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

URGI – Bio-informatics Platform

INRA de Versailles, France

Anne-Françoise Adam/Nathalie Choisne

PAG - January, 16th 2011

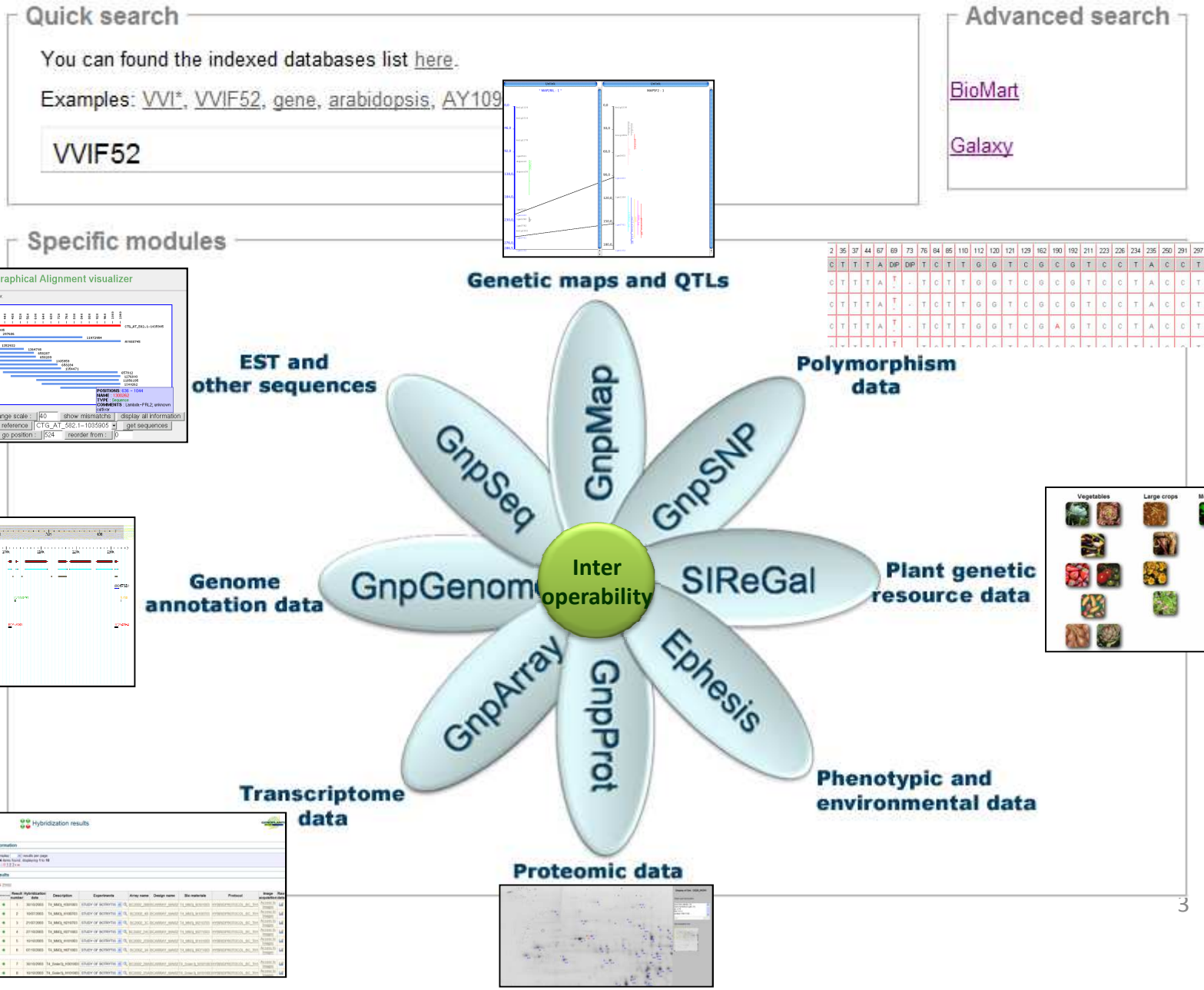
ALIMENTATION
AGRICULTURE
ENVIRONNEMENT

URGI home page
http://urgi.versailles.inra.fr

Access to GnpIS portal

Access to Vitis resources

GnpIS: a data warehouse



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

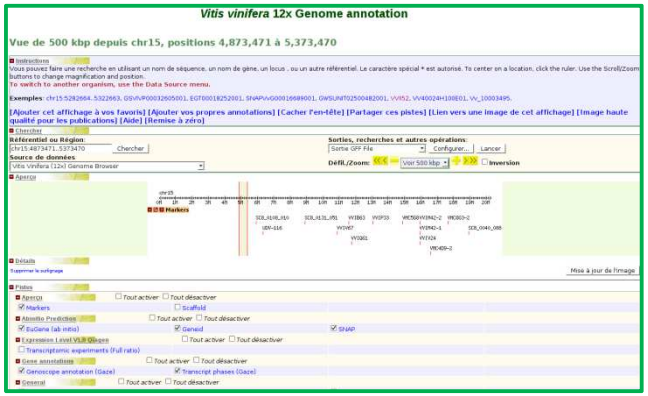
Mapped loci: 4

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	ChBi_080717	Vitis vinifera L.	1	43.4	framework	-	-
SC8_0084_087	Chardonnay_080717	Vitis vinifera L.	1	46.2	framework	-	-

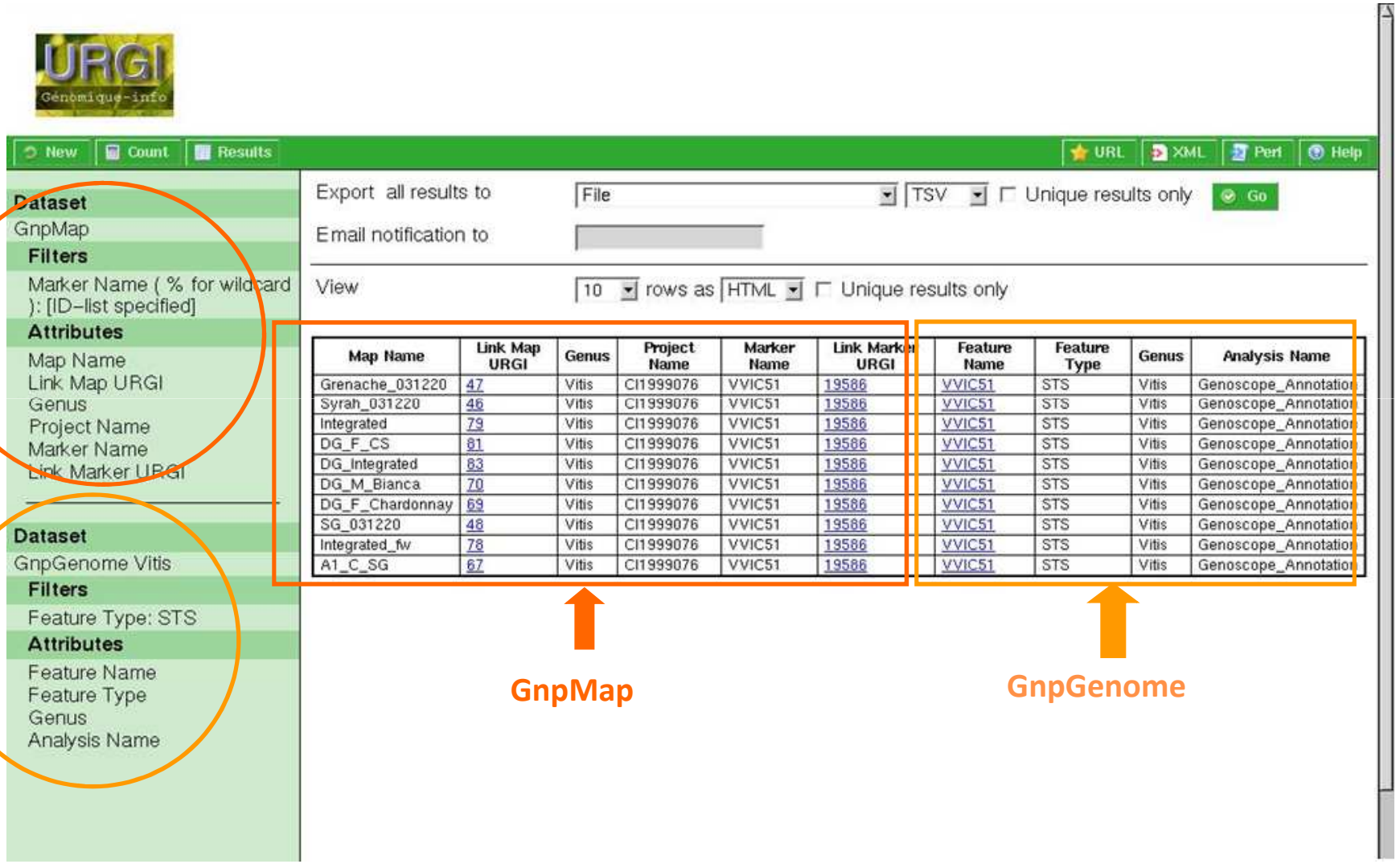
|◀◀ ◀ ▶ ▶▶| 1 items found, displaying 1 to 1 | Display 10 results per page

SC8_0084_087 Submit

Go to GnpGenome



Advanced search : BioMart

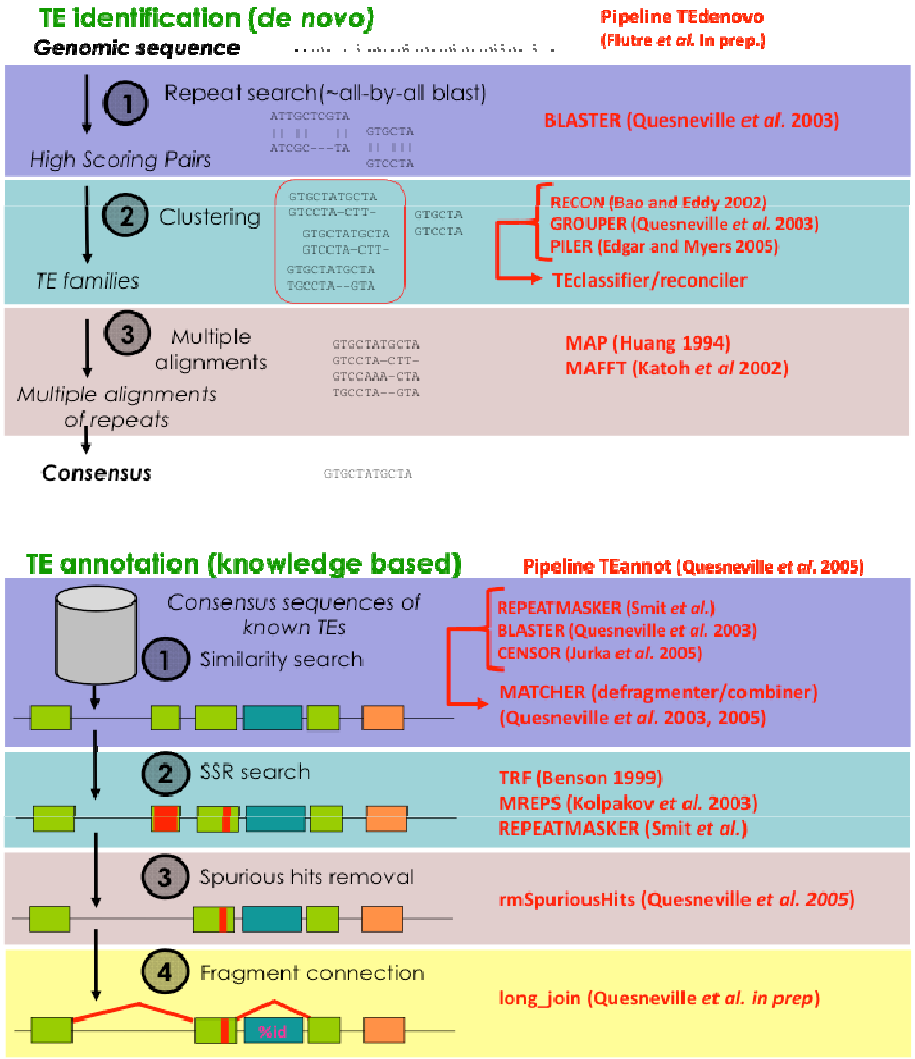


Map Name	Link Map URGI	Genus	Project Name	Marker Name	Link Marker URGI	Feature Name	Feature Type	Genus	Analysis Name
Grenache_031220	47	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Syrah_031220	46	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Integrated	79	Vitis	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

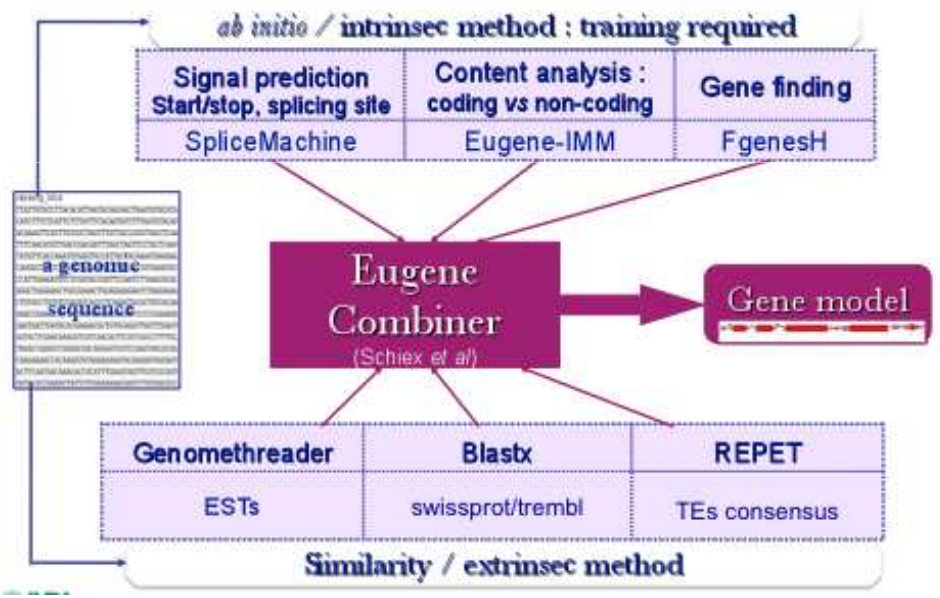
URGI pipelines

Pipeline for Structural Annotation

Transposable Elements : REPET



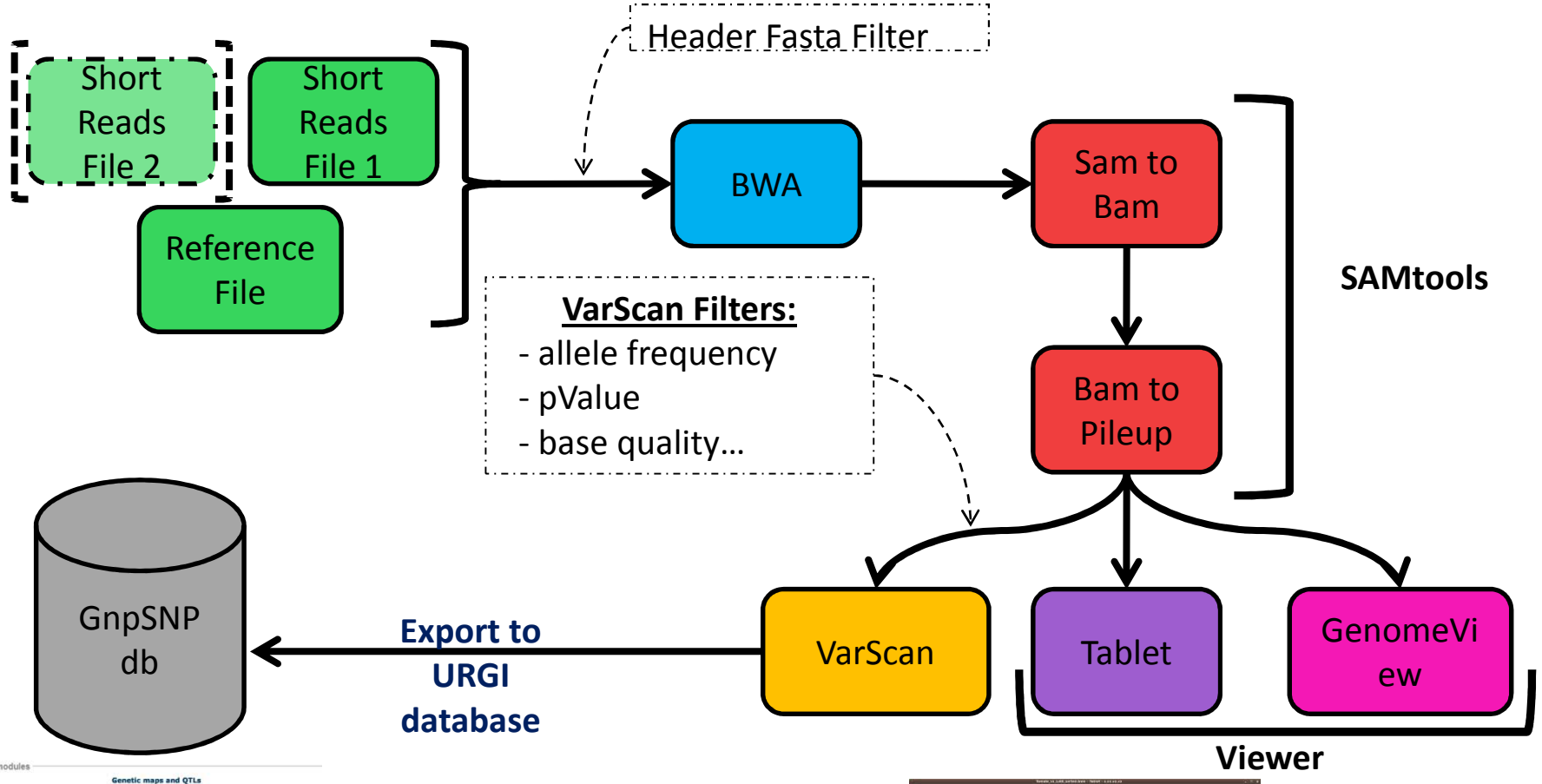
Genes : EuGene

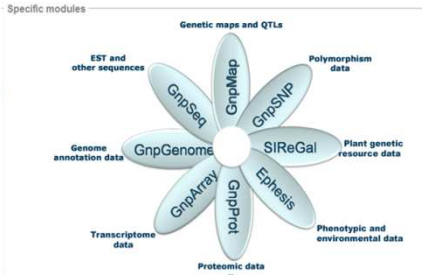


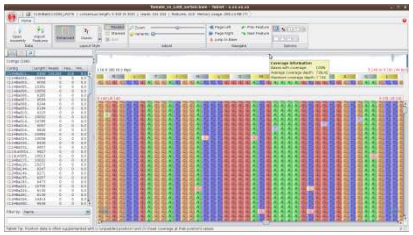
Foissac S, Gouzy J, Rombauts S, Mathé C, Amselem J, Van de Peer Y, Rouzé R, Schiex T (2008) Genome Annotation in Plants and fungi : Eugene as a model platform Curr Bioinf 3:87-97

Pipeline for SNP detection: MAPHiTS

Mapping Analysis Pipeline for High-Throughput Sequences

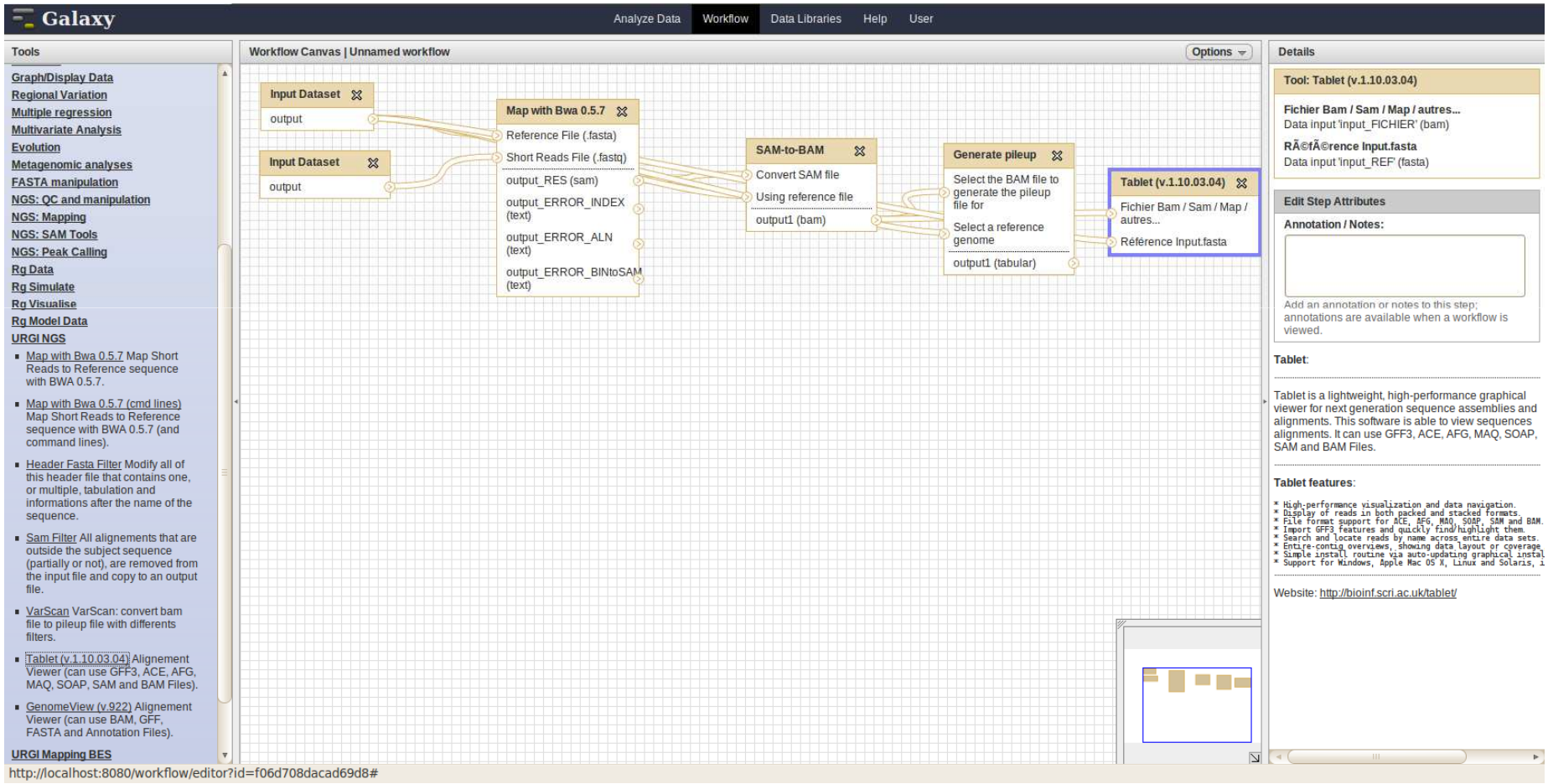




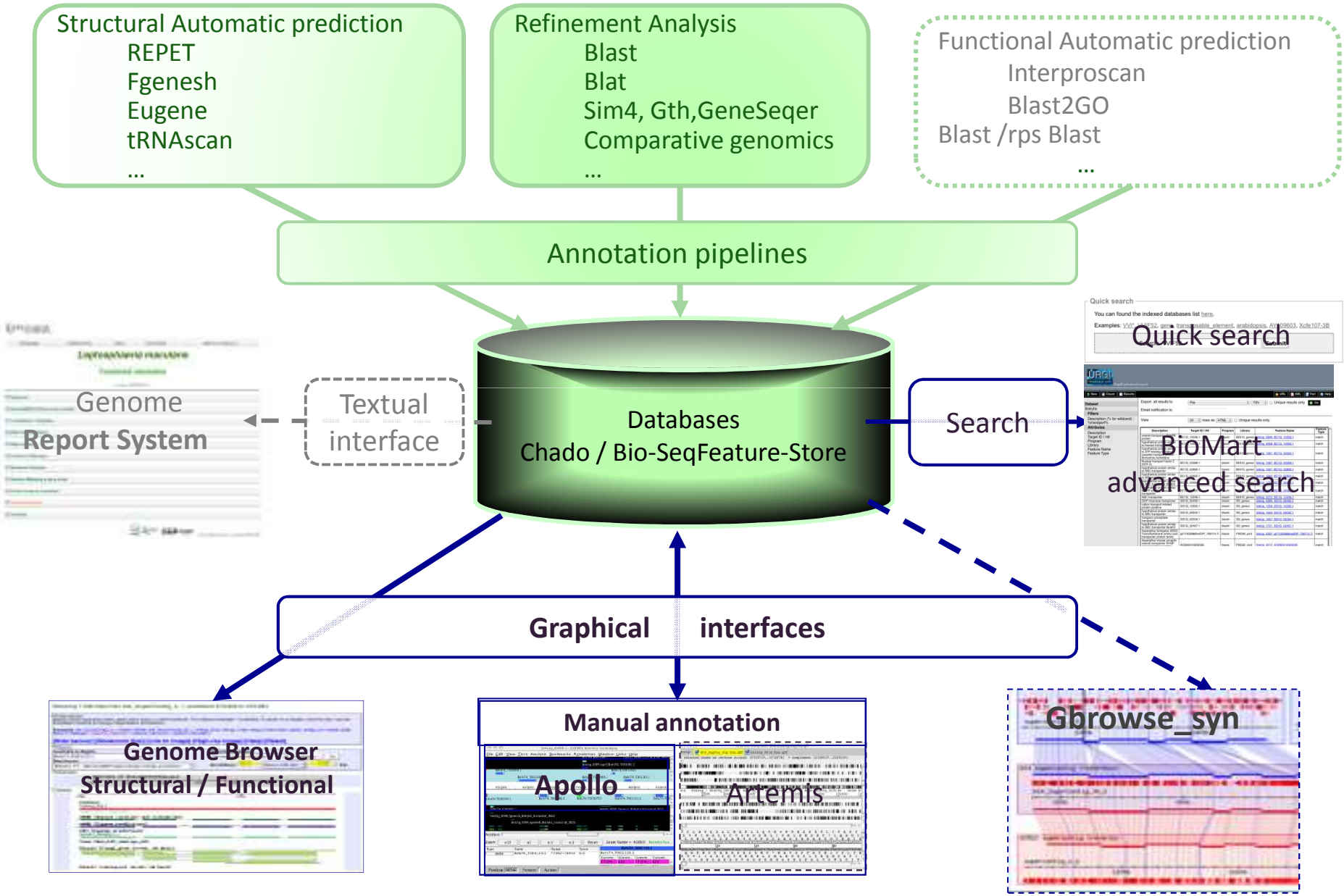


MAPHiTS workflow in Galaxy

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



Pipelines, DBs, Interfaces

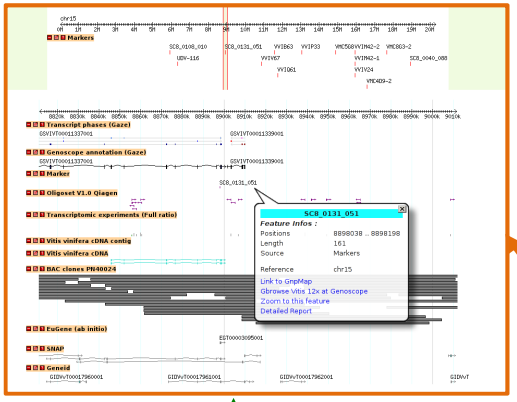


Vitis vinifera resources

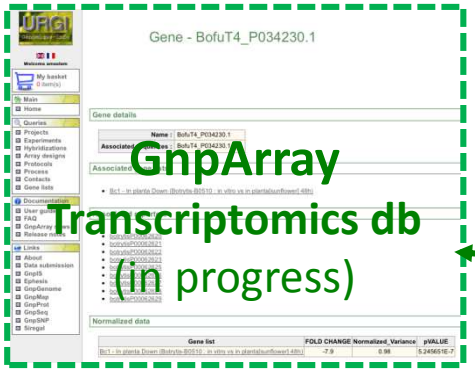
http://urgi.versailles.inra.fr/index.php/urgi/Species/Vitis

ALIMENTATION
AGRICULTURE
ENVIRONNEMEN

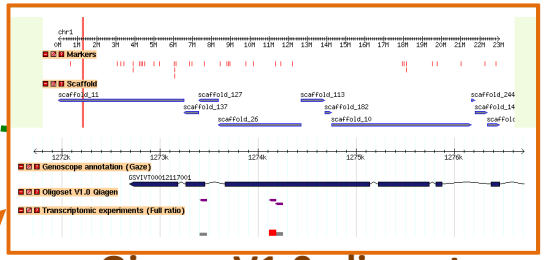
Markers



GnpArray
Transcriptomics db
(in progress)



Transcriptomics data
(GRASP project)

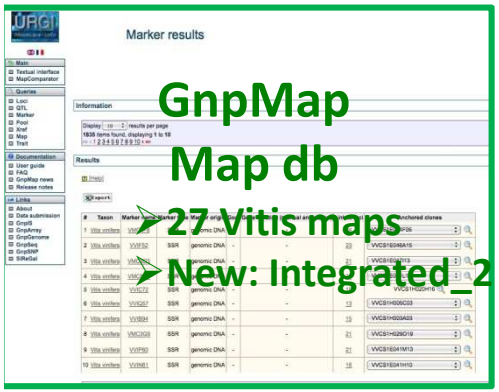


Qiagen V1.0 oligoset

GnpMap
Map db

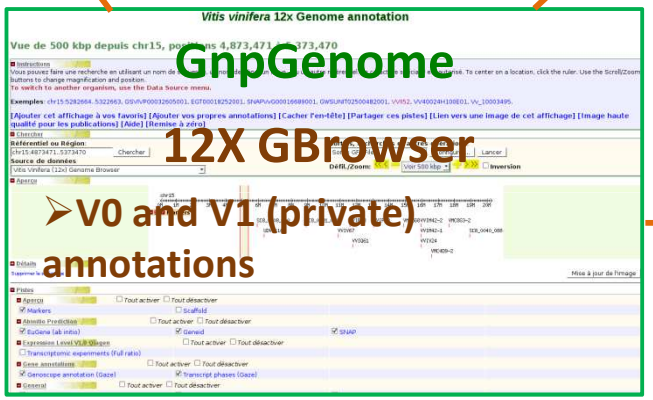
➢27 Vitis maps

➢New: Integrated_2

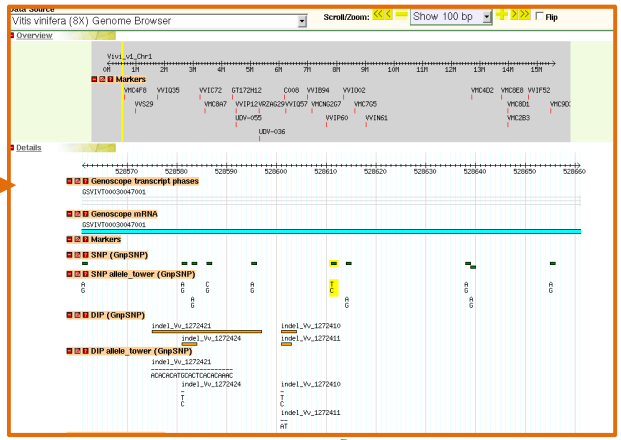


GnpGenome
12X GBrowser

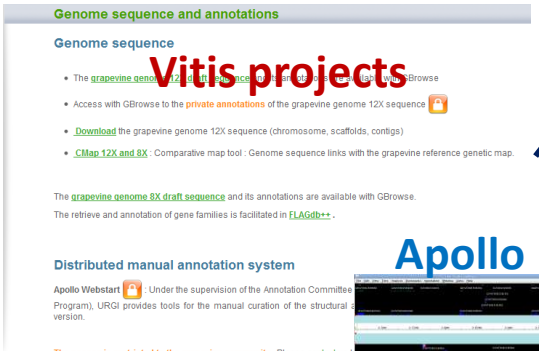
➢V0 and V1 (private) annotations



Polymorphism data



Vitis projects



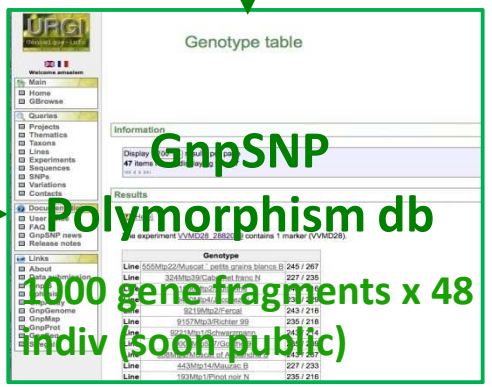
Apollo

SiREGAL
Genetic resources db

➢Vassal collection (7000 accessions)

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)

	automatic annotation	manual annotation
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.

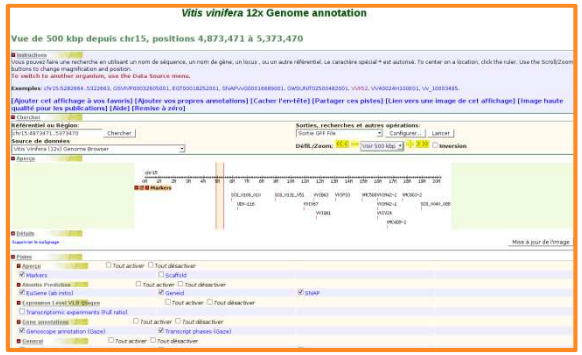
The retrieve and annotation of gene families is facilitated in FLAGdb++ .

Distributed manual annotation system

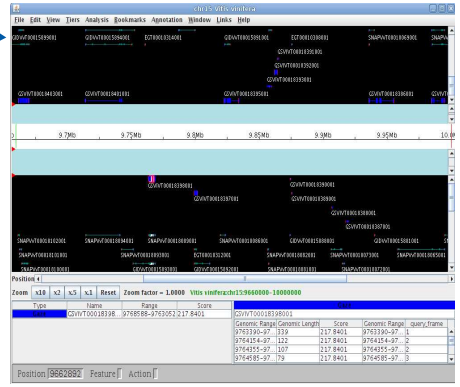
Apollo Webstart : Under the supervision of the Annotation Committee of the IGGP (International Grape Genome Program), URGI provides tools for the manual curation of the structural annotation of the grapevine genome 12X version.

The access is restricted to the grapevine community . Please contact us to get access.

12X Gbrowse
(public and private data)



Apollo : Genome Annotation and Curation Tool



Apollo : Genome Annotation and Curation Tool

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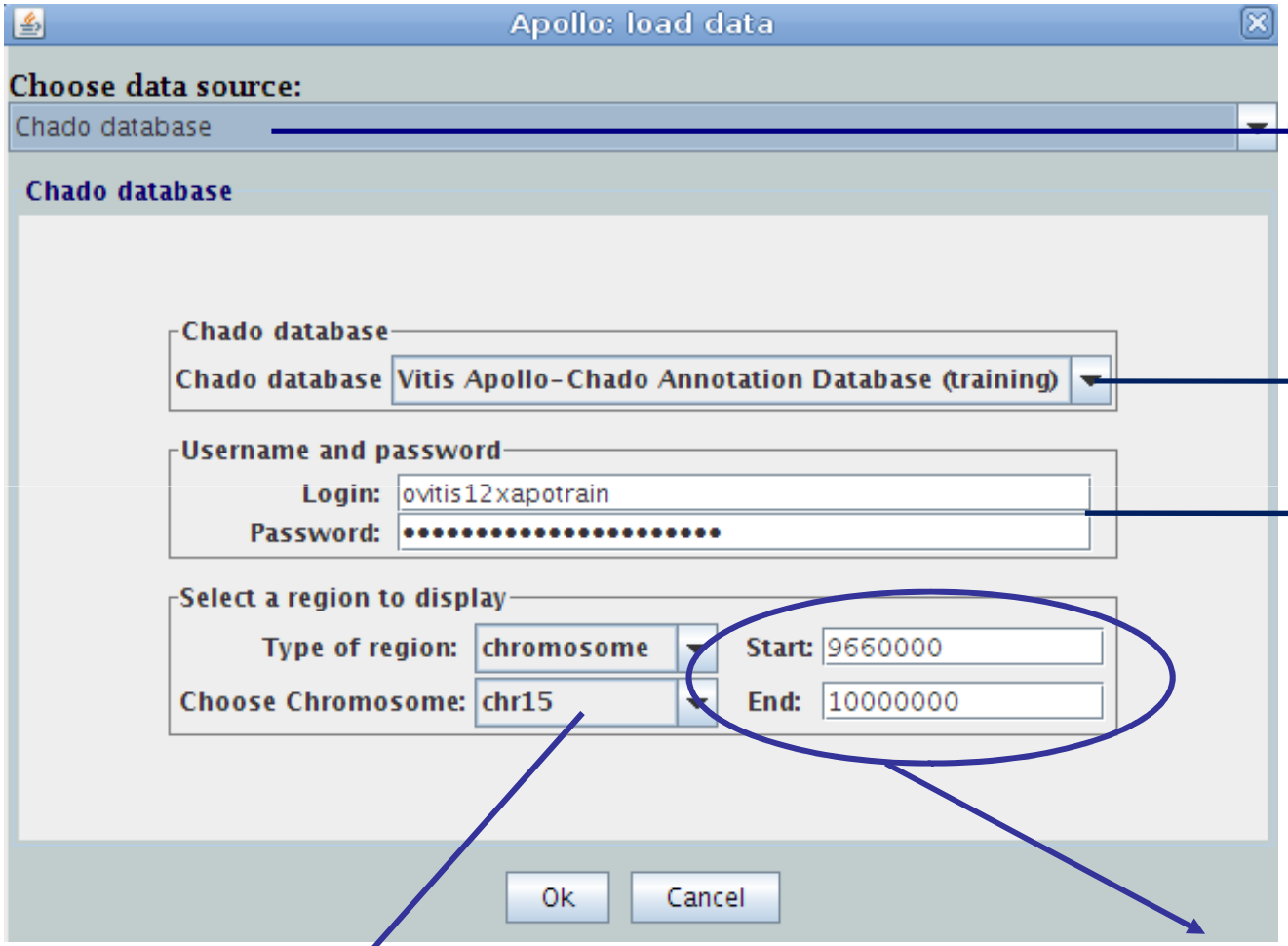


Select Chado database

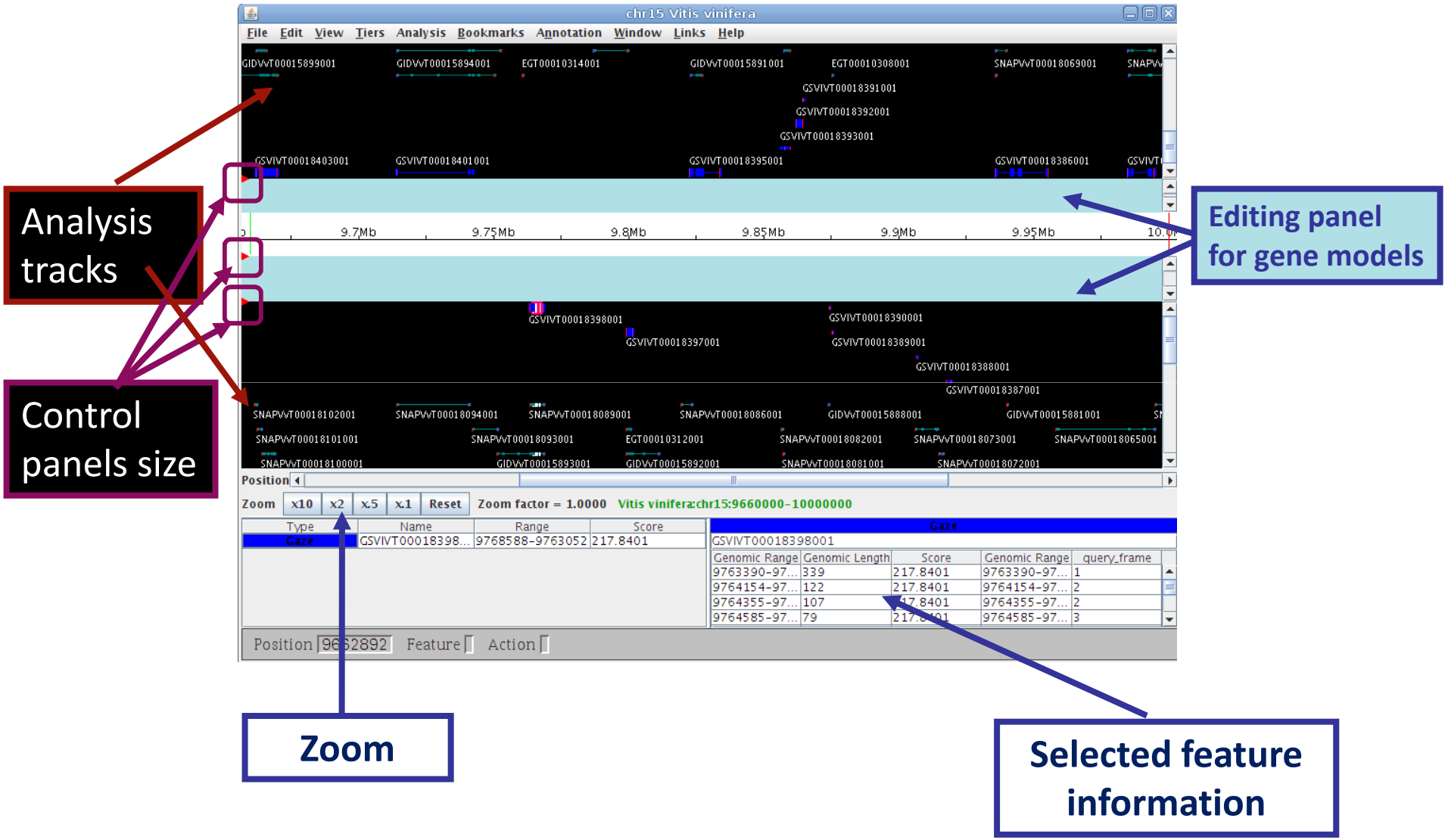
Select Vitis database

login/password for write mode

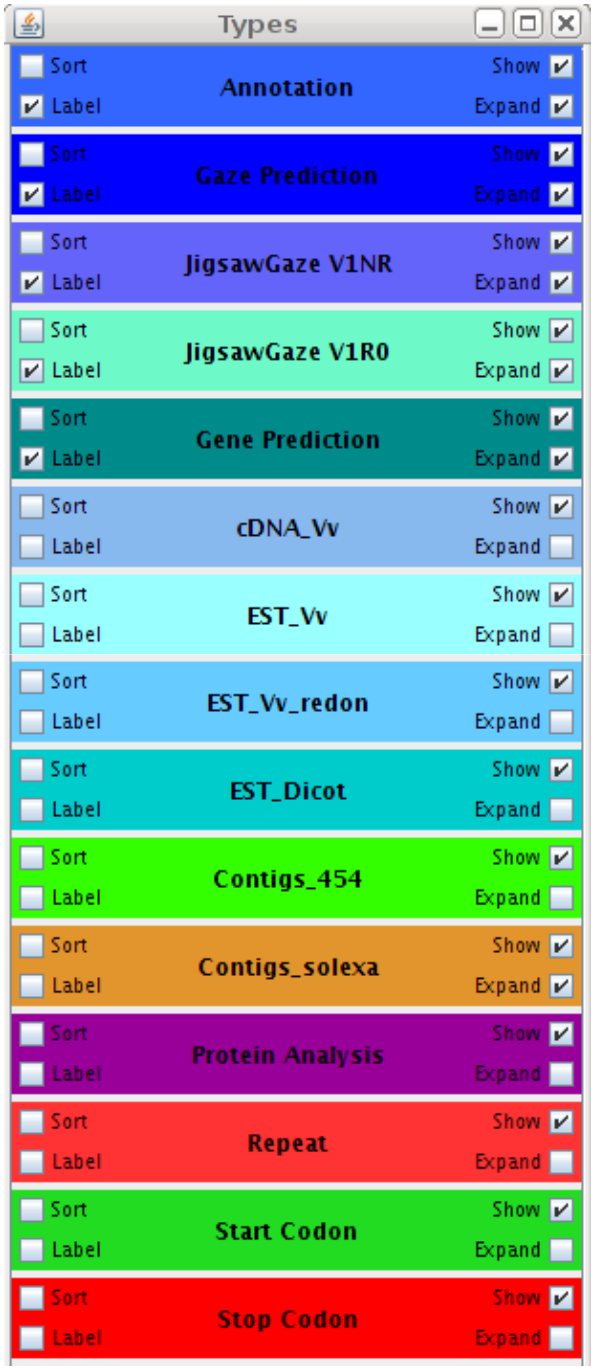
chr1, chr1_random, ... chrUn

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

Apollo Editing and curating interface



Evidences available in Apollo



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*)

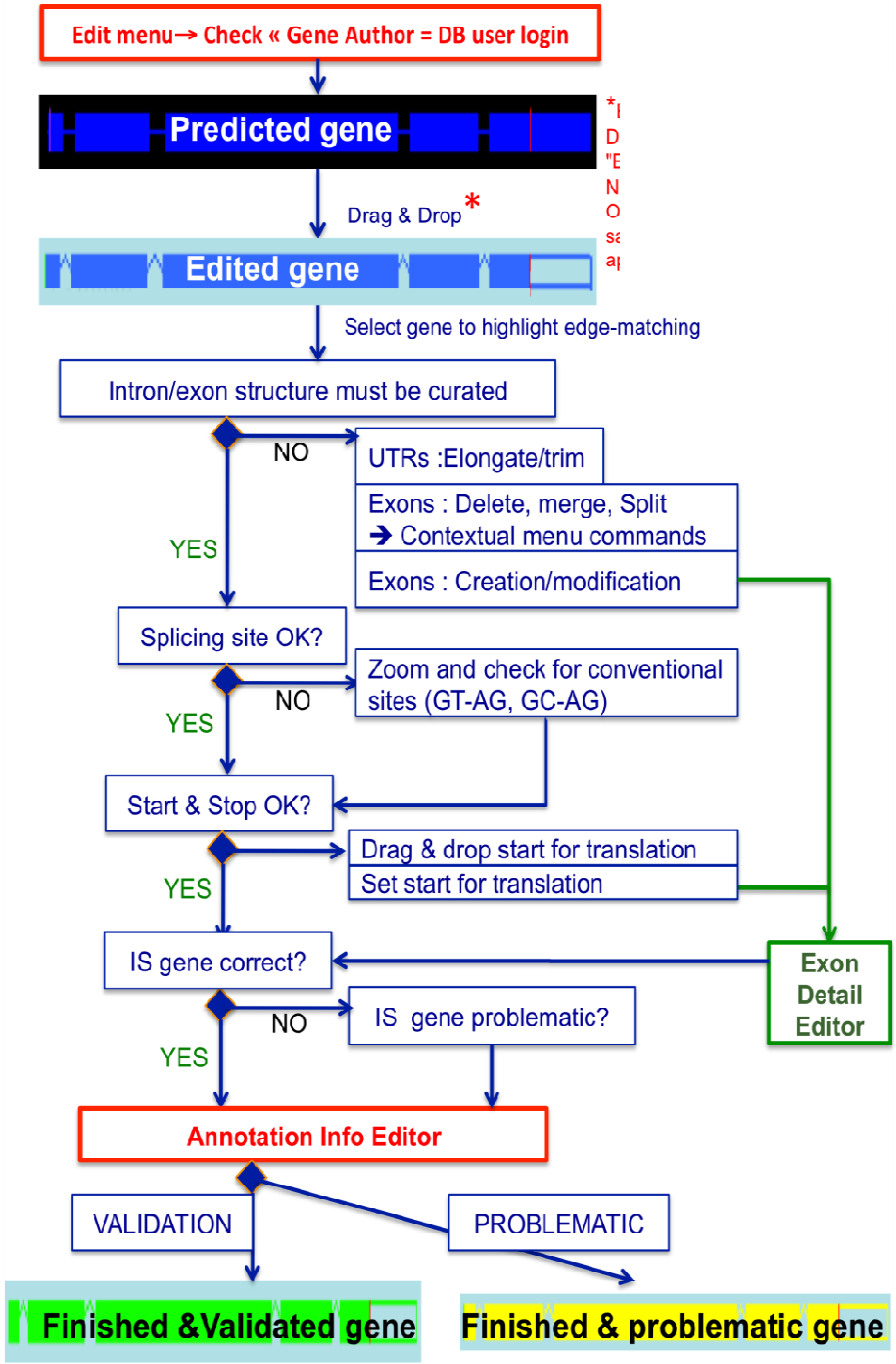
***Vitis vinifera* 454 contigs assembly**

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

Genewise (Uniprot)

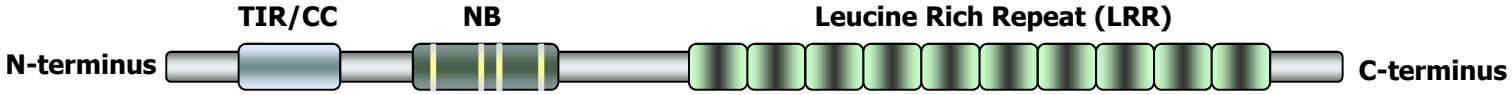
Repeats : RepeatMasker and TRF (Tandem Repeat Finder)

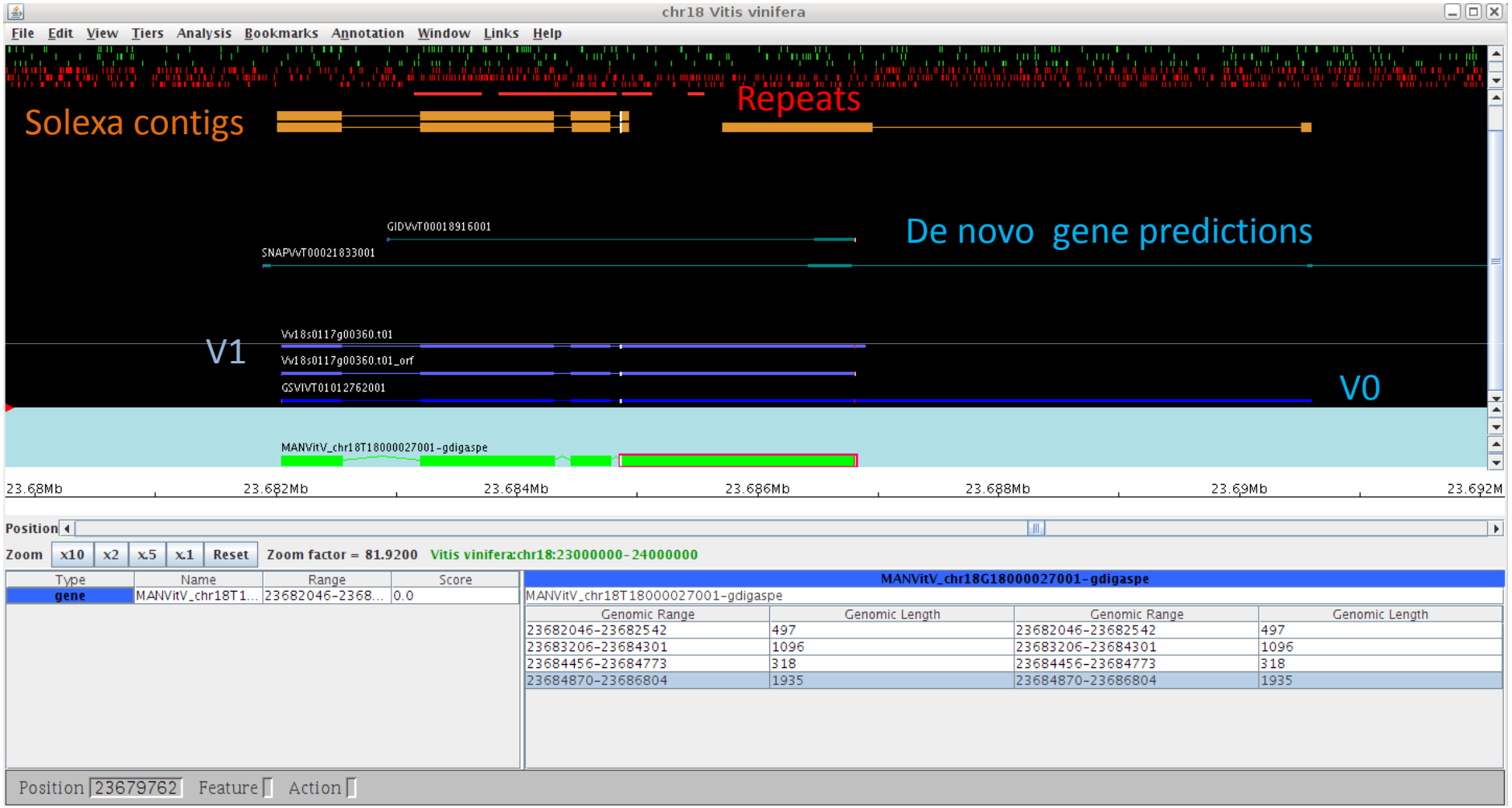
Annotation rules for gene editing



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

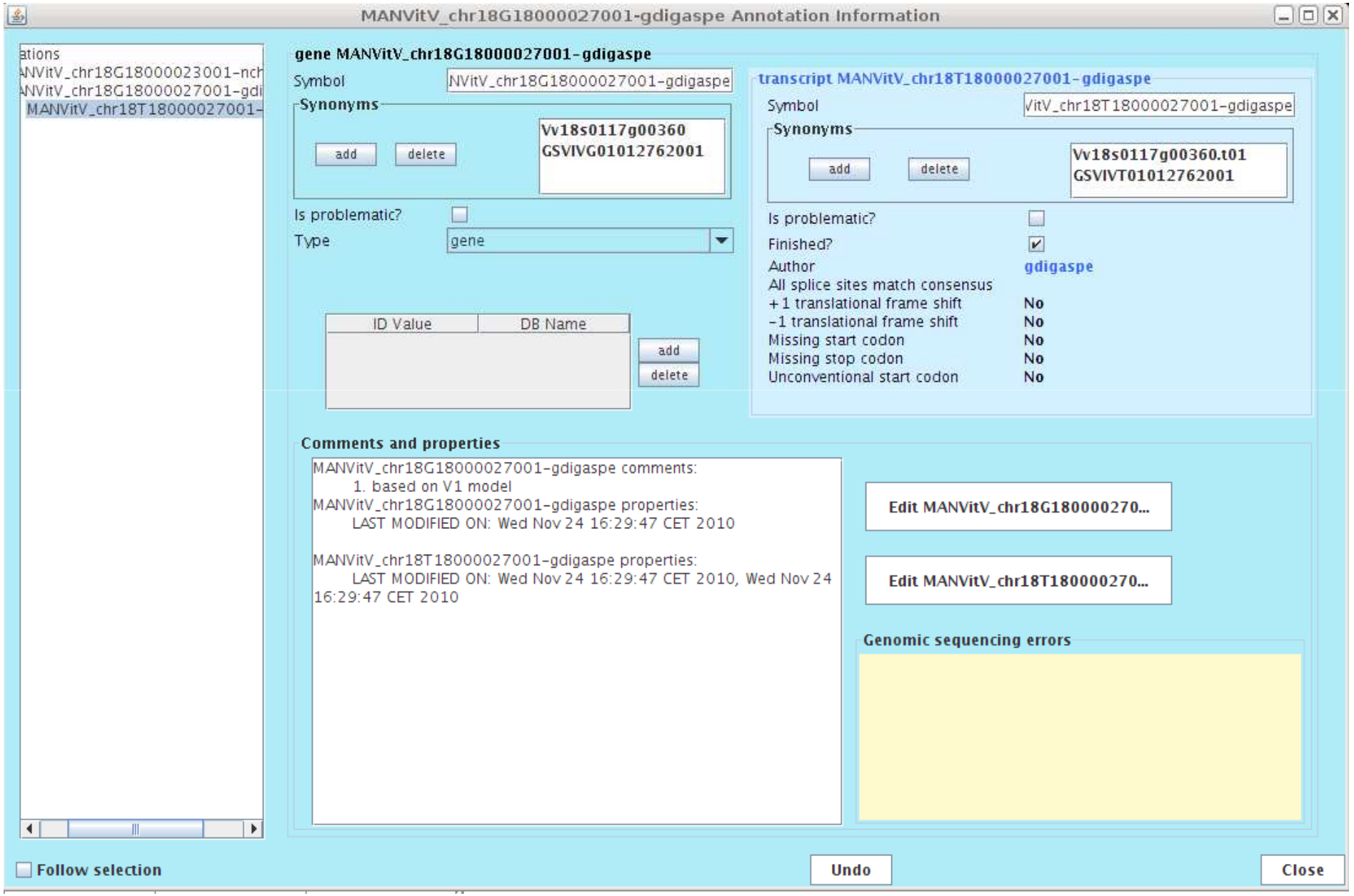
The NBS-LRR gene family





Valided gene by Gabriele Di Gaspero

Annotation info editor



Save gene models manual annotation

Apollo (private website)

Write

Read

Chado

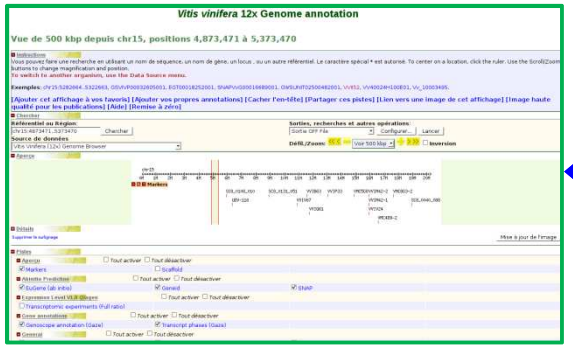
Export Edited genes (GFF3)

New complete release

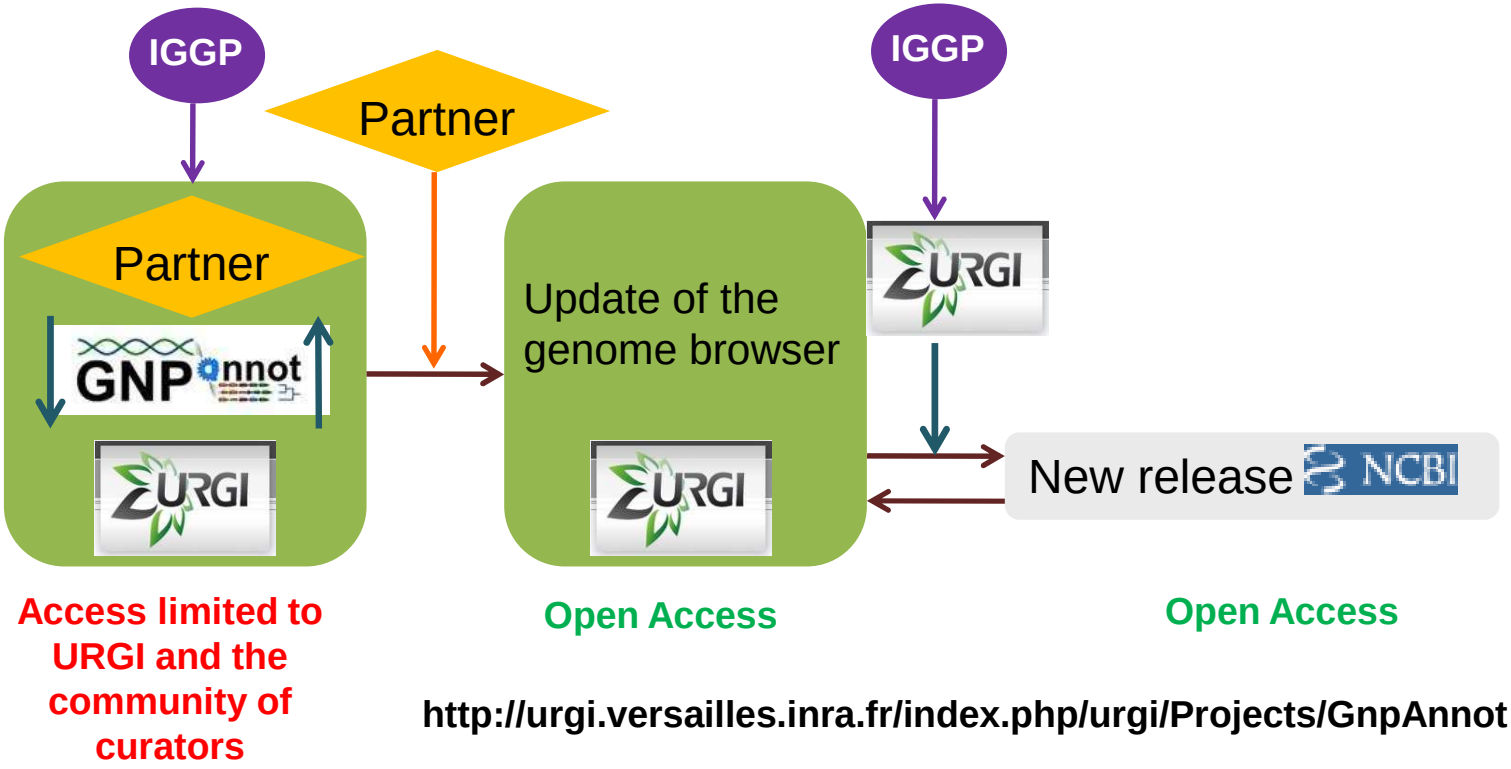
Bio:Seq: Feature store

Read

Gbrowse update



Perspectives/Conclusion



http://urgi.versailles.inra.fr/index.php/urgi/Projects/GnpAnnot

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

=> Basis for the functional annotation

Acknowledgment

URGI – INRA de Versailles

M. Alaux
F. Alfama
J. Amselem
S. Arnoux
M. Bras
B. Brault
L. Brigitte
N. Choisne
S. Durand
T. Flutre
C. Hoede
O. Inizan
V. Jamilloux
A. Keliet
E. Kimmel
J. Kreplak
N. Lapalu
I. Luyten
N. Mohellibi
C. Pommier
S. Reboux
D. Steinbach
D. Valdenaire
D. Verdelet
M. Zytnicki
H. Quesneville

URGV – INRA Evry

A-F Adam-Blondon
Cécile Guichard
Sébastien Aubourg

University of Padova, Italy

Giorgio Vallé

IGA, Udine, Italy

Michele Morgante

University of Verona, Italy

Mario Pezzotti
Massimo Delledonne