (99%)
TaaCsp3BFhA_0101L21

- TaaCsp3BFhA_0101J20
- TaaCsp3BFhA_0051L08
- TaaCsp3BFhA_0067B14
- TaaCsp3BFhA_0070F11

Ta#S32672838-3B
Xwmc430-3B
Ta#S260291
Xgpcw7757-3B

Xwmc430-3B

Position: 132001..132001
Source: FPC
Reference: ctg6
[Zoom to this feature](#)
[Detailed Report](#)
[Link to GnpMap](#)
[external link to CMap \(CCG Murdoch\)](#)



WMC430	SSR	Wheat	Framework Feb07	5B	154.00 cM XWMC430	View on Map	Feature Details
Xwmc430	SSR	Wheat	RL4452*AC Domain SO 05/08	5B	163.00 cM wmc0430, wmc430, WMC430, Xw...	View on Map	Feature Details
Xwmc430	SSR	Wheat	Somers Consensus April 04	3B	3.00 cM wmc0430, wmc430, Xwmc0430	View on Map	Feature Details
Xwmc430	SSR	Wheat	Somers Consensus April 04	5B	154.00 cM wmc0430, wmc430, Xwmc0430	View on Map	Feature Details
Xwmc430	SSR	Wheat	Somers Grain Genes Consensus Map	3B	3.00 cM wmc0430, wmc430, WMC430, Xwm...	View on Map	Feature Details
Xwmc430	SSR	Wheat	Somers Grain Genes Consensus Map	5B	154.00 cM wmc0430, wmc430, WMC430, Xwm...	View on Map	Feature Details
wmc430	SSR	Wheat	5B Consensus November 2011	5B	148.27 cM	View on Map	Feature Details



Galaxy@URGI

Galaxy / URGI Analyze Data Workflow Shared Data Visualization Help User Using 21%

Tools

search tools

Get Data
[Text Manipulation](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[Convert Formats](#)
[Alternative splicing tools](#)
[Vcf utils](#)
[Operate on Genomic Intervals](#)
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[NGS: QC and manipulation](#)
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[URGI: BAC analysis](#)
[URGI: MAPHITS - PreProcess Tools](#)
[URGI: MAPHITS - Tools](#)
[URGI: MAPHITS - PostProcess Tools](#)
[URGI: MAPHITS - SNPs Chip Tools](#)
[URGI: S-MART](#)
[URGI: Differential expression](#)
[Analysis Tools](#)

History

Interop_JA
748.1 KB

12: Select on data 7

7: Column Join on data 5 and data 1

5: Normalized Data Gene upregulated inPlanta.csv

1: Botrytis_functional annotation

Welcome to URGI server

i

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 - DEA: Differential Expression Analysis.
 - Go to Shared Data -> Published Pages -> DEA tutorial.
 - SMART Documentation is [here](#)
- You can also download data from GnpIS URGI information system marts by selecting Get Data -> Biomart INRA URGI GnpIS

!

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URGI

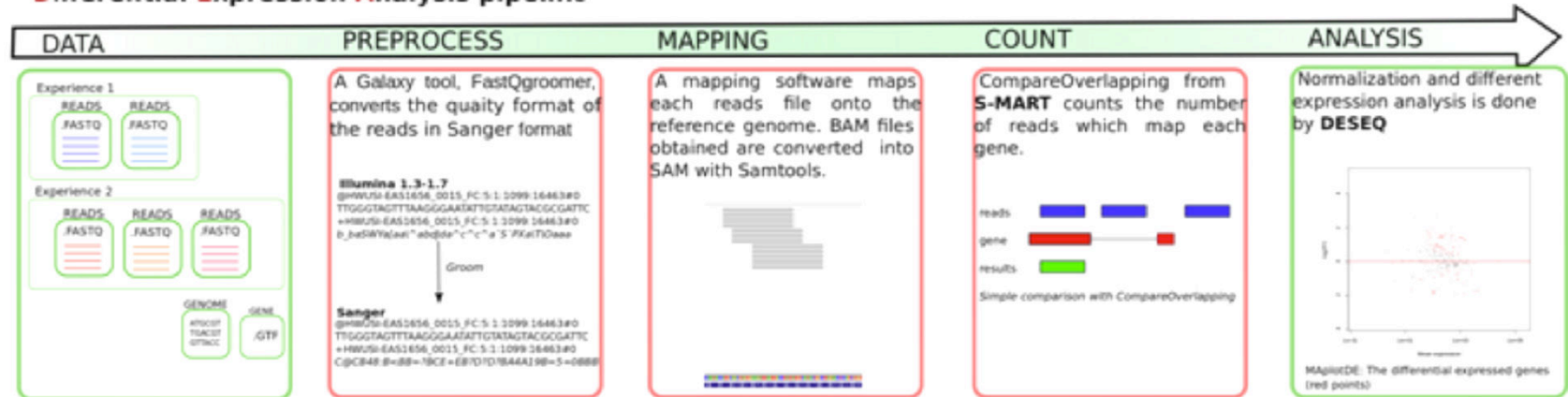
intensive biomedical research. The [Galaxy team](#) is a part of [BX](#) at [Emory University](#). The [Galaxy Project](#) is supported in part by [Penn State](#), and [Emory University](#).

getData from URGI BioMart

Pipelines: MAPHITS, DEA S-MART toolbox

Welcome to the Differential Expression Analysis tutorial page.

Differential Expression Analysis pipeline



Parallelized steps of DEA

This pipeline performs differential expression analysis on two different conditions.

One reference genome (fasta format), one gene annotation file (gtf format) and several RNA-seq samples are required.

A parallel version for some steps are available. Parallelized and not-parallelized steps share usually the same options and interface. However, for specific case, some options are mandatory for the parallelized version.

Step 0: Upload RNA-seq samples.

Step 1: Clean the annotation file.

Step 2: Groom RNA-seq files. (Available in a parallel version)

Step 3: Map RNA-seq samples to the genome reference, using TopHat1/2 or GSNAP. (Available in a parallel version)

Step 4: Convert bam files (given by TopHat) to sam files. (Available in a parallel version)

Step 5: Count reads number per annotation using S-MART (CompareOverlapping). (Available in a parallel version)

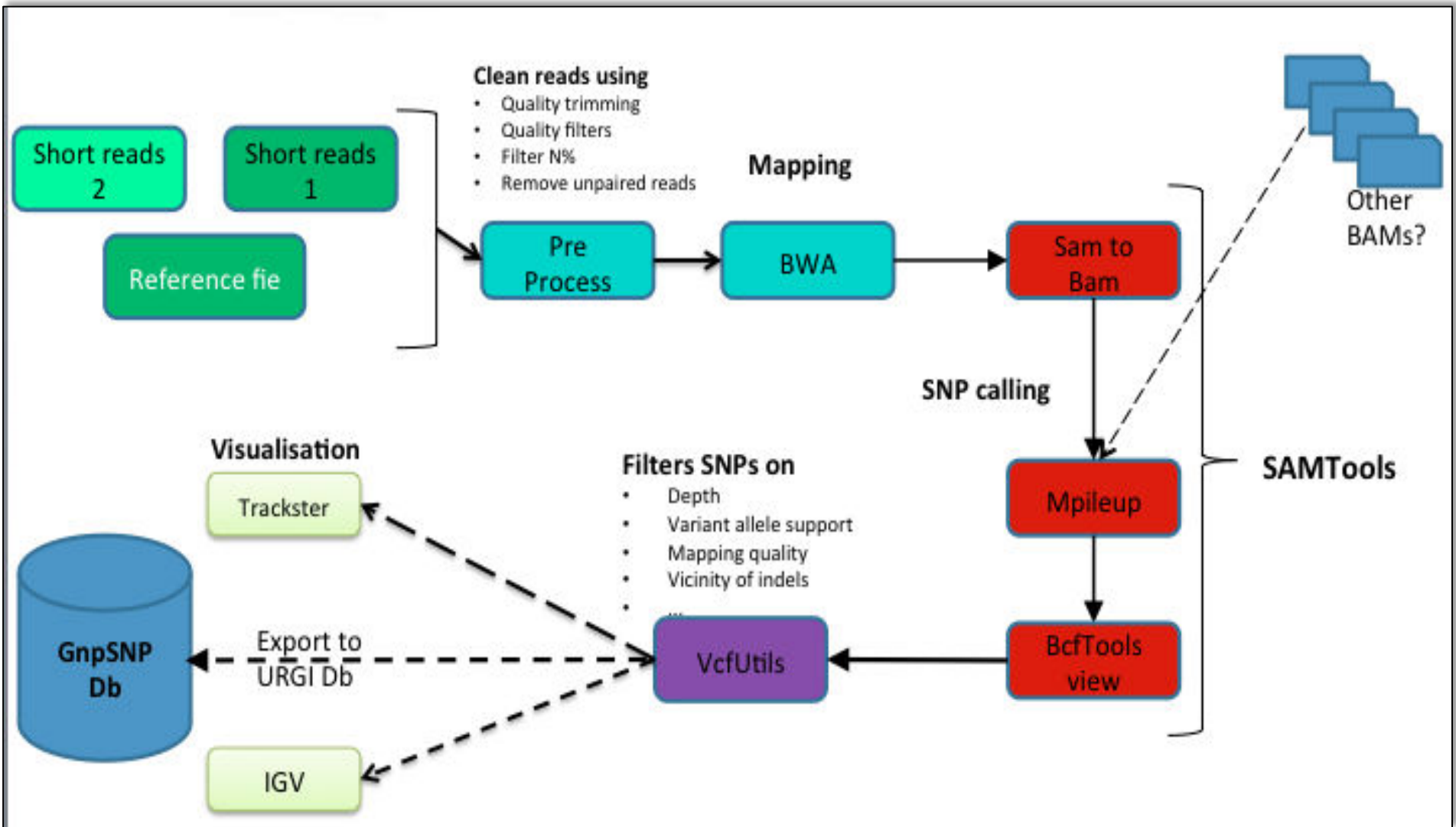
Step 6: Build input files for DESeq. (Available in a parallel version)

Step 7: Launch DESEQ to normalize and analyze data

The results of step 1 to 6 are tar files. If you want to use those files in Galaxy, you can use this tool: "Untar".

Workflows for parallel and non-parallel version are available. You just need to edit step1 to adapt it to your experience.

MAPHiTS: Mapping Analysis Pipeline for High-Throughput Sequences



Galaxy / URGI

Tools

URGI: MAPHITS - SNPs Chip Tools

URGI: S-MART

CONVERSION TOOLS

- [convert transcript file](#) Convert a file from a format to another.
- [coordinates to sequence](#) Coordinates to Sequences: Extract the sequences from a list of coordinates.
- [mapper analyzer](#) Read the output of an aligner, print statistics and possibly translate into GFF, BED or GBrowse formats.

WIG TOOLS

- [get WIG data](#) Compute the average data for some genomic coordinates using WIG files
- [get WIG distance](#) Compute the average data around some genomic coordinates using WIG files (thus covering a large proportion of the genome).
- [get WIG profile](#) Compute the average profile of some genomic coordinates using WIG files (thus covering a large proportion of the genome).

MERGE TOOLS

- [clusterize by sliding windows](#) Produces a GFF3 file that clusters a list of transcripts using a sliding window. Cluster the data into regions (defined by size and overlap with next region).
- [collapse reads](#) Merges two genomic features if they have exactly the same genomic coordinates.
- [merge sliding windows clusters](#) Merges two files containing the results of a sliding windows clustering.
- [merge transcript lists](#) Merge the elements of two lists of genomic coordinates.

COMPARISON TOOLS

- [compare overlapping](#) Print all the transcripts from a first file which overlap with the transcripts from a second file.
- [compare overlapping small query](#) Provide the queries that overlap with a reference, when the query data set is small.
- [compare overlapping small reference](#) Provide the queries that overlap with a reference, when the reference dataset is small.
- [get difference](#) Gets all the regions of the genome, except the one given in an annotation file. Alternatively, it may also give all the elements from the first set which does not overlap with the second set (at the nucleotide level).
- [get differential expression](#) Get the differential expression between 2 conditions using Fisher's exact test, on regions defined by a third file.

SELECTION TOOLS

- [get exons](#) Get the exons of a set of transcripts.
- [get introns](#) Get the introns of a set of transcripts.
- [get flanking](#) Get the flanking regions of a set of reference.
- [restrict from size](#) Select the elements of a list of sequences or transcripts with a given size.
- [restrict transcript list](#) Select the features which are located in a given locus.
- [select by tag](#) Keep the genomic coordinates such that a value of a given tag.
- [compute coverage](#) Compute the coverage of a set with respect to another set.
- [count read GC percent](#) Count GC percent for each read against a genome.

MODIFICATION TOOLS

- [clean transcript file](#) Clean a transcript file so that it is useable for S-MART.
- [change GFF features](#) Change a feature in a GFF file (the feature is the 3rd column).
- [change tag name](#) Change the name of a tag in a GFF file.
- [modify genomic coordinates](#) Extend or shrink a list of genomic coordinates.
- [modify sequence list](#) Extend or shrink a list of sequences.
- [trim sequences](#) Remove the 5' and/or 3' adapters of a list of reads.

VISUALIZATION TOOLS

- [get distance](#) Give the distances between every data from the

Applications Dood Intra GPI Conf DocWiki BIBL BIOINFO Trans Traf Maps Visio Autres favoris

Galaxy / URGi Analyze Data Workflow Shared Data Visualization Help User Using 21%

Tools

search tools

Get Data

- Upload File from your computer
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- BX table browser
- EBI SRA ENA SRA
- Get Microbial Data
- BioMart Central server
- BioMart INRA URGi GnpIs**
- CBI Rice Mart rice mart
- GrameneMart Central server
- modENCODE fly server
- Flymine server
- Flymine test server
- modENCODE modMine server
- MouseMine server
- Ratmine server
- YeastMine server
- metabolicMine server
- modENCODE worm server
- WormBase server
- Wormbase test server

Welcome to URGi server

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History

Interop_JA

0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

New Count Results

URL XML Perl

Dataset
Botrytis_functional_annotator

Filters

Feature Type :
signal_peptide
Start < : 1
End < : 30
Program : signalp

Attributes

Reference Feature
Feature Type
Start (-1)
End
Program
Library
HIT
Description
Analysis source name

Export all results to Galaxy TSV Unique results only Go

Email notification to

View 10 rows as TSV Unique results only

Reference Feature	Feature Type	Start (-1)	End	Program	Library	HIT	Description	Analysis source	name	DB	Xref	DB	DB X:
BofuT4_P000030.1	signal_peptide	0	25	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000070.1	signal_peptide	0	18	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000200.1	signal_peptide	0	18	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000210.1	signal_peptide	0	19	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000260.1	signal_peptide	0	19	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000270.1	signal_peptide	0	19	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000290.1	signal_peptide	0	17	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000390.1	signal_peptide	0	17	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000440.1	signal_peptide	0	19	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp
BofuT4_P000590.1	signal_peptide	0	3	signalp	model	SignalP	polypeptide_iprscan_annotation	GFF_source					signalp

Tools

search tools

Get Data

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[Convert Formats](#)

[Alternative splicing tools](#)

[Vcf utils](#)

[Operate on Genomic Intervals](#)

[Emboss Tools](#)

[FASTA manipulation](#)

[NGS: QC and manipulation](#)

[NGS: Mapping](#)

[NGS: RNA Analysis](#)

[NGS: SAM Tools](#)

[NGS: Peak Calling](#)

[VCF Tools](#)

[URGI: Get Data for grapevine](#)

[URGI: BAC analysis](#)

[URGI: MAPHITS - PreProcess Tools](#)

[URGI: MAPHITS - Tools](#)

[URGI: MAPHITS - PostProcess Tools](#)

[URGI: MAPHITS - SNPs Chip Tools](#)

[URGI: S-MART](#)

[URGI: Differential expression Analysis Tools](#)

[Tools for APLIBIO pipelines](#)

Workflows

- All workflows

Welcome to URGI server

i

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w

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History

Interop_JA
0 bytes

i Botrytis_functional_annotation%20

Galaxy / URGI

Analyze Data Workflow Shared Data Visualization Help User

Tools

search tools

Get Data

Text Manipulation

Filter and Sort

- Filter data on any column using simple expressions
- Sort data in ascending or descending order
- Select lines that match an expression
- GFF
- Extract features from GFF data
- Filter GFF data by attribute using simple expressions
- Filter GFF data by feature count using simple expressions
- Filter GTF data by attribute values list

Join, Subtract and Group

- Join two Datasets side by side on a specified field
- Compare two Datasets to find common or distinct rows
- Subtract Whole Dataset from another dataset
- Group data by a column and perform aggregate operation on other columns.
- Column Join

Convert Formats

Alternative splicing tools

Vcf utils

Operate on Genomic Intervals

Emboss Tools

FASTA manipulation

NGS: QC and manipulation

NGS: Mapping

NGS: RNA Analysis

Column Join (version 1.1.0)

Choose the first file for the join:

Use this column and columns to left the 'hinge' (matching data for each join):

All columns to left of selected column (plus selected column) will be used. Select 2 for pileup

Include these column:

Multi-select list - hold the appropriate key while clicking to select multiple columns

Fill empty columns:

Choose the second file for the join:

Additional Inputs

Execute

What it does

This tool allows you to join several files with the same column structure into one file, removing certain columns if necessary. The user needs to select a 'hinge', which is the number of left-most columns to match on. They also need to select the columns to include in the join, which should include the hinge columns, too.

Note that the files are expected to have the same number of columns. If for some reason the join column is missing (this only applies to the last column(s)), the tool attempts to handle this situation by inserting an empty item (or the appropriate filler) for that column on that row. This could lead to the situation where a row has a hinge but entirely empty or filled columns, if the hinge exists in at least one file but every file that has it is missing the join column. Also, note that the tool does not distinguish between a file missing the hinge altogether and a file having the hinge but missing the column (in both cases the column would be empty or filled). There is an example of this below.

General Example

Given the following files:

```

FILE 1
chr2 1 T 6 .C., I$$III
chr2 2 G 6 .N., III@II
chr2 3 C 7 .C., I$IIIII
chr2 4 G 7 .G., I#IIIII
chr2 5 G 7 .N., IIII#BI
chr2 6 A 7 .T., I$IDIII
chr1 1 C 1 .:, I
    
```

GnpArray / Gene list results

RESULTS

Number of unique reporters in your query: 211
 Number of unique genes in your query: 35690
 3 Items found, displaying 1 to 3 | Display | 4 results per page

#	Gene list name	Creation date	Description	Project	Experiments	Regulation	Reporter normalized data	Gene normalized data
1	Bot- in planta Up Botrytis B051D_in_vitro vs in planta(Sunflowered 489) (277 genes)	2009/03/09	Variance analysis wa. - 2 mos	Botrytis_on_Sunflower_2008	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Up regulated		Export
2	Bot- in planta Down Botrytis B051D_in_vitro vs in planta(Sunflowered 489) (277 genes)	2009/03/09	Variance analysis wa. - 2 mos	Botrytis_on_Sunflower_2008	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Down regulated		Export
	Botrytis_on_Sunflower_2008			STUDY OF BOTRYTIS-SUNFLOWER INTERACTION		Unchanged		Export

History

Interop_JA
481.2 KB

5: Normalized Data Gene upregulated InPlanta.csv
278 lines
format: csv, database: ?
uploaded csv file

1	2	3
Reporter name	Sequence db ID	FOLD CH
B4BC_116_249_C09	B4BC_116_249_C09	8.0
B5BC_116_281_B07	B5BC_116_281_B07	4.5
BC1G_00109.1	BC1G_00109.1	2.2
BC1G_00913.1	BC1G_00913.1	1.7
BC1G_01483.1	BC1G_01483.1	23.0

1: Botrytis functional annotation

Load Gene expression data from GnpIS

Join on Gene name column

Galaxy / URGI

Analyze Data Workflow Shared Data Visualization Help User

Using 21%

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NGS: RNA Analysis

Column Join (version 1.1.0)

Choose the first file for the join:
1: Botrytis_functional_annotation

Use this column and columns to left the 'hinge' (matching data for each join):
c1

All columns to left of selected column (plus selected column) will be used. Select 2 for pileup

Include these column:
c1
c2
c3
c4

Multi-select list - hold the appropriate key while clicking to select multiple columns

Fill empty columns:
No

Choose the second file for the join:
5: Normalized_Data_G_nPlanta.csv

Additional inputs

Add new Additional Input

Execute

History

Interop_JA
481.2 KB

5: Normalized_Data_Gene_upregulated_InPlanta.csv
278 lines
format: csv, database: ?
uploaded csv file

1	2	3
Reporter name	Sequence db ID	FOLD CH
B4BC_116_249_C09	B4BC_116_249_C09	8.0
B5BC_116_281_B07	B5BC_116_281_B07	4.5
BC1G_00109.1	BC1G_00109.1	2.2
BC1G_00913.1	BC1G_00913.1	1.7
BC1G_01483.1	BC1G_01483.1	23.0

1: Botrytis_functional_annotation

What it does

This tool allows you to join several files with the same column structure into one file, removing certain columns if necessary. The user needs to select a 'hinge', which is the number of left-most columns to match on. They also need to select the columns to include in the join, which should include the hinge columns, too.

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FILE 1

```
chr2 1 T 6 .C... I$SIII
chr2 2 G 6 .N... III@II
chr2 3 C 7 .C... I$IIIII
chr2 4 G 7 .G... I#IIIII
chr2 5 G 7 .N... IIII#BI
chr2 6 A 7 .T... I$IDIII
chr1 1 C 1 *. I
```



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BofuT4_P003870.1	signal_peptide	0	19	BofuT4_P003870.1	18.0
BofuT4_P004830.1	signal_peptide	0	17	BofuT4_P004830.1	39.0
BofuT4_P005170.1	signal_peptide	0	20	BofuT4_P005170.1	6.0
BofuT4_P007640.1	signal_peptide	0	18	BofuT4_P007640.1	13.0
BofuT4_P010370.1	signal_peptide	0	18	BofuT4_P010370.1	5.4
BofuT4_P010380.1	signal_peptide	0	18	BofuT4_P010380.1	58.0
BofuT4_P010920.1	signal_peptide	0	19	BofuT4_P010920.1	2.2
BofuT4_P011170.1	signal_peptide	0	19	BofuT4_P011170.1	9.8
BofuT4_P011370.1	signal_peptide	0	20	BofuT4_P011370.1	2.9
BofuT4_P011380.1	signal_peptide	0	16	BofuT4_P011380.1	5.9
BofuT4_P011810.1	signal_peptide	0	19	BofuT4_P011810.1	61.0
BofuT4_P014350.1	signal_peptide	0	23	BofuT4_P014350.1	43.0
BofuT4_P015800.1	signal_peptide	0	18	BofuT4_P015800.1	30.0
BofuT4_P018370.1	signal_peptide	0	20	BofuT4_P018370.1	36.0
BofuT4_P019100.1	signal_peptide	0	19	BofuT4_P019100.1	6.2
BofuT4_P025640.1	signal_peptide	0	17	BofuT4_P025640.1	46.0
BofuT4_P030940.1	signal_peptide	0	18	BofuT4_P030940.1	3.3
BofuT4_P031660.1	signal_peptide	0	18	BofuT4_P031660.1	74.0
BofuT4_P033100.1	signal_peptide	0	19	BofuT4_P033100.1	4.9
BofuT4_P035820.1	signal_peptide	0	17	BofuT4_P035820.1	2.1
BofuT4_P035890.1	signal_peptide	0	19	BofuT4_P035890.1	22.0
BofuT4_P036980.1	signal_peptide	0	20	BofuT4_P036980.1	6.0
BofuT4_P043000.1	signal_peptide	0	19	BofuT4_P043000.1	9.8
BofuT4_P047700.1	signal_peptide	0	17	BofuT4_P047700.1	6.9
BofuT4_P047740.1	signal_peptide	0	25	BofuT4_P047740.1	24.0
BofuT4_P055300.1	signal_peptide	0	15	BofuT4_P055300.1	2.7
BofuT4_P056080.1	signal_peptide	0	19	BofuT4_P056080.1	3.6
BofuT4_P059250.1	signal_peptide	0	19	BofuT4_P059250.1	60.0
BofuT4_P059260.1	signal_peptide	0	19	BofuT4_P059260.1	26.0
BofuT4_P059350.1	signal_peptide	0	19	BofuT4_P059350.1	6.2
BofuT4_P059480.1	signal_peptide	0	19	BofuT4_P059480.1	36.0
BofuT4_P061530.1	signal_peptide	0	18	BofuT4_P061530.1	154.0
BofuT4_P061550.1	signal_peptide	0	19	BofuT4_P061550.1	2.4
BofuT4_P061870.1	signal_peptide	0	22	BofuT4_P061870.1	11.0
BofuT4_P063500.1	signal_peptide	0	17	BofuT4_P063500.1	7.5

History

Interop_JA
744.0 KB

12: Select on data 7

7: Column Join on data 5 and data 1

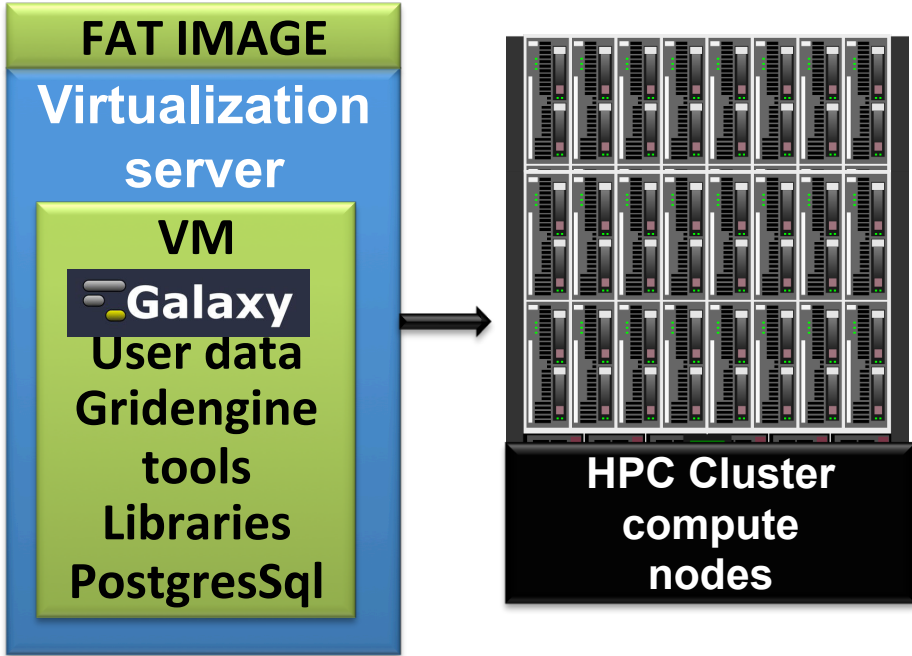
5: Normalized Data Gene upregulated InPlanta.csv

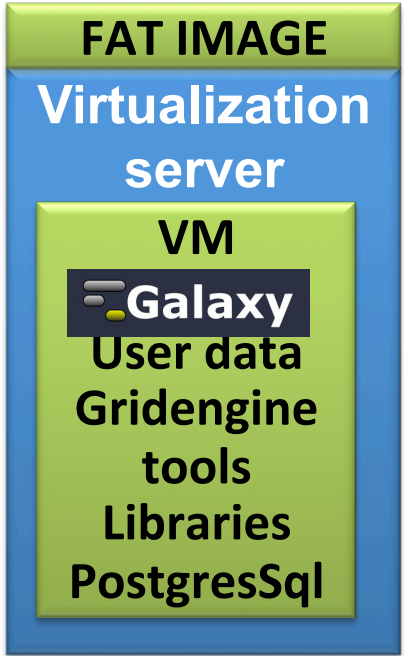
1: Botrytis functional annotation



➤ A Virtual vs physical instance

- For easier monitoring
- To better adapt memory, cpu, storage according to the use

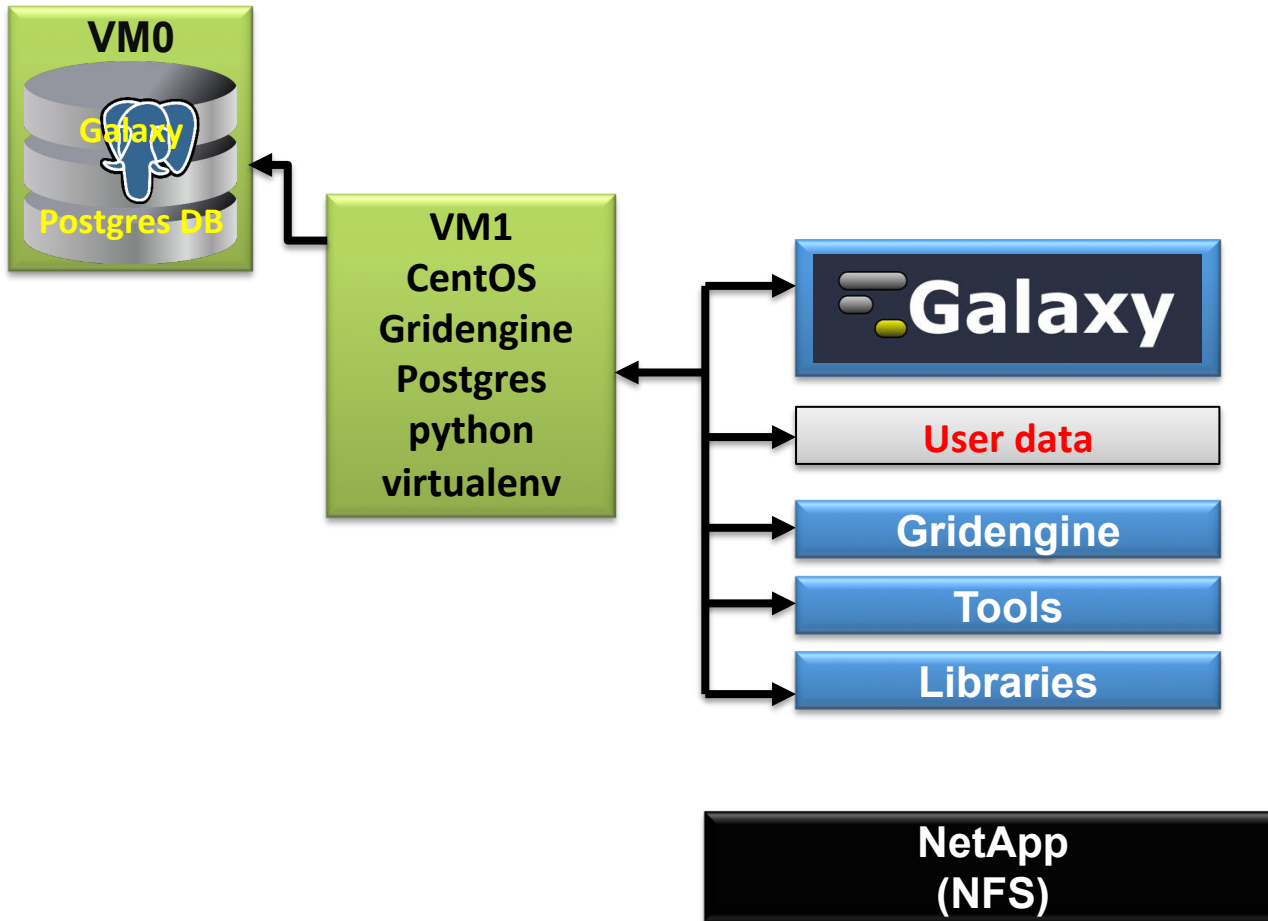




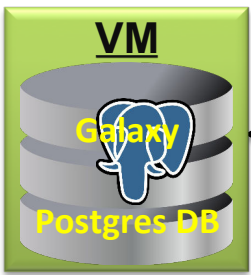
CONS of FAT image

- At each distribution : an entire VM creation
- Duplicated application, dependencies, ...
- Maintenance issues (backup, size ...)

“SLIM” Image



“SLIM” Images



VM
CentOS
Gridengine
Postgres
python
virtualenv

Job submission

Submission proxy node

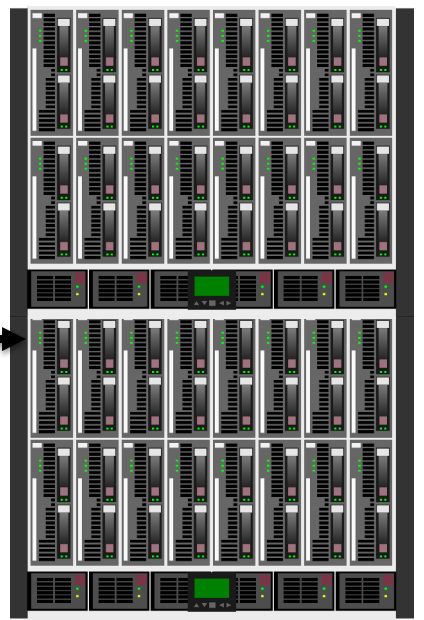
Galaxy

User data

Gridengine

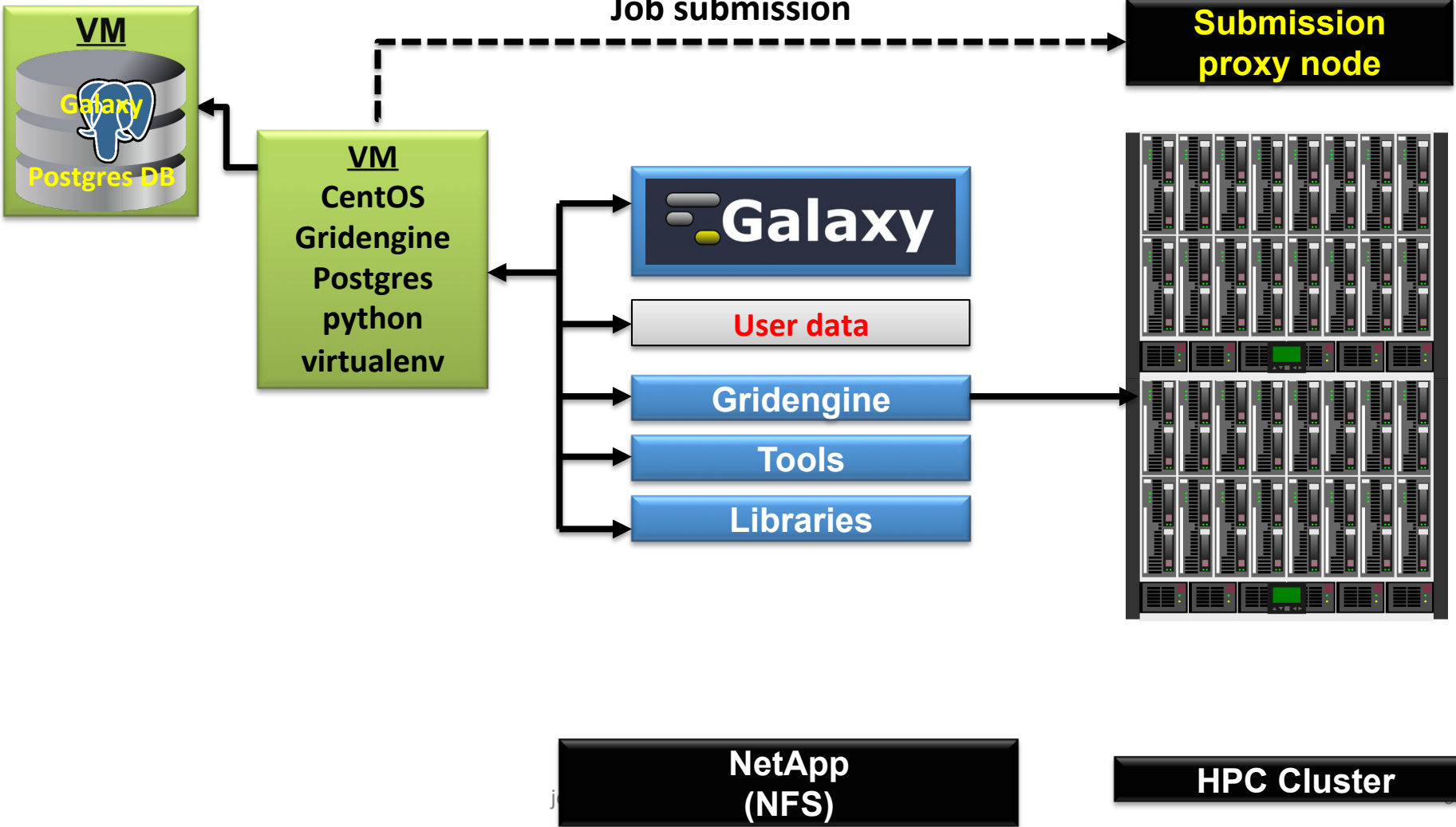
Tools

Libraries

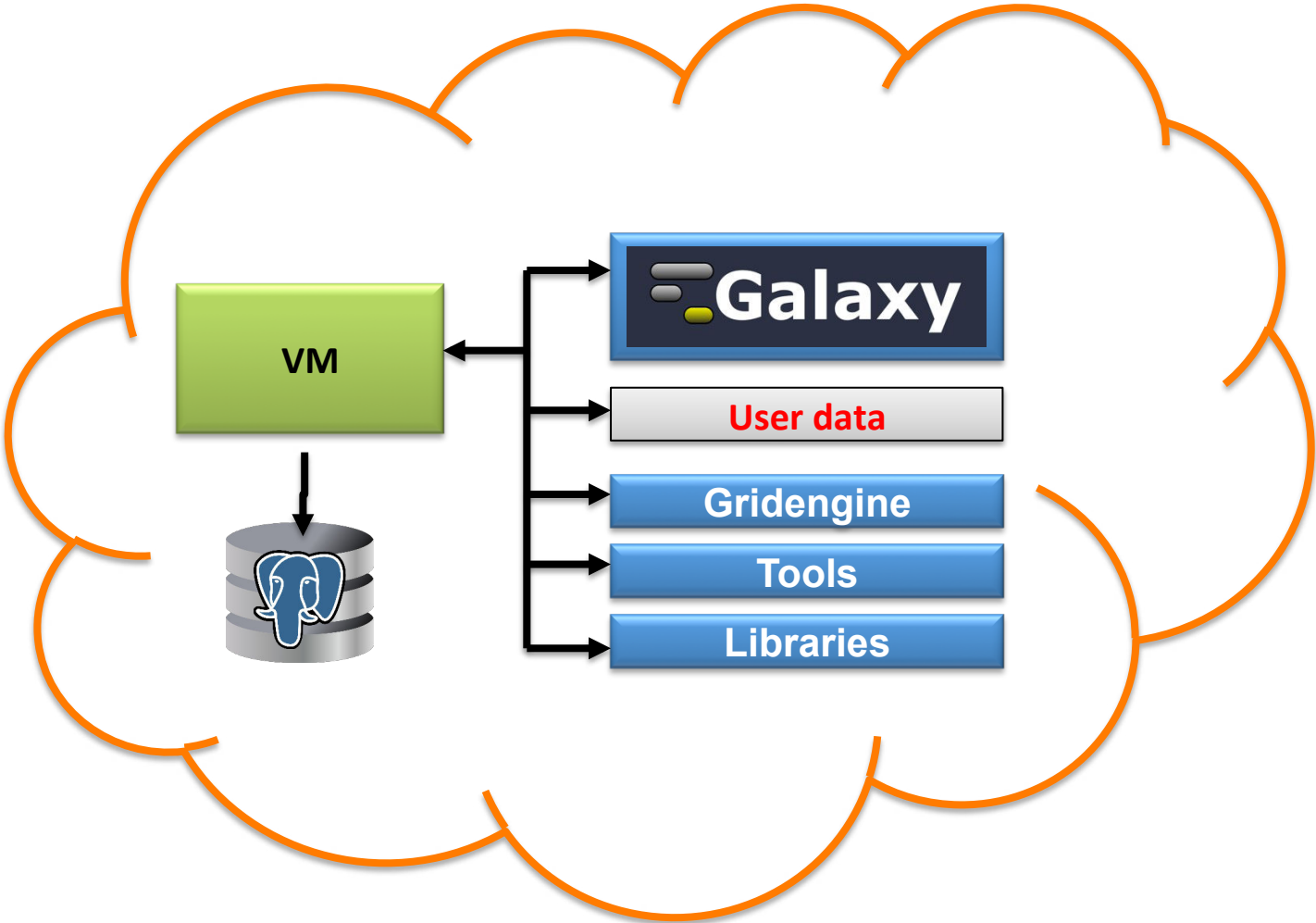


NetApp (NFS)

HPC Cluster



Next step: cloud





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URGI-team

