



Bio-informatic resources for genomic and genetic information system in grapevine

URGI – Bio-informatics Platform
INRA de Versailles, France



Anne-Françoise Adam/Nathalie Choise
PAG - January, 16th 2011

ALIMENTATION
AGRICULTURE
ENVIRONNEMENT



URGI home page

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

Access to GnpIS portal

Access to Vitis resources

The screenshot shows the URGI website home page. At the top, there is a navigation bar with links for FEEDBACK, CONTACT, SITE MAP, and ABOUT US, along with a Register button. The main header features the URGI logo and the text "PLANT AND FUNGI DATA INTEGRATION". Below this is a green navigation menu with categories: Platform, Research, Projects, Data, Tools, and Species. A search bar is located on the right side of the menu. The main content area is divided into several sections. On the left, there is a text block describing URGI as a research unit in genomics and bioinformatics at INRA, dedicated to plant and crop parasites. In the center, there is a circular diagram of tools including GnpMap, GnpSeq, GnpGenome, GnpArray, GnpPro, SIREGal, and Ethesis. Below this is a "GNPIS PORTAL" section with a corn image and a "SPECIES" section with a list of tools like structural variants, genomics, TE annotation, molecular evolution, REPET package, Pipelines, heterochromatin, and TE classification. At the bottom, there is a "RESEARCH" section. On the right side, there is a "WHAT'S NEW?" section with an RSS icon, listing updates for GnpIS 1.6.1, Siregal 1.6.1, and REPET 1.3.12. At the bottom of the page, there is an "EVENTS" section with two entries: "07 Sep 2010 Development of a workflow for" and "02 Dec 2010 Siregal and Ethesis steering".

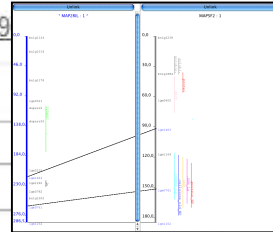
GnpIS: a data warehouse

Quick search

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

Examples: [VVI](#), [VVIF52](#), [gene](#), [arabidopsis](#), [AY109](#)

VVIF52

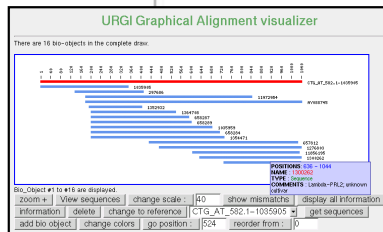


Advanced search

[BioMart](#)

[Galaxy](#)

Specific modules



Genetic maps and QTLs

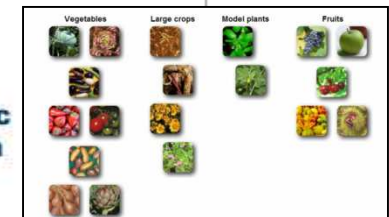
2	36	37	44	67	69	73	76	84	85	110	112	120	121	129	162	190	192	211	223	226	234	235	250	291	297
C	T	T	A	D	P	T	C	T	G	G	T	C	G	C	G	T	C	C	T	A	C	C	T		
C	T	T	A	T		T	C	T	G	G	T	C	G	C	G	T	C	C	T	A	C	C	T		
C	T	T	A	T		T	C	T	G	G	T	C	G	C	G	T	C	C	T	A	C	C	T		
C	T	T	A	T		T	C	T	G	G	T	C	G	A	G	T	C	C	T	A	C	C	T		

EST and other sequences

Polymorphism data

Genome annotation data

Plant genetic resource data



Transcriptome data

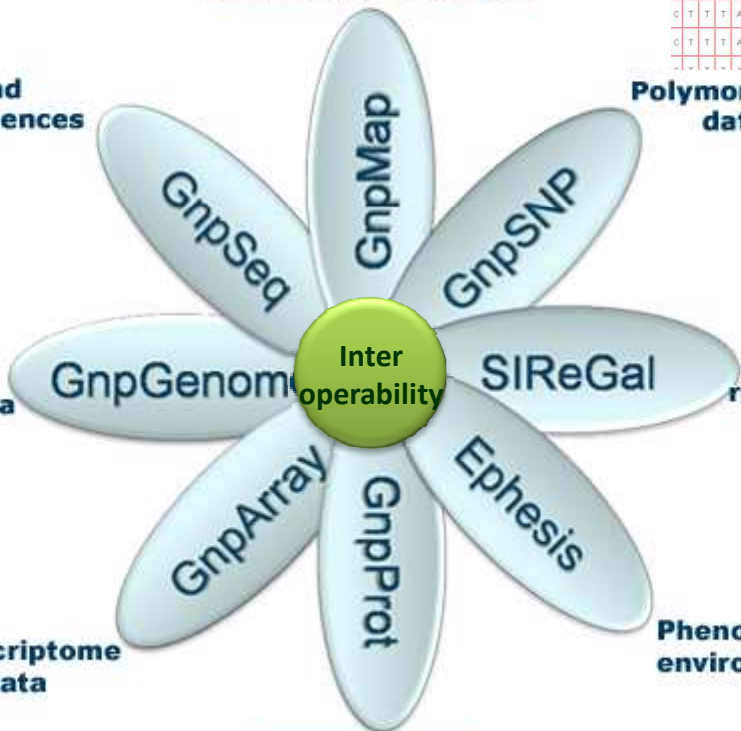
Phenotypic and environmental data

Hybridization results

Accession	Date	Description	Experiment	Array name	Design name	Site name	Product	Accession	Year
1	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
2	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
3	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
4	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
5	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
6	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
7	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008
8	20080808	TA_SAME_1000000	ARRAY OF ARABIDOPSIS	AR_1	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	TA_SAME_1000000_000000	2008



Interoperability



Quick search

Go to GnpMAP

SC8_0084_087 Submit

genome-vitis12x mapping

+ Feature (1)

SC8_0084_087 ★★★★★

Marker details

Marker name	SC8_0084_087
Taxon	Vitis vinifera L.
Marker type	SSR
Marker origin	Genome Sequence
Goal	Mapping
Gene function (manual annotation)	-
Target	GRAPESEQ
Origin laboratory	URGV
Readthrough	-
Insert length	-

Mapped loci

Mapped loci: 4

Locus name	Map name	Taxon	Linkage group	Distance	Reliability / (source map name)	Link to QTL	Link to QTL large
SC8_0084_087	Integrated_2_080717	Vitis vinifera L.	1	43.5	framework	-	-
SC8_0084_087	Bianca_080717	Vitis vinifera L.	1	40.9	framework	-	-
SC8_0084_087	ChRI_080717	Vitis vinifera L.	1	43.4	framework	-	-
SC8_0084_087	Chardonnay_080717	Vitis vinifera L.	1	46.2	framework	-	-

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

SC8_0084_087 Submit

Go to GnpGenome

Vitis vinifera 12x Genome annotation

Vue de 500 kbp depuis chr15, positions 4,873,471 à 5,373,470

Annotations: Vous pouvez faire une recherche en utilisant un nom de séquence, un nom de gène, un locus, ou un autre référentiel. Le caractère spécial * est autorisé. To center on a location, click the ruler. Use the ScrollZoom buttons to change magnification and position. To switch to another organism, use the Data Source menu.

Exemples: chr15:5282664..5322963, GSVAVP001205001, EGF001825201, SWAPV0001698001, GWSVJ0250042001, VV052_VV40024130801_VV_10003495.

[Ajouter cet affichage à vos favoris] [Ajouter vos propres annotations] [Cacher Fen-ête] [Partager ces pistes] [Lien vers une image de cet affichage] [Image haute qualité pour les publications] [Aide] [Réinitialiser à zéro]

Rechercher ou Régler: chr15:4873471..5373470 Rechercher Sorties, recherches et autres opérations: Exporter en PDF, Télécharger, Lancer

Source de données: Vitis vinifera 12x Genomes Browser DVH/Zoom: 500 bp | Voir 500 kbp | 300 | Inversion

Détails: Exporter le schéma, Mise à jour de l'image

Filtres: Afficher / Masquer, Tout activer / Tout désactiver

Annotations: Afficher / Masquer, Tout activer / Tout désactiver

Annotations Prédictes: Afficher / Masquer, Tout activer / Tout désactiver

Annotations (à venir): Afficher / Masquer, Tout activer / Tout désactiver

Expressions Locus: Afficher / Masquer, Tout activer / Tout désactiver

Transcriptomic experiments (Full rates): Afficher / Masquer, Tout activer / Tout désactiver

Gene annotations: Afficher / Masquer, Tout activer / Tout désactiver

Genomic annotation (Gaps): Afficher / Masquer, Tout activer / Tout désactiver

Genomic: Afficher / Masquer, Tout activer / Tout désactiver

Advanced search : BioMart



URGI Genomique-info

New Count Results URL XML Perl Help

Export all results to: File TSV Unique results only Go

Email notification to:

View: 10 rows as HTML Unique results only

Map Name	Link Map URGI	Genus	Project Name	Marker Name	Link Marker URGI	Feature Name	Feature Type	Genus	Analysis Name
Grenache_031220	47	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Syrah_031220	46	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Integrated	79	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_F_CS	81	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_Integrated	83	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_M_Bianca	70	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_F_Chardonnay	69	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
SG_031220	48	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Integrated_fw	78	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
A1_C_SG	67	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation

Dataset
GnpMap

Filters
Marker Name (% for wildcard): [ID-list specified]

Attributes
Map Name
Link Map URGI
Genus
Project Name
Marker Name
Link Marker URGI

Dataset
GnpGenome Vitis

Filters
Feature Type: STS

Attributes
Feature Name
Feature Type
Genus
Analysis Name

GnpMap ↑

GnpGenome ↑



URGI pipelines

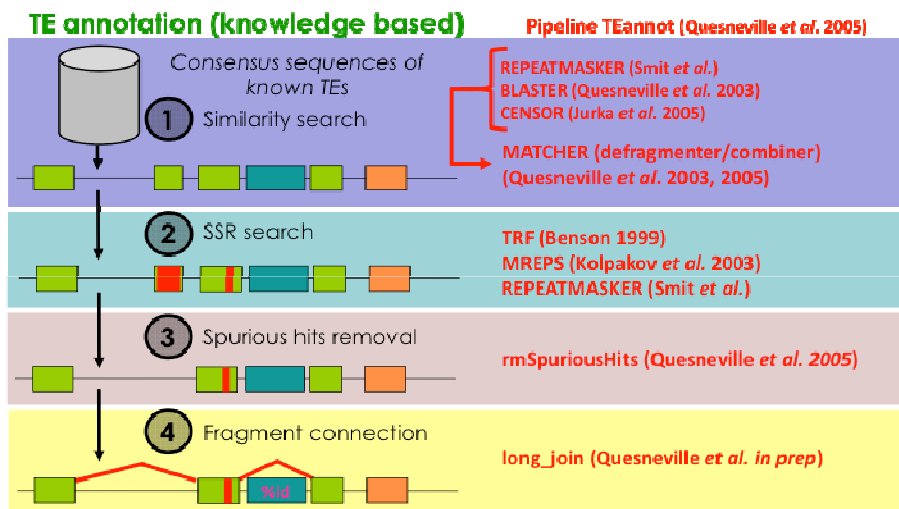
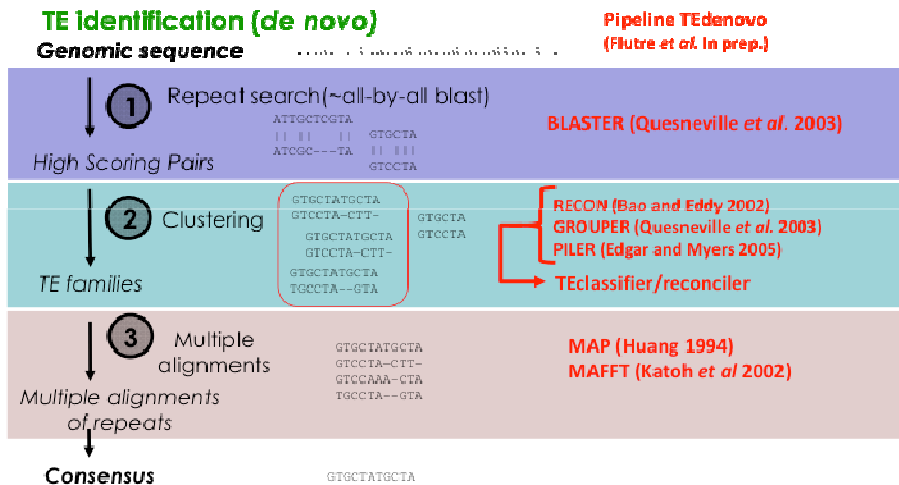


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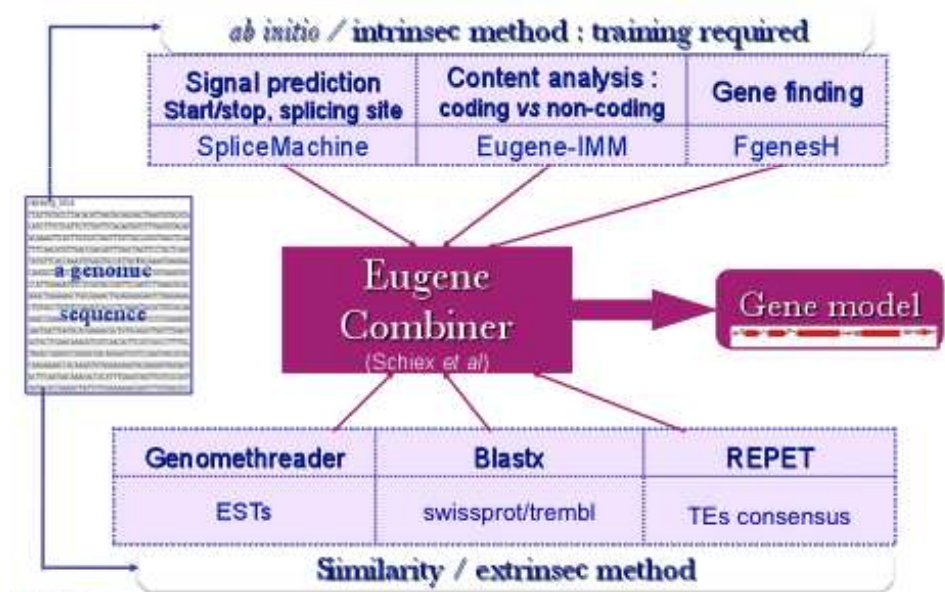


Pipeline for Structural Annotation

Transposable Elements : REPET



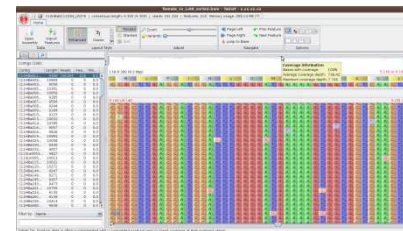
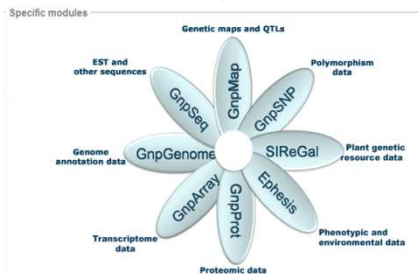
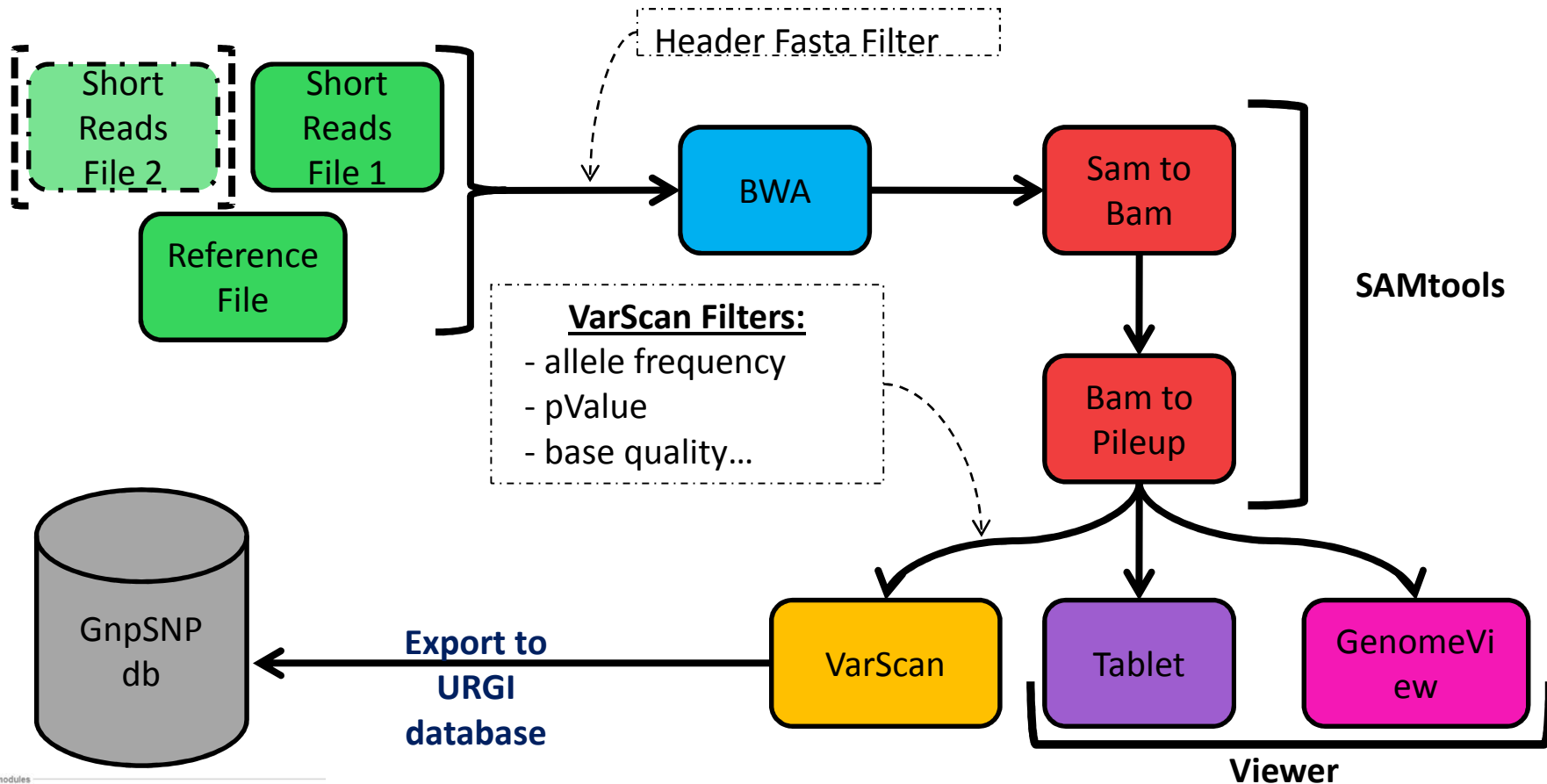
Genes : EuGene



Foissac S, Gouzy J, Rombauts S, Mathé C, Amselem J, Van de Peer Y, Rouzé R, Schiex T (2008) Genome Annotation in Plants and fungi : Eugene as a model platform *Curr Bioinf* 3:87-97

Pipeline for SNP detection: MAPHiTS

Mapping Analysis Pipeline for High-Throughput Sequences



MAPHiTS workflow in Galaxy

(a web-based platform for genomic research : <http://usegalaxy.org>)

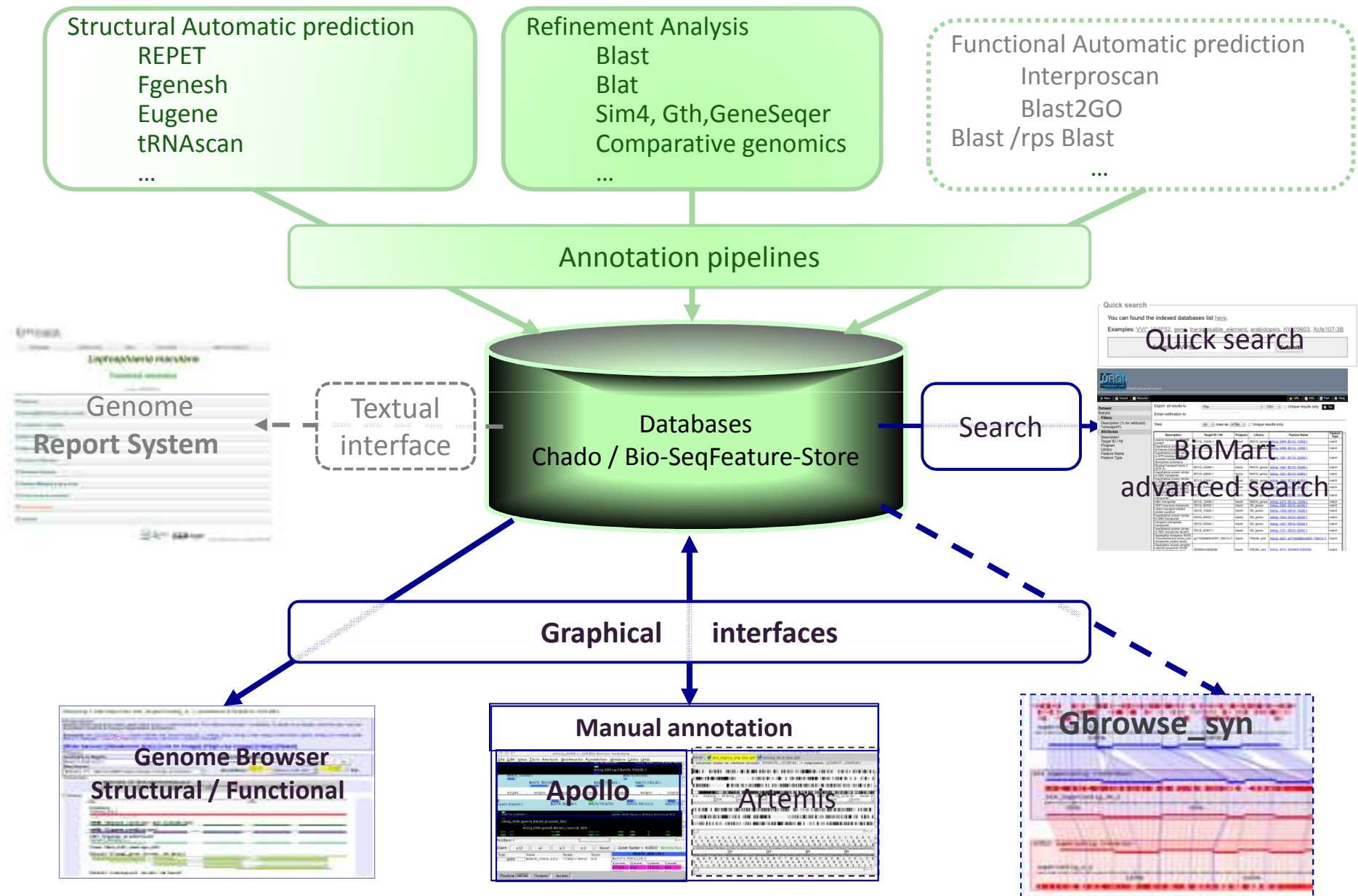
The screenshot displays the Galaxy web interface for a workflow named "Unnamed workflow". The workflow canvas contains the following steps:

- Input Dataset** (two instances) connected to **Map with Bwa 0.5.7**.
- Map with Bwa 0.5.7** outputs: output_RES (sam), output_ERROR_INDEX (text), output_ERROR_ALN (text), output_ERROR_BINtoSAM (text).
- SAM-to-BAM** (Convert SAM file) receives input from the SAM output of the previous step and outputs: output1 (bam).
- Generate pileup** (Using reference file) receives input from the BAM output and outputs: output1 (tabular).
- Tablet (v.1.10.03.04)** (Alignment Viewer) receives input from the pileup output and outputs: Fichier Bam / Sam / Map / autres... and Référence Input.fasta.

The left-hand menu lists various tools, including "URGI NGS" and "Tablet (v.1.10.03.04)". The right-hand panel provides details for the selected "Tablet" tool, including its version, input/output files, and a list of features such as high-performance visualization, support for multiple file formats, and search capabilities.

http://localhost:8080/workflow/editor?id=f06d708dacad69d8#

Pipelines, DBs, Interfaces





Vitis vinifera resources

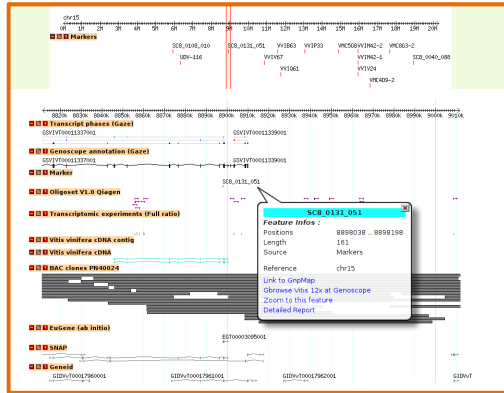
<http://urgi.versailles.inra.fr/index.php/urgi/Species/Vitis>



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Markers



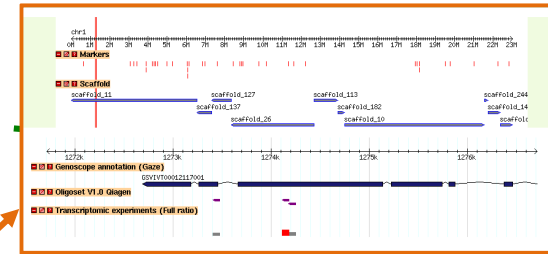
Gene - BofuT4_P034230.1

GnpArray

Transcriptomics db (in progress)

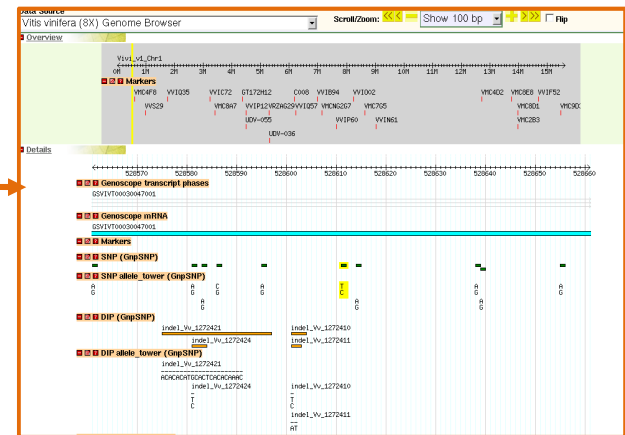
Gene details, Annotations, Normalized data

Transcriptomics data (GRASP project)



Qiagen V1.0 oligoset

Polymorphism data



GnpMap

Map db

- 27 Vitis maps
- New: Integrated_2

GnpGenome

12X GBrowser

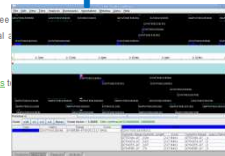
V0 and V1 (private) annotations

Vitis projects

Genome sequence and annotations

- Access with GBrowse to the private annotations of the grapevine genome 12x sequence
- Download the grapevine genome 12x sequence (chromosome, scaffolds, contigs)
- CMap 12x and 8x: Comparative map tool: Genome sequence links with the grapevine reference genetic map.

Apollo



SiREGAL

Genetic resources db

Plante: Vigne

- Vassal collection (7000 accessions)
- Centre de Ressources Génétiques (CRG)
- Réseau National de Conservation des Ressources Génétiques

GnpSNP

Polymorphism db

1000 gene fragments x 48 indiv (soon public)

Grapevine genome annotation



automatic annotation

12X-V0
12X-V1 (private)



manual annotation

Ex: famille TPS (Martin et al 2010)

Quantity



whole genome scale

genes scale

Availability



fast

low, progressive

Quality



- weaknesses of gene predictors
- errors in spliced alignments
- poor justifications
- limited functional annotations
- error propagation

- checked and curated predictions
- optimised parameters/tools
- based on knowledge/experiments
- systematic justifications
- deep functional annotations
- links to references




COMPLEMENTARITY

Platform for distributed curation of the annotation

<http://urgi.versailles.inra.fr/index.php/urgi/Species/Vitis/Resources/Genome-sequence-and-annotations>

Genome sequence and annotations

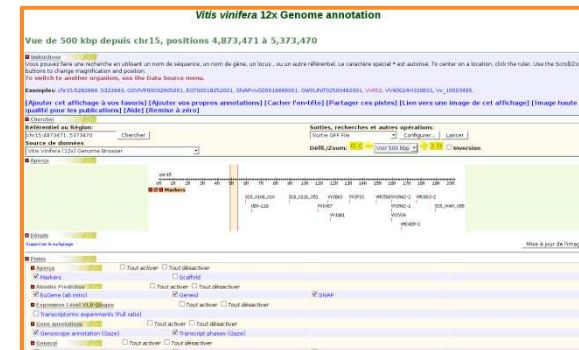
Genome sequence

- The [grapevine genome 12X draft sequence](#) and its annotations are available with GBrowse
- Access with GBrowse to the **private annotations** of the grapevine genome 12X sequence 
- [Download](#) the grapevine genome 12X sequence (chromosome, scaffolds, contigs)
- [CMap 12X and 8X](#) : Comparative map tool : Genome sequence links with the grapevine reference genetic map.


The [grapevine genome 8X draft sequence](#) and its annotations are available with GBrowse.

The retrieve and annotation of gene families is facilitated in [FLAGdb++](#).

12X Gbrowse (public and private data)

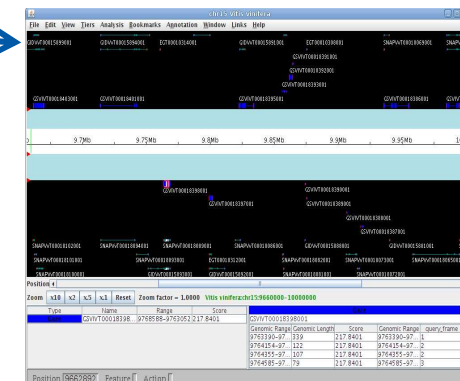


Distributed manual annotation system

Apollo Webstart . Under the supervision of the Annotation Committee of the [IGGP](#) (International Grape Genome Program), URGI provides tools for the manual curation of the structural annotation of the grapevine genome 12X version.

The access is restricted to the **grapevine community**. Please [contact us](#) to get access.

Apollo : Genome Annotation and Curation Tool



Apollo : Genome Annotation and Curation Tool

The screenshot shows the Apollo Genome Editor website. At the top, there is a navigation bar with links for FEEDBACK, CONTACT, SITE MAP, and ABOUT US. The main header features the EURLGI logo and the text "PLANT AND FUNGI DATA INTEGRATION". A "Register" button is located in the top right corner. Below the header is a green navigation menu with tabs for Platform, Research, Projects, Data, Tools, and Species. A search bar is positioned to the right of the menu. The "Tools" section is active, displaying a list of tools on the left: SRS (registered access), Triannot Pipeline, S-MART, Full list, Blast, Gnpis, REPET, Apollo, and BLASTER. The main content area is titled "Apollo Genome Editor" and includes a breadcrumb trail: "You are here: Home / Data / Apollo". The text describes the Apollo genome editor as an application for browsing and editing genomic sequences. It notes that manual gene curation is available for specific genomes, with access restricted to their respective consortia. A list of these consortia is provided: Botrytis cinerea, Leptosphaeria maculans, Tuber melanosporum, Vitis vinifera, and Tranznet. Below this, there is a section for "Apollo webstart access for projects" which includes links to download and read a PDF file (ApolloWebstart.pdf, 328.04 kB) and an introduction to Apollo and rules for gene edition (Apollo_intro_and_rules.pdf, 2.00 MB). A red arrow points from the "Tranznet" link in the list to the text "Apollo WebStart" on the right side of the page.

FEEDBACK | CONTACT | SITE MAP | ABOUT US

EURLGI PLANT AND FUNGI DATA INTEGRATION Register

Platform Research Projects Data Tools Species SEARCH

Tools

You are here: Home / Data / Apollo

Apollo Genome Editor

Apollo genome editor: an application for browsing and editing genomic sequences.

Apollo has been set up to allow manual gene curation on different genomes. The access is restricted to their respective consortia. Please [contact us](#) to get access if you belong to one of them:

- Botrytis cinerea
- Leptosphaeria maculans
- Tuber melanosporum
- Vitis vinifera
- Tranznet

Apollo webstart access for projects

Download and READ before launching Apollo-webstart [ApolloWebstart.pdf \(328.04 kB\)](#)

Introduction to Apollo and rules to follow for gene edition [Apollo_intro_and_rules.pdf \(2.00 MB\)](#)

- For Linux, Mac (10.5 or higher (Leopard), Windows user
 - [Botrytis cinerea](#)
 - [Leptosphaeria maculans](#)
 - [Tuber melanosporum](#)
 - [Vitis vinifera](#)
 - [Tranznet](#)

→ Apollo WebStart

Apollo : Genome Annotation and Curation Tool

The screenshot shows the 'Apollo: load data' dialog box. It has a title bar with a close button. The main content is organized into sections: 'Choose data source:', 'Chado database', 'Username and password', and 'Select a region to display'. The 'Choose data source:' section has a dropdown menu currently set to 'Chado database'. The 'Chado database' section has a dropdown menu set to 'Vitis Apollo-Chado Annotation Database (training)'. The 'Username and password' section has a 'Login:' field with 'ovitis12xapotrain' and a 'Password:' field with masked characters. The 'Select a region to display' section has a 'Type of region:' dropdown set to 'chromosome', a 'Choose Chromosome:' dropdown set to 'chr15', a 'Start:' text box with '9660000', and an 'End:' text box with '10000000'. At the bottom are 'Ok' and 'Cancel' buttons. Annotations include arrows pointing from text boxes to these fields: 'Select Chado database' points to the top dropdown; 'Select Vitis database' points to the middle dropdown; 'login/password for write mode' (in a red box) points to the password field; 'chr1, chr1_random, ... chrUn' points to the 'Choose Chromosome:' dropdown; and 'Fill with the start and end position of region you need to display' points to the 'Start:' and 'End:' text boxes. A blue oval highlights the 'Start:' and 'End:' fields.

Choose data source:
Chado database

Chado database

Chado database
Chado database Vitis Apollo-Chado Annotation Database (training)

Username and password
Login: ovitis12xapotrain
Password:

Select a region to display
Type of region: chromosome Start: 9660000
Choose Chromosome: chr15 End: 10000000

Ok Cancel

Select Chado database

Select Vitis database

login/password for write mode

chr1, chr1_random, ... chrUn

Fill with the start and end position of region you need to display

Apollo Editing and curating interface

Analysis tracks

Control panels size

Editing panel for gene models

Zoom

Selected feature information

Type	Name	Range	Score	Gaze	
Gaze	GSVIVT00018398...	9768588-9763052	217.8401	GSVIVT00018398001	
				Genomic Range	Genomic Length
				9763390-97...	339
				9764154-97...	122
				9764355-97...	107
				9764585-97...	79

Evidences available in Apollo

Types		
<input type="checkbox"/> Sort	Annotation	Show <input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> Label		Expand <input checked="" type="checkbox"/>
<input type="checkbox"/> Sort	Gaze Prediction	Show <input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> Label		Expand <input checked="" type="checkbox"/>
<input type="checkbox"/> Sort	JigsawGaze V1NR	Show <input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> Label		Expand <input checked="" type="checkbox"/>
<input type="checkbox"/> Sort	JigsawGaze V1R0	Show <input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> Label		Expand <input checked="" type="checkbox"/>
<input type="checkbox"/> Sort	Gene Prediction	Show <input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> Label		Expand <input checked="" type="checkbox"/>
<input type="checkbox"/> Sort	cDNA_Vv	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	EST_Vv	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	EST_Vv_redon	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	EST_Dicot	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	Contigs_454	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	Contigs_solexa	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input checked="" type="checkbox"/>
<input type="checkbox"/> Sort	Protein Analysis	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	Repeat	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	Start Codon	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>
<input type="checkbox"/> Sort	Stop Codon	Show <input checked="" type="checkbox"/>
<input type="checkbox"/> Label		Expand <input type="checkbox"/>

VO annotation from Genoscope (GAZE prediction)

V1 annotation from CRIBI (JigsawGaze V1NR) : non repetitive sequences

V1 annotation from CRIBI (JigsawGaze V1R0) : repetitive sequences

Ab initio prediction : Geneid, SNAP, Eugene

Vitis vinifera cDNA

Vitis vinifera public ESTs

Vitis vinifera public ESTs (redondant)

Dicotyledons public ESTs (except *Vitaceae*)

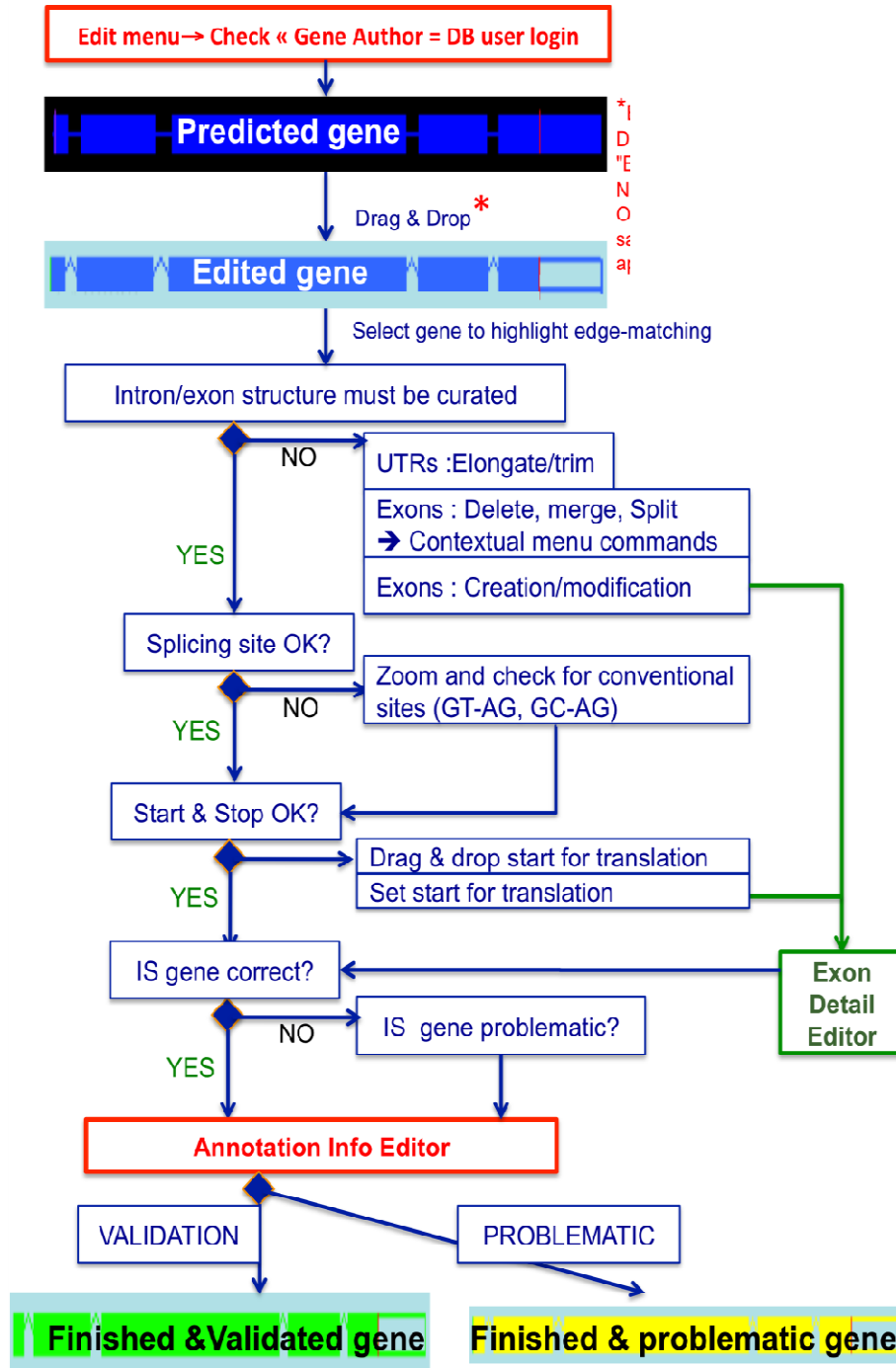
Vitis vinifera 454 contigs assembly

Vitis vinifera G-Mo.R-Se (Gene Modelling using RNA-Seq) coding models

Genewise (Uniprot)

Repeats : RepeatMasker and TRF (Tandem Repeat Finder)

Annotation rules for gene editing



NBS-LRR jamboree
Versailles, 22-24th November 2010

The NBS-LRR gene family



chr18 Vitis vinifera

File Edit View Tiers Analysis Bookmarks Annotation Window Links Help

Solexa contigs **Repeats**

De novo gene predictions

V1 V0

MANVitV_chr18T18000027001-gdigaspe

23.68Mb 23.682Mb 23.684Mb 23.686Mb 23.688Mb 23.69Mb 23.692Mb

Position

Zoom Zoom factor = 81.9200 Vitis vinifera:chr18:23000000-24000000

Type	Name	Range	Score	MANVitV_chr18G18000027001-gdigaspe			
gene	MANVitV_chr18T1...	23682046-2368...	0.0	MANVitV_chr18G18000027001-gdigaspe			
				Genomic Range	Genomic Length	Genomic Range	Genomic Length
				23682046-23682542	497	23682046-23682542	497
				23683206-23684301	1096	23683206-23684301	1096
				23684456-23684773	318	23684456-23684773	318
				23684870-23686804	1935	23684870-23686804	1935

Position Feature Action

Valided gene by Gabriele Di Gaspero

Annotation info editor

MANVitV_chr18G18000027001-gdigaspe Annotation Information

Annotations
MANVitV_chr18G18000023001-ncf
MANVitV_chr18G18000027001-gdi
MANVitV_chr18T18000027001-

gene MANVitV_chr18G18000027001-gdigaspe

Symbol

Synonyms

<input type="button" value="add"/>	<input type="button" value="delete"/>	<input type="text" value="Vv18s0117g00360"/> <input type="text" value="GSVIVG01012762001"/>
------------------------------------	---------------------------------------	--

Is problematic?

Type

ID Value	DB Name

transcript MANVitV_chr18T18000027001-gdigaspe

Symbol

Synonyms

<input type="button" value="add"/>	<input type="button" value="delete"/>	<input type="text" value="Vv18s0117g00360.t01"/> <input type="text" value="GSVIVT01012762001"/>
------------------------------------	---------------------------------------	--

Is problematic?

Finished?

Author **gdigaspe**

All splice sites match consensus

+1 translational frame shift **No**

-1 translational frame shift **No**

Missing start codon **No**

Missing stop codon **No**

Unconventional start codon **No**

Comments and properties

MANVitV_chr18G18000027001-gdigaspe comments:
1. based on V1 model

MANVitV_chr18G18000027001-gdigaspe properties:
LAST MODIFIED ON: Wed Nov 24 16:29:47 CET 2010

MANVitV_chr18T18000027001-gdigaspe properties:
LAST MODIFIED ON: Wed Nov 24 16:29:47 CET 2010, Wed Nov 24 16:29:47 CET 2010

Genomic sequencing errors

Follow selection

Save gene models manual annotation

Apollo (private website)



Write

Chado

Read

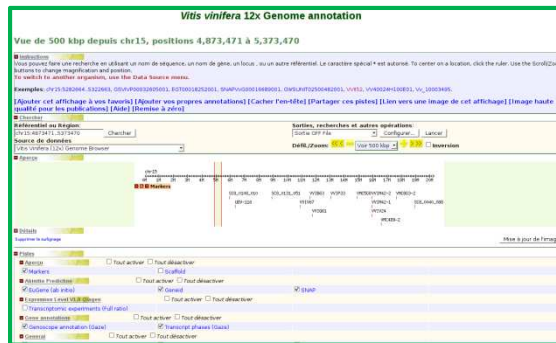
Export Edited genes (GFF3)

Problematic genes

In progress genes

Finished genes

Gbrowse update

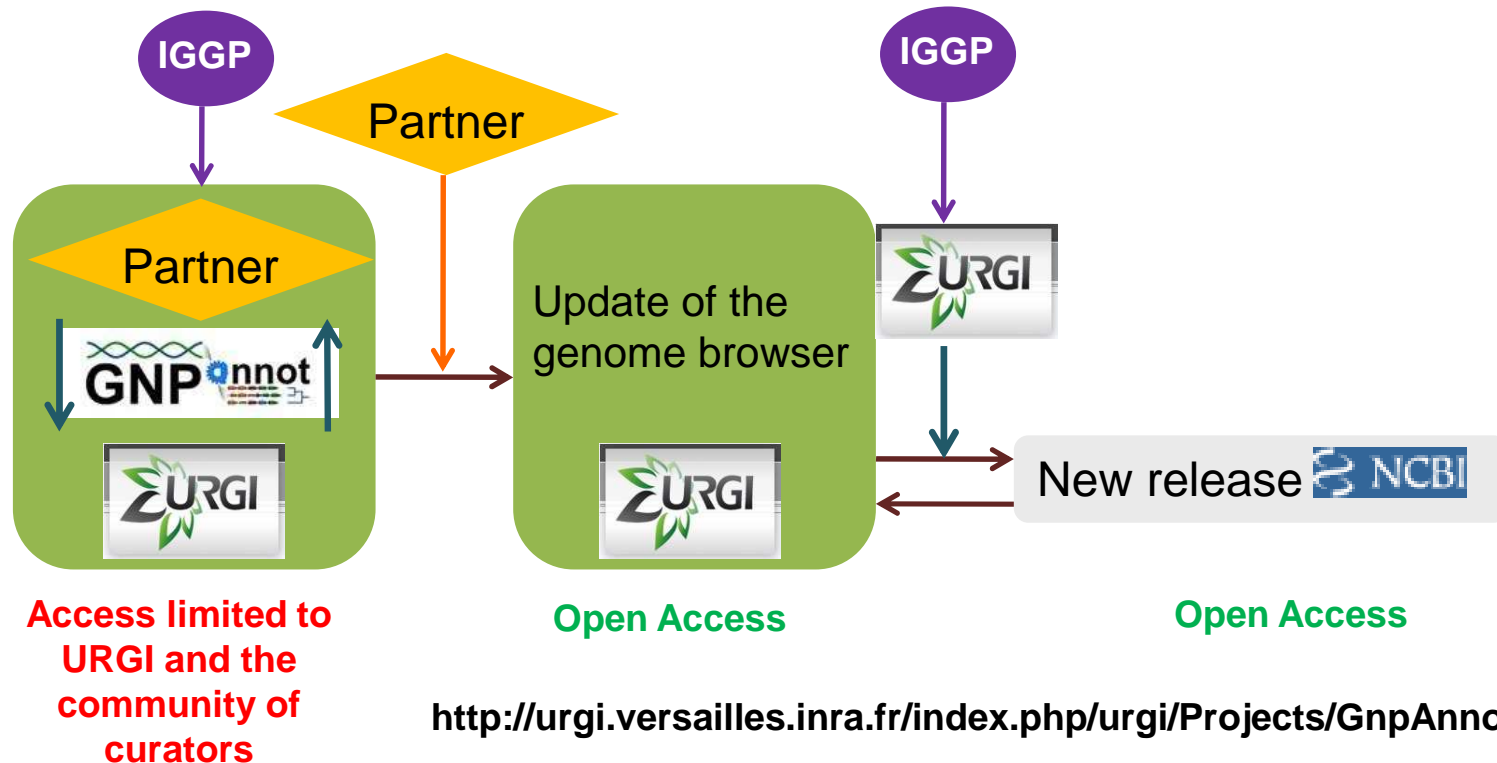


Read

Bio:Seq:
Feature
store

New complete
release

Perspectives/Conclusion



Towards a V2 version of the annotation, based on the V1 and including curated gene models

=> Basis for the functional annotation



Acknowledgment



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- | | |
|-------------------|-----------------------|
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