

# ***Botrytis/Sclerotinia* resources: an integrated system for structural and functional genome annotation**

BSPGW, Sept 17th, 2011



J. Amselem, N. Lapalu

ALIMENTATION  
AGRICULTURE  
ENVIRONNEMENT

The INRA logo consists of the letters 'INRA' in a large, bold, green, sans-serif font.

**Quick search**

You can find the indexed databases list

Examples: VVI\*, VVIF52, gene, arabidop

VVIF52

**Advanced search**

[BioMart](#)

[Galaxy](#)

**Genome annotation**

**Maps**

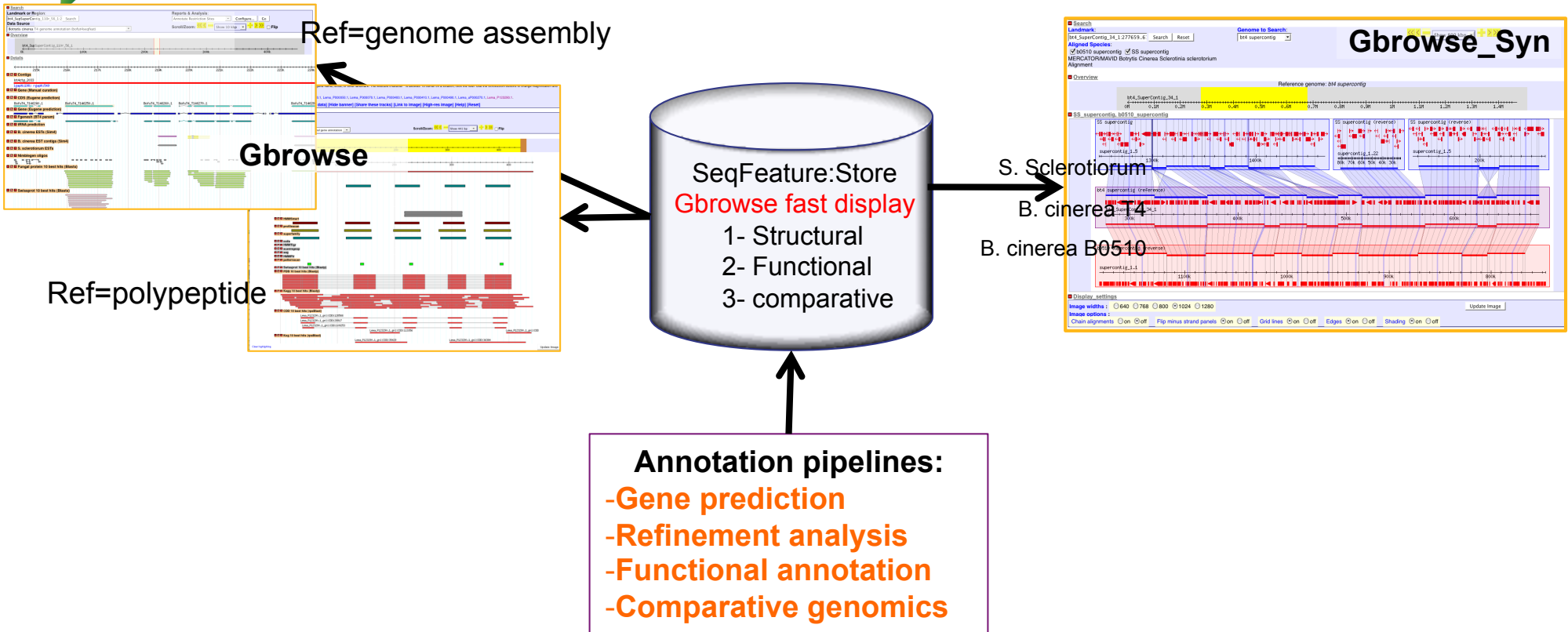
**Transcriptome**

**DNA Polymorphisms**

**Interop.**

**Genetic resources**





# Distributed annotation system

Ref=genome assembly

**Gbrowse**

Ref=polypeptide

SeqFeature:Store  
Gbrowse fast display

- 1- Structural
- 2- Functional
- 3- comparative

**Gbrowse\_Syn**

S. Sclerotiorum  
B. cinerea T4  
B. cinerea B0510

**Annotation pipelines:**

- Gene prediction
- Refinement analysis
- Functional annotation
- Comparative genomics

Chado  
Edition

Structural & functional annotation

Manual curation  
**Apollo**

**Genome Report System + manual curation**

*Botrytis cinerea* T4 GRS

Search by ontology (ID or term)

Search by ontology:  Envoyer

Search by gene name

Search name:  Envoyer

Search by keyword on whole GnpIS





# Distributed annotation system

Ref=genome assembly

**Gbrowse**

**Gbrowse**

Ref=polypeptide

SeqFeature:Store  
**Gbrowse fast display**  
 1- Structural  
 2- Functional  
 3- comparative

**Gbrowse\_Syn**

Aligned Species: 2 of 10510 supercontig: 2 of 85 supercontig: MER10201MAY02 Botrytis Oenocarpa Sclerotium

Reference genome: bld supercontig

SS supercontig: b0510 supercontig

S. Sclerotiorum  
 B. cinerea T4  
 B. cinerea B0510

S. Sclerotiorum

B. cinerea T4

B. cinerea B0510

Advanced search  
 BioMart

Please restrict your query using criteria below

Dataset: Botrytis\_functional\_annotation

Filter: Start > -1, End <= 25, Feature Type: signal\_peptide

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

Feature: Reference Feature (% for wildcard), Example: BofuT4\_P0001%

Feature Type: search polypeptide, polypeptide, domain, signal\_peptide

Feature Name (% for wildcard), Example: BofuT4\_P000%

Feature Location: Start <

Description (% for wildcard), Example: %Euchromatin%

**Annotation pipelines:**

- Gene prediction
- Refinement analysis
- Functional annotation
- Comparative genomics

**Quick search**  
 Lucene/Hibernate

GnpIS - Genetic & Genomic Information System

Quick search: You can find the indexed databases for: VVIF52

Advanced search: Submit

Specific modules: Genetic maps and QTLs, EST and other sequences, Polymorphism data, Plant genetic resources data, Proteomic data

Manual curation  
 Apollo

URGI

Homepage | GnpGenome | FunAnnot Browser | Blast | Downloads | Retrieve sequence

**Botrytis cinerea T4 GRS**

Search by ontology (ID or term): Envoyer

Search by gene name: BofuT4\_P000210.1 Envoyer

Search by keyword on whole GnpIS

URGI | GNPennet | Genome Report System - copyright INRA 2009

Chado  
 Edition  
 Structural & functional annotation

Genome Report System  
 + manual curation

URGI

Homepage | GnpGenome | FunAnnot Browser | Blast | Downloads | Retrieve sequence

**Botrytis cinerea T4 GRS**

Search by ontology (ID or term): Envoyer

Search by gene name: BofuT4\_P000210.1 Envoyer

Search by keyword on whole GnpIS

URGI | GNPennet | Genome Report System - copyright INRA 2009



# Quick and advanced search

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

## Quick search

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

Examples: [VVI\\*](#), [VVIF52](#), [gene](#), [transposable\\_element](#), [arabidopsis](#), [AY109603](#), [Xcfe107-3B](#)

Search:

## Advanced search

[BioMart](#)

[Galaxy](#)

## Specific modules

Genetic maps and QTLs

### Quick search based on :

- hibernate search
- Apache Lucene™ full-featured text search engine library

**Galaxy**  
Set of tools  
for data mining

**Biomart based  
advanced search**



Microarray  
data

omic and  
omic data

The screenshot shows the GnpIS website interface. At the top, a browser address bar is highlighted with an orange box, containing the URL `http://urgi.versailles.inra.fr/gnpis/`. Below the browser, the website header includes the URGI logo, the title "GnpIS - Genetic & Genomic Information System", and the INRA logo. On the left side, there is a navigation menu with sections: "Queries" (Quick, Advanced, Biomart, Galaxy), "Documentation" (User guide, News, Release notes), and "GnpIS" (Data submission, GnpArray, GnpGenome, GnpMap, GnpSeq, GnpSNP, Siregal). The main content area features a "Quick search" section with a text input field containing "transport" and a "Submit" button. A dropdown menu is open below the input field, listing "Species", "All", "Wheat genome", "Vitis genome", and "Fungi genome". To the right, there is an "Advanced search" section with links for "BioMart" and "Galaxy". A large orange box on the right contains the text "Keywords", "Gene id", "Sequence id", and "...". A red box at the bottom left contains the text "User guide". An orange arrow points from the "User guide" box to the "User guide" link in the navigation menu. Another orange arrow points from the "Keywords" box to the search input field.

# Quick search

[Botrytis \(B0510\) functional](#)
[Botrytis \(T4\) functional](#)
[Botrytis \(T4\) genome](#)
[Leptosphaeria genome](#)

[Leptosphaeria functional](#)

**+ Feature (498)**

- [bt4 SuperContig 12 1...](#) ★★★★★
- [bt4 SuperContig 171 ...](#) ★★★★★
- [bt4 SuperContig 50 1...](#) ★★★★★
- [bt4 SuperContig 51 1...](#) ★★★★★
- [bt4 SuperContig 313 ...](#) ★★★★★
- [bt4 SuperContig 69 1...](#) ★★★★★
- [bt4 SuperContig 69 1...](#) ★★★★★
- [bt4 SuperContig 103 ...](#) ★★★★★
- [bt4 SuperContig 103 ...](#) ★★★★★
- [bt4 SuperContig 153 ...](#) ★★★★★

144 < 1 2 3 4 5 6 7 8 9 10 > || 498 items found

Link to GBrowse

**Search**

Landmark or Region:  Search

Data Source: Botrytis cinerea T4 genome annotation

Reports & Analysis: Annotate Restriction Sites

Scroll/Zoom: <<< < > >>> Show 2.078 kbp

**Overview**

**Details**

- Contigs**
  - bt4ctg\_0287
  - lgapN:341; rgapN:150
- Gene (Manual curation)**
  - BoFu14\_1022650.1
- CDS (Eugene prediction)**
  - BoFu14\_1022650.1
- tRNA prediction**
- B. cinerea ESTs (Sim4)**
- B. cinerea EST contigs (Sim4)**
- S. sclerotiorum ESTs**
- Nimblegen oligos**
- Fungal protein 10 best hits (Blastx)**
- Swissprot 10 best hits (Blastx)**

**bt4\_SuperContig\_12\_1\_bt4ctg\_0287\_Q4WK80**

**Feature Info:**

- Length: 2552
- Ref: start..end: bt4\_SuperContig\_12\_1:175717..178268
- Hit: start..end: [Q4WK80: 1..762](#)
- Hit length: 780
- Hit coverage: 97.69%
- Hit identity: 84.38%
- Hit desc: Protein transport protein sec23 - Aspergillus fumigatus (Sartoryia fumigata)

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



# Quick search

Botrytis (B0510) functional
Botrytis (T4) functional
Botrytis (T4) genome
Leptosphaeria genome

Leptosphaeria functional

+ **Feature (3275)**

<a href="#">BofuT4_P100220.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P080330.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P141780.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P020460.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P000560.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P012860.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P006320.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P024090.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P100350.1</a>	★ ★ ★ ★
<a href="#">BofuT4_P127990.1</a>	★ ★ ★ ★

100 < 1 2 3 4 5 6 7 8 9 10 > >> | 3275 items found, displaying

Homepage
GnpGenome
FunAnnot Browser
Blast
Downloads


*Botrytis cinerea* T4 GRS

Functional annotation

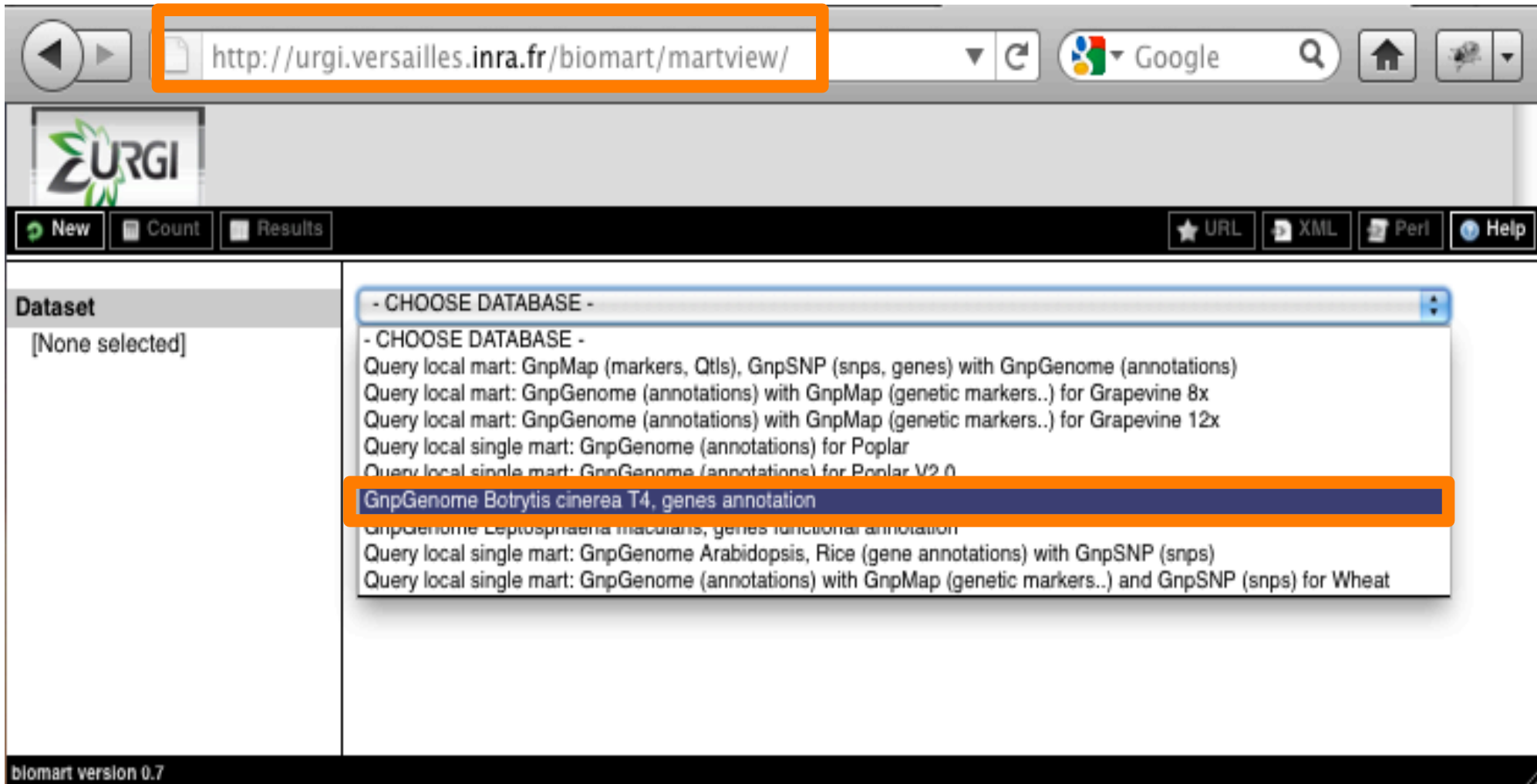
BofuT4\_P100220.1

- + Gene Identifier
- + DbXrefs
- + 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 Genome Report System



# Biomart based advanced search



http://urgi.versailles.inra.fr/biomart/martview/

URGI

New Count Results URL XML Perl Help

Dataset  
[None selected]

- CHOOSE DATABASE -

- CHOOSE DATABASE -
- Query local mart: GnpMap (markers, Qtls), GnpSNP (snps, genes) with GnpGenome (annotations)
- Query local mart: GnpGenome (annotations) with GnpMap (genetic markers..) for Grapevine 8x
- Query local mart: GnpGenome (annotations) with GnpMap (genetic markers..) for Grapevine 12x
- Query local single mart: GnpGenome (annotations) for Poplar
- Query local single mart: GnpGenome (annotations) for Poplar V2.0
- GnpGenome Botrytis cinerea T4, genes annotation**
- GnpGenome Leptosphaeria maculans, genes functional annotation
- Query local single mart: GnpGenome Arabidopsis, Rice (gene annotations) with GnpSNP (snps)
- Query local single mart: GnpGenome (annotations) with GnpMap (genetic markers..) and GnpSNP (snps) for Wheat

biomart version 0.7

# Biomart : request form

New Count Results URL XML Perl Help

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

Feature

Reference Feature (% for Wildcard). Example: BofuT4\_P0001%

Feature Type

match  
polypeptide  
polypeptide\_domain  
signal\_peptide

**Signal\_peptide**

Feature Name (% for wildcard). Example: BofuT4\_P009%

Feature Location

Start < 1  
Start >  
End < 30  
End >

**Start=1  
End=30**

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

**Iprscan\_annotation**

DB Xref DB

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

DB Xref Accession (% for wildcard)



# Biomart results

**Results**

Please restrict your query using criteria below

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  TSV  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
<a href="#">BoluT4_P000030.1</a>	signal_peptide	0	25	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BoluT4_P000070.1</a>	signal_peptide	0	18	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BoluT4_P000200.1</a>	signal_peptide	0	18	signalp	model	SignalP		polypeptide_iprscan_annotation	GFF_source	signalp
<a href="#">BoluT4_P000210.1</a>	signal_peptide	0	19	signalp	model				_source	signalp
<a href="#">BoluT4_P000260.1</a>	signal_peptide	0	19	signalp	model				_source	signalp
<a href="#">BoluT4_P000270.1</a>	signal_peptide	0	19	signalp	model				_source	signalp
<a href="#">BoluT4_P000290.1</a>	signal_peptide	0	17	signalp	model				_source	signalp
<a href="#">BoluT4_P000390.1</a>	signal				model				_source	signalp
<a href="#">BoluT4_P000440.1</a>	signal				model				_source	signalp
<a href="#">BoluT4_P000590.1</a>	signal_peptide	0	3	signalp	model				_source	signalp

**Link to GRS**

URGI  
GnpIS advanced search

Botrytis cinerea T4 GRS  
Functional annotation  
BoluT4\_P000210.1

Analysis	Start	End	Length	Location	Reliability class	Signal Peptide CutOff	Mitochondrion CutOff
targetp	1	19	19	Secretory pathway 3	0.820	0.301	
signalp	1	19	18				
tmhmm					Not result		

DB Xref Accession (% for wildcard)



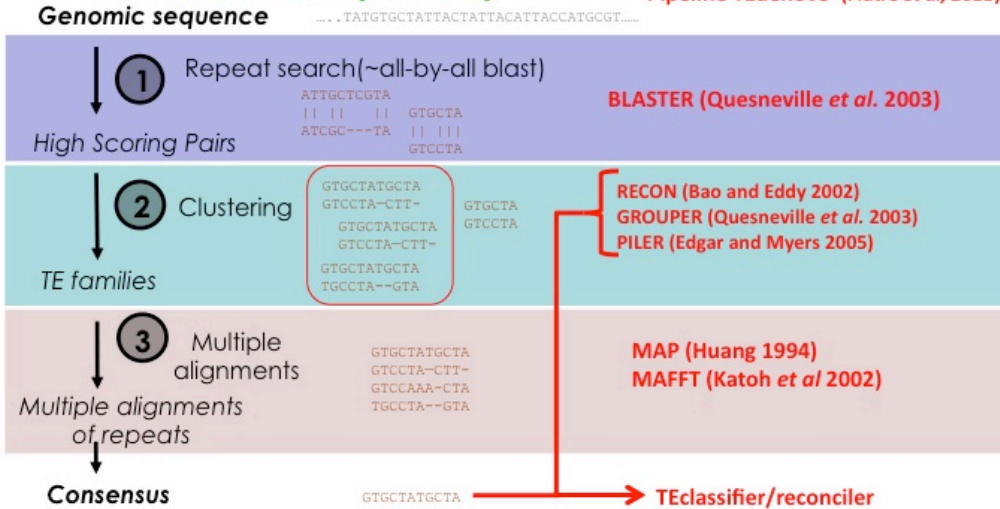
# Pipelines

## Transposable Elements: REPET package

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

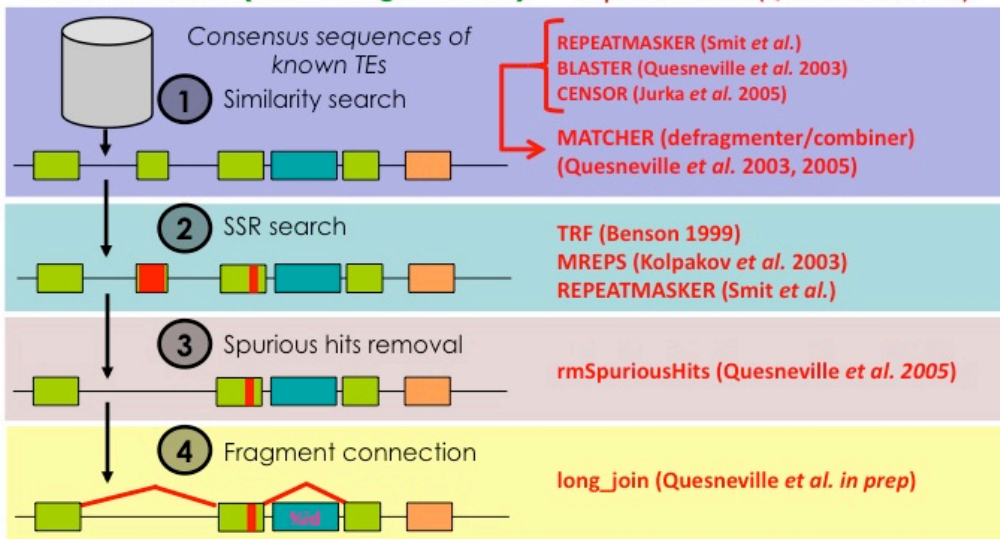
### • TE identification (de novo)

Pipeline TEdenovo (Flutre *et al.*, 2011)



### • TE annotation (knowledge based)

Pipeline TEannot (Quesneville *et al.* 2005)



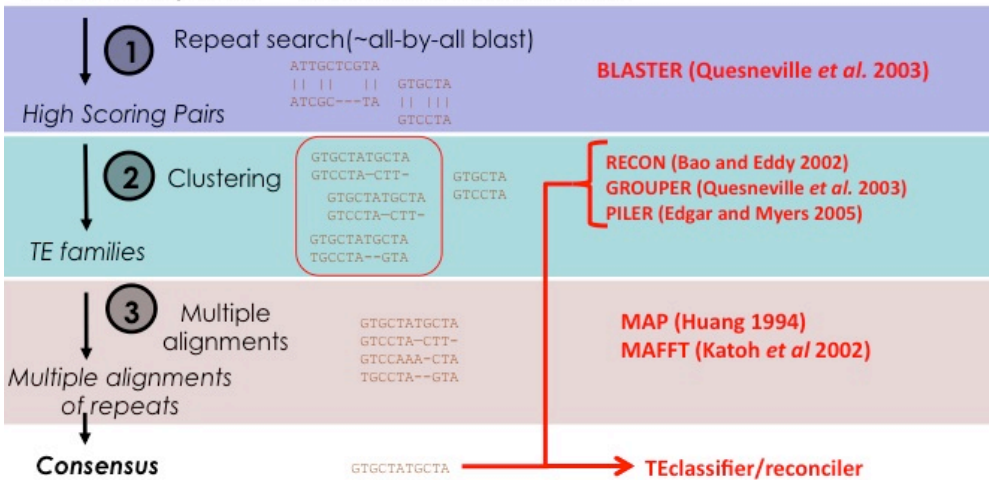
## Transposable Elements: REPET package

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

### • TE identification (de novo)

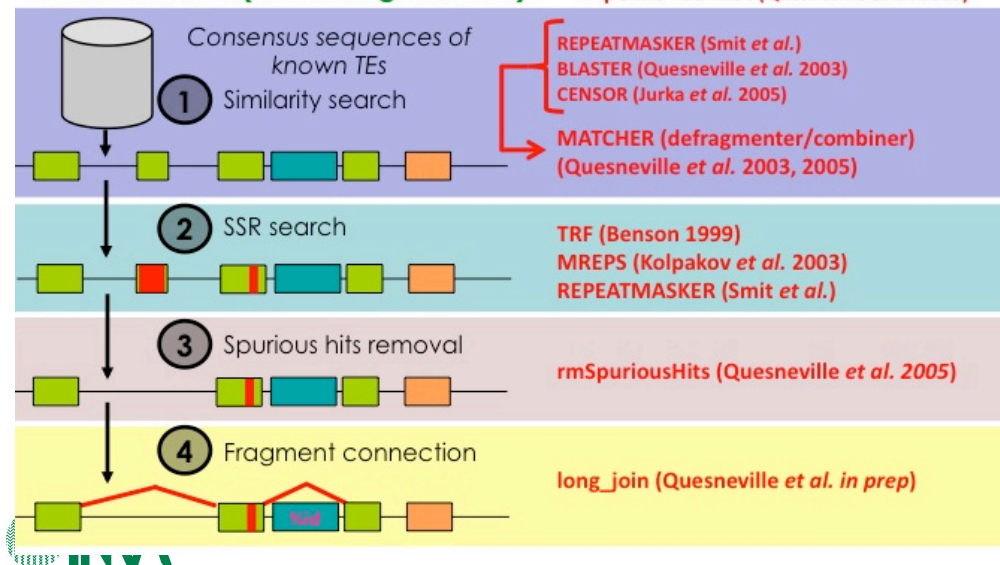
Pipeline TEdenovo (Flutre et al, 2011)

Genomic sequence ...TATGTGCTATTACTATTACATTACCATGCGT...



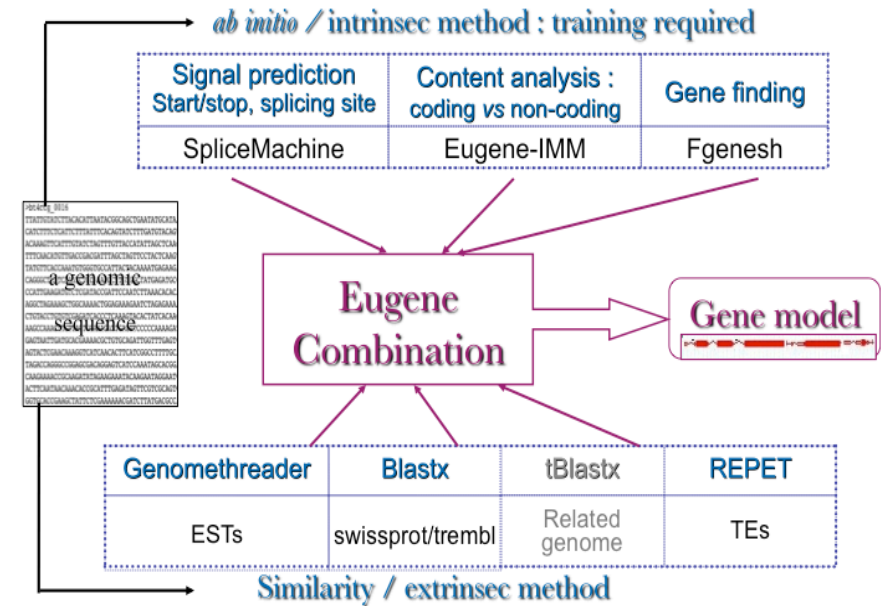
### • TE annotation (knowledge based)

Pipeline TEannot (Quesneville et al. 2005)



## Genes prediction: EuGene

<http://eugene.toulouse.inra.fr/>



J. Anselme 06/10/09

# Functional annotation pipeline

Predicted polypeptides

Protein domain identification

*InterProScan*



InterPro





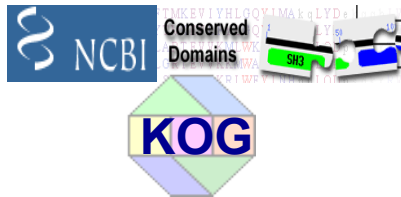
Predicted polypeptides



Blast similarities



rpsBlast  
Conserved domains



Protein domain identification

*InterProScan*

Coils, Patternscan, Profilescan,  
Scanregexp, seg

InterPro



# Functional annotation pipeline

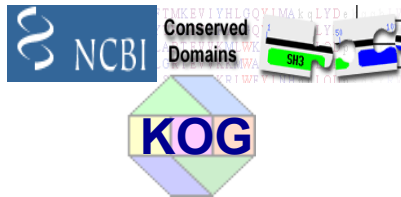
Predicted polypeptides



Blast similarities



rpsBlast  
Conserved domains



Protein domain identification

*InterProScan*

Coils, Patternscan, Profilescan, Scanregexp, seg

InterPro



Localization Targeting



SignalP  
TargetP



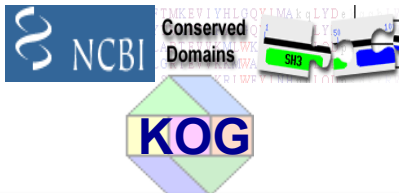
# Functional annotation pipeline

Predicted polypeptides

Blast similarities



rpsBlast  
Conserved domains



Protein domain identification

InterProScan



Coils, Patternscan, Profilescan,  
Scanregex, seg

InterPro



Localization  
Targeting



SignalP  
TargetP

GFF3

Chado  
DB:SeqFeatureStore

INRA URGI

Homepage GnpGenome Blast Downloads Retrieve sequence

*Leptosphaeria maculans*

Functional annotation

**Genome Report System**

**Gene/Protein**

- + Sequence
- + Domain/Motif (Interproscan results)
- + Localization / Targeting
- + Blast based analysis
- + Other reports
- + Functional Gbrowse
- + Structural Gbrowse
- + Genome Mapping at gene locus

INRA URGI GNP nnot

Genome Report System - copyright INRA 2009

INRA

*Leptosphaeria maculans* Functional annotation

Showing 441 bp from Locus\_012220.1, positions 1 to 441

**Gbrowse**

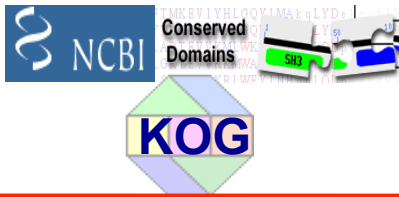
Ref=polypeptide

Predicted polypeptides

Blast similarities



rpsBlast  
Conserved domains



Protein domain identification

InterProScan

Localization Targeting



SignalP  
TargetP

*Botrytis* T4, B05.10  
and *Sclerotinia*  
predicted genes  
annotated

INRA URGI

Homepage GnpGenome Blast Downloads Retrieve sequence

*Leptosphaeria maculans*

Functional annotation

**Genome Report System**

**Gene/Protein**

- + Sequence
- + Domain/Motif (InterproScan results)
- + Localization / Targeting
- + Blast based analysis
- + Other
- + Functional Gbrowse
- + Structural Gbrowse
- + Genome Mapping at gene locus

INRA URGI GNP annot

Chado  
DB:SeqFeatureStore

INRA

*Leptosphaeria maculans* Functional annotation

Showing 441 bp from Locus\_012220.1, positions 1 to 441

**Gbrowse**

Ref=polypeptide

## Interfaces & dataflow

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

**Botrytis portal**

2 ways to access data

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

**GnpIS portal**



# Interfaces and dataflow : *B. cinerea*

**Botrytis portal Sequences & Databases**

The screenshot shows the ZURGI Plant and Fungi Data Integration portal. The main content area displays information about Botrytis cinerea sequences and databases, including a list of databases and a search bar.

**Transcriptomics GnpArray**

The screenshot shows the GnpArray interface for the gene BofuT4\_P034230.1. It displays a list of associated reports and a table of normalized data.

**Gbrowse\_syn Botrytis T4 Botrytis B0510 Sclerotinia**

The screenshot shows the Gbrowse\_syn interface, displaying a genomic map with various features and tracks for Botrytis T4, Botrytis B0510, and Sclerotinia.

**Structural annotation GnpGenome**

The screenshot shows the GnpGenome interface for Botrytis cinerea T4 Supercontigs. It displays a genomic map with various features and tracks, including gene models and annotations.

**Genome Report System Botrytis T4 Botrytis B0510 Sclerotinia**

The screenshot shows the Genome Report System interface for Botrytis T4, Botrytis B0510, and Sclerotinia. It displays a list of reports and a search bar.

**Genes curation/Validation**

The screenshot shows the Genes curation/Validation interface, displaying a genomic map with various features and tracks, including gene models and annotations.

**GnpIS portal**

The screenshot shows the GnpIS portal interface, displaying a search bar and a list of specific modules for genetic and genomic information.



# Interfaces and dataflow : *B. cinerea*

**Botrytis portal Sequences & Databases**

Genome sequences and databases

**Advanced search**

Please restrict your query using criteria below

- Feature
  - Reference Feature (% for wildcard): Example: BofuT4\_P0001%
- Feature Name (% for wildcard): Example: BofuT4\_P009%
- Feature Location
  - Start <
  - Start >
  - End <
  - End >
- HIT (% for wildcard): Example: 3b95\_%
- Description (% for wildcard): Example: %Euchromatic%

**Transcriptomics GnpArray**

Gene - BofuT4\_P034230.1

Gene details

Associated reports

Gene list	FOLD CHANGE	Normalized_Variance	eVALUE
BofuT4_P034230.1	0.000000000000000000	0.000000000000000000	0.000000000000000000

**Gbrowse\_syn Botrytis T4 Botrytis B0510 Sclerotinia**

**Structural annotation GnpGenome**

Botrytis cinerea T4 Supercontigs / contigs annotation

Showing 26.64 kbp from B4\_SuperContig\_0\_1, positions 120,110 to 146,747

**Results Quick search**

Welcome amsterdam

Display 10 results per page  
4 items found, displaying 1 to 4

Query parameters: BofuT4\_P034230.1 BofuT4\_P046390.1

Feature [genome-botrytis] (4)	Gene [transcriptome] (2)
BofuT4_P034230.1	BofuT4_P034230.1
BofuT4_P034230.1	BofuT4_P046390.1
BofuT4_P046390.1	-
BofuT4_P046390.1	-

**Genome Report System Botrytis T4 Botrytis B0510 Sclerotinia**

Leptosphaeria maculans

- Sequence
- Domains/Motif (Interproscan results)
- Localization / Target
- Blast based analysis
- Other analysis
- Functional Browse
- Structural Browse
- Genome Mapping at gene locus

**Genes curation/Validation**

bricq\_0006 Botrytis fuckeliana

Type	Name	Score	Match
uniprot_trembl	bricq_uniprot_fm_21815-19167	0.0	Putative uncharacterized protein - Phaeosphaeria nodorum (Phaeosphaeria nodorum)
FNCSI3_proc	bricq_FNCSI3_fm_21813-19760	0.0	Genome: Genome: score: expect: query_fm: Match: Match: 21810-1: 2058 0.0 1 1-683 683
FNCSI3_proc	bricq_FNCSI3_fm_21766-19783	0.0	
uniprot_trembl	bricq_uniprot_fm_21613-19783	0.0	
FNCSI3_proc	bricq_FNCSI3_fm_21613-19783	0.0	

**GnpIS portal**

GnpIS - Genetic & Genomic Information System

Specific modules

- Genetic maps and QTLs
- Polymorphism data
- Plant genetic resources data
- Microarray data
- Proteomic data
- EST and other sequences
- Genome annotation data
- GnpGenome
- GnpMap
- GnpSeq
- GnpSNP
- GnpArray
- SIReGal
- Epiplex
- CyberMap
- CyberSeq
- CyberSNP





# Interfaces and dataflow : *B. cinerea*

**Botrytis portal Sequences & Databases**

This interface provides access to genomic sequences and databases for *Botrytis cinerea*. It includes a search bar, a list of species, and a detailed view of genomic data.

**Structural annotation GnpGenome**

This interface displays the structural annotation of the *Botrytis cinerea* T4 Supercontigs. It shows a genomic map with various features and annotations.

**Genes curation/Validation**

This interface is used for the curation and validation of genes. It displays a list of genes with their names, IDs, and scores, along with a detailed view of a specific gene.

**Transcriptomics GnpArray**

This interface displays transcriptomics data for the gene BofuT4\_P034230.1. It includes a list of transcripts and a table of normalized data.

**Gbrowse\_syn Botrytis T4 Botrytis B0510 Sclerotinia**

This interface provides a genomic browser view for *Botrytis T4*, *Botrytis B0510*, and *Sclerotinia*. It shows genomic tracks and annotations for these species.

**Genome Report System Botrytis T4 Botrytis B0510 Sclerotinia**

This interface provides a genome report system for *Botrytis T4*, *Botrytis B0510*, and *Sclerotinia*. It includes a search bar and a list of reports.

**GnpIS portal**

This interface is the GnpIS portal, providing genetic and genomic information. It includes a search bar and a central hub for various data types.



# Interfaces and dataflow : *B. cinerea*

**Botrytis portal  
Sequences &  
Databases**

**Biomart  
Advance search**

**Transcriptomics  
GnpArray**

**Gbrowse\_syn  
Botrytis T4  
Botrytis B0510  
Sclerotinia**

**Structural  
annotation  
GnpGenome**

**Galaxy  
to cross  
and mine data**

**Genome Report System  
Botrytis T4  
Botrytis B0510  
Sclerotinia**

**Genes  
curation/  
Validation**

**GnpIS portal**



# Interfaces and dataflow : *B. cinerea*

**Botrytis portal Sequences & Databases**

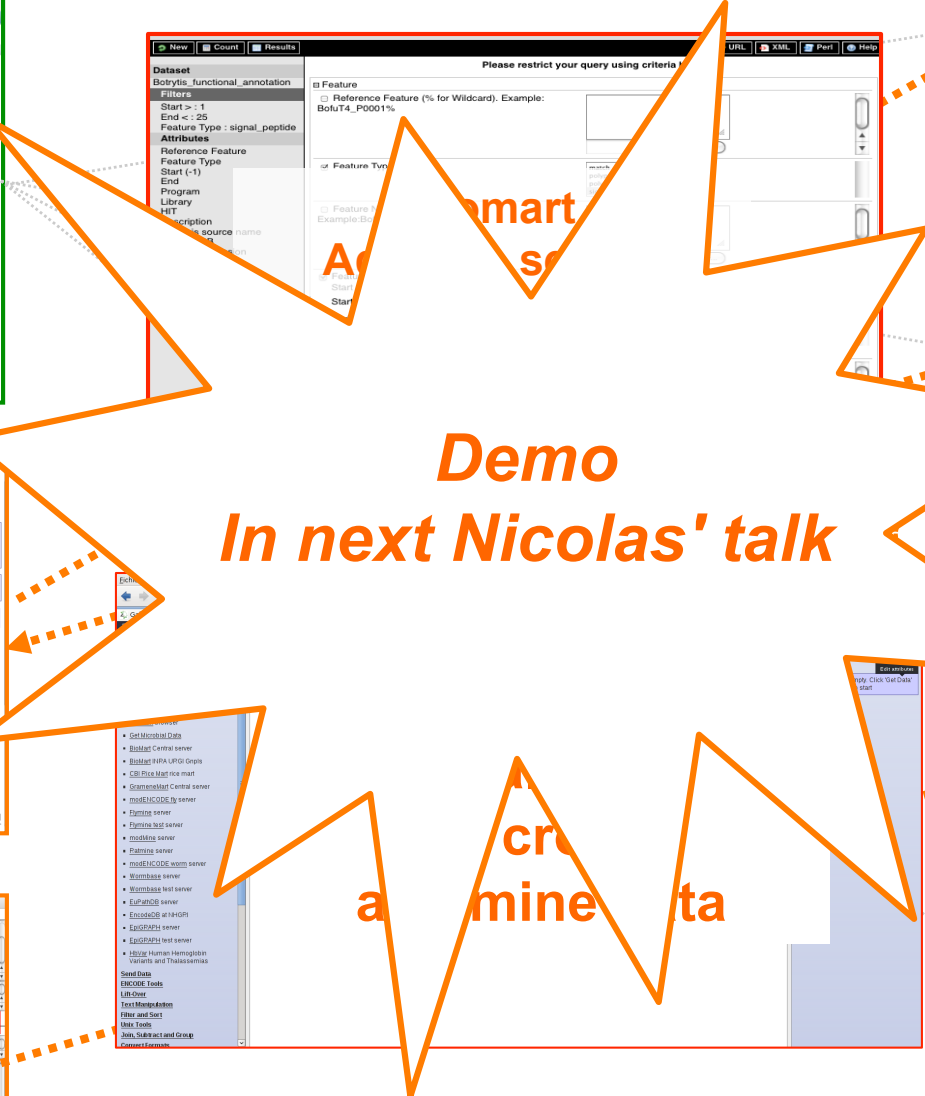
**Smart search**

**Transcriptomics GnpArray**

**Gbrowse\_syn Botrytis T4 Botrytis B0510 Sclerotinia**

**Structural annotation GnpGenome**


**Genes curation/Validation**



**Genome Report System**

**Botrytis T4 Botrytis B0510 Sclerotinia**

**GnpIS portal**

 **Queries**

- Projects**
- Experiments**
- Hybridizations**
- Array designs**
- Protocols**
- Process**
- Gene lists**




Log in


 **My basket**  
0 Item(s)

 **Main**  
 Home


 **Global queries**  
 Contacts

 **Queries**

- Projects
- Experiments
- Hybridizations
- Array designs
- Protocols
- Process
- Gene lists

 **Documentation**

- User guide
- FAQ
- GnpArray news
- Release notes

 **GnpIS**

- Data submission
- GnpIS
- Ephasis
- GnpGenome
- GnpMap
- GnpProt
- GnpSeq
- GnpSNP
- Siregal
- Synteny

## GnpArray

Welcome on the URGI Transcriptome web interface page.

GnpArray is part of the [GnpIS](#) platform like [GnpSeq](#), [GnpMap](#) and [GnpSNP](#).

The database is a repository for all transcriptome data such as microarray or macroarray data.

Complex query forms are available to search for precise information.

All result pages offer links to associated data (with in some cases links to external resources), then it provides the ability to query.

### Overview of the database content

<a href="#">Projects</a>	3
<a href="#">Experiments</a>	3
<a href="#">Hybridizations</a>	60
<a href="#">Array designs</a>	3
<a href="#">Arrays</a>	48
<a href="#">Taxons</a>	4
<a href="#">Protocols</a>	21
<a href="#">Gene lists</a>	9

### GnpArray news

■ **September 01, 2011**

GnpArray 1.8.8 is now available. See the [release notes](#) for more information about changes.

Changes:

- add taxon related objects count on taxon card

■ **May 03, 2011**

**Gene lists associated to a project**

- 1- Gene list in "Queries" menu
- 2- select project & data
- 3- Display results

**Gene lists:**  
*In planta* upregulated  
*In planta* down regulated  
 Unchanged

#	Gene list name	Creation date	Description	Project	Experiments	Regulation	Reporter normalized data	Gene normalized data
1	Bc1 - In planta Up (Botrytis-B0510 : in vitro vs in planta[sunflower] 48h) (277 genes)	2009/03/09	Variance analysis wa... > more	Botrytis_on_Sunflower_2008	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Up regulated	-	<a href="#">Display data</a>
2	Bc1 - In planta Down (Botrytis-B0510 : in vitro vs in planta[sunflower] 48h) (306 genes)	2009/03/09	Variance analysis wa... > more	Botrytis_on_Sunflower_2008	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Down regulated	-	<a href="#">Display data</a>
3	Bc1 - In planta Unchanged (Botrytis-B0510 : in vitro vs in planta[sunflower] 48h) (20306 genes)	2009/03/09	Variance analysis wa... > more	Botrytis_on_Sunflower_2008	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Unchanged	-	<a href="#">Display data</a>



Gene list query

Query parameters

By default the query accepts wildcards (% and \_) and is case sensitive for the gene names. See the user guide for more information.

Projects: All Botrytis\_on\_Sunflower\_2009 INRA\_AJ\_GDC

Sort results by: Gene list name

Results

1- Gene list in "Queries" menu  
2- select project & data  
3- Display results  
4- Display Gene list details

## Gene list details

### Results

[Help]

« 4 5 6 7 8 9 10 11 12 13 » | 277 items found, displaying 71 to 80 | Display 10 results per page

##	Gene name	Associated sequences	FOLD CHANGE	Normalized_Variance	pVALUE
71	<a href="#">BofuT4_P014290.1</a>	<a href="#">BofuT4_P014290.1</a>	6.8	0.92	2.97187E-6
72	<a href="#">BofuT4_P014350.1</a>	<a href="#">BofuT4_P014350.1</a>	43.0	0.99	2.868724E-7
73	<a href="#">BofuT4_P015750.1</a>	<a href="#">BofuT4_P015750.1</a>	7.7	0.96	2.523899E-6
74	<a href="#">BofuT4_P015800.1</a>	<a href="#">BofuT4_P015800.1</a>	30.0	0.97	7.024053E-7
75	<a href="#">BofuT4_P016040.1</a>	<a href="#">BofuT4_P016040.1</a>	3.9	0.92	7.381806E-7
76	<a href="#">BofuT4_P018370.1</a>	<a href="#">BofuT4_P018370.1</a>	36.0	0.98	5.72899E-7

## Gene list results



### Results

[Help]

Number of unique reporters in your query: 211

Number of unique genes in your query: 35690

« 1 2 3 » | 3 items found, displaying 1 to 3 | Display 10 results per page

#	Gene list name	Creation date	Description	Project	Experiments	Regulation	Reporter normalized data	Gene normalized data
1	<a href="#">Bc1 - In planta Up (Botrytis-B0510 - in vitro vs in planta(sunflower) 48h)</a> (277 genes)	2009/03/09	Variance analysis wa... > more	<a href="#">Botrytis_on_Sunflower_2009</a>	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Up regulated	-	<a href="#">Display data</a>
2	<a href="#">Bc1 - In planta Down (Botrytis-B0510 - in vitro vs in planta(sunflower) 48h)</a> (306 genes)	2009/03/09	Variance analysis wa... > more	<a href="#">Botrytis_on_Sunflower_2009</a>	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Down regulated	-	<a href="#">Display data</a>
3	<a href="#">Bc1 - In planta Unchanged (Botrytis-B0510 - in vitro vs in planta(sunflower) 48h)</a> (2036 genes)	2009/03/09	Variance analysis wa... > more	<a href="#">Botrytis_on_Sunflower_2009</a>	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Unchanged	-	<a href="#">Display data</a>



Gene list query

Query parameters

By default the query accepts wildcards (% and \_) and is case sensitive for the text file. See the user guide for more information.

Projects : **5** Sunflower\_2008

Data type : All

Separated by : semicolon

**Results**

[Help]

«« < 4 5 6 7 8 9 10 11 12 13 > »» | 277 items found, displaying 71 to 80 | Display 10 results per page

##	Gene name	Associated sequences	FOLD CHANGE	Normalized_Variance	pVALUE
71	<a href="#">BofuT4_P014290.1</a>	<a href="#">BofuT4_P014290.1</a>	6.8	0.92	2.97187E-6
72	<a href="#">BofuT4_P014350.1</a>	<a href="#">BofuT4_P014350.1</a>	43.0	0.99	2.868724E-7
73	<a href="#">BofuT4_P015750.1</a>	<a href="#">BofuT4_P015750.1</a>	7.7	0.96	2.523899E-6
74	<a href="#">BofuT4_P015800.1</a>	<a href="#">BofuT4_P015800.1</a>	30.0	0.97	7.024053E-7
75	<a href="#">BofuT4_P016040.1</a>	<a href="#">BofuT4_P016040.1</a>	3.9	0.92	7.381806E-7
76	<a href="#">BofuT4_P018370.1</a>	<a href="#">BofuT4_P018370.1</a>	36.0	0.98	5.72899E-7

## Gene - BofuT4\_P014290.1

**Gene details**

Name : BofuT4\_P014290.1

Associated sequences : [BofuT4\\_P014290.1](#)

**Associated gene lists**

- [Bc1 - In planta Up \(Botrytis-B0510 : in vitro vs in planta\[sunflower\] 48h\)](#)

**Associated reporters**

- [botrytisP00047432](#)
- [botrytisP00047435](#)
- [botrytisP00047436](#)
- [botrytisP00047437](#)
- [botrytisP00047438](#)
- [botrytisP00047439](#)
- [botrytisP00047440](#)
- [botrytisP00047433](#)
- [botrytisP00047441](#)

**Normalized data**

Gene list	FOLD CHANGE	Normalized_Variance	pVALUE
<a href="#">Bc1 - In planta Up (Botrytis-B0510 : in vitro vs in planta[sunflower] 48h)</a>	6.8	0.92	2.97187E-6

- 1- Gene list in "Queries" menu
- 2- select project & data
- 3- Display results
- 4- Display Gene list details
- 5- Display Gene card**

Results

Creation date	Description	Project	Experiments	Regulation	Reporter normalized data	Gene normalized data
20080309	Variance analysis wa... <a href="#">&gt; more Botrytis_on_Sunflower_2008</a>	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Up regulated	-	<a href="#">[i]</a> <a href="#">[m]</a>	
20080309	Variance analysis wa... <a href="#">&gt; more Botrytis_on_Sunflower_2008</a>	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Down regulated	-	<a href="#">[i]</a> <a href="#">[m]</a>	
20080309	Variance analysis wa... <a href="#">&gt; more Botrytis_on_Sunflower_2008</a>	STUDY OF BOTRYTIS-SUNFLOWER INTERACTION	Unchanged	-	<a href="#">[i]</a> <a href="#">[m]</a>	

31



Reference=supercontigs



**Search**

Landmark or Region:  Search

Data Source: Botrytis cinerea T4 genome annotation (bofut4seqfeat)

Reports & Analysis: Annotate Restriction Sites

Scroll/Zoom:     Show 10 kbp    Flip

**Overview**

**Details**

215k 216k 217k 218k 219k 220k 221k 222k 223k 224k

**Contigs**

bt4ctg\_2033  
lgapN:198; rgapN:549

**Gene (Manual curation)**

**CDS (Eugene prediction)**

BoFuT4\_T146240.1 BoFuT4\_T146250.

**Gene (Eugene prediction)**

**Fgenesh (BT4 param)**

**tRNA prediction**

**B. cinerea ESTs (Sim4)**

**B. cinerea EST contigs (Sim4)**

**S. sclerotiorum ESTs**

**Nimblegen oligos**

**Fungal protein 10 best hits (Blastx)**

**Swissprot 10 best hits (Blastx)**

**bt4\_SupSuperContig\_110r\_56\_1\_bt4ctg\_2033\_AO09010200449**

**Feature Infos :**

Length	2054
Ref: start.end	bt4_SupSuperContig_110r_56_1: 219955..222000
Hit: start.end	AO090102000449: 35..667
Hit length	698
Hit coverage	88.40%
Hit identity	33.39%
Hit desc	Aspergillus oryzae predicted protein

[Zoom to this feature](#)

[Detailed Report](#)

Reference=supercontigs

**Search**  
Landmark or Region: bt4\_SupSuperContig\_110r\_56\_1:2 Search  
Data Source: Botrytis cinerea T4 genome annota

**Overview**  
bt4\_SupSuperContig\_110r\_56\_1:2

**Details**

**Contigs**  
bt4ctg\_2033  
lgapN:198; rgapN:549

**Gene (Manual curation)**  
BoFuT4\_T146240.1  
BoFuT4\_T146250.1

**Gene (Eugene prediction)**  
BoFuT4\_T146240.1  
BoFuT4\_T146250.1

**Fgenesh (BT4 param)**

**tRNA prediction**

**B. cinerea ESTs (Sim4)**

**B. cinerea EST contigs (Sim4)**

**S. sclerotiorum ESTs**

**Nimblegen oligos**

**Fungal protein 10 best hits (Blastx)**

**Swissprot 10 best hits (Blastx)**

**Feature Infos :**  
Length 2381  
Ref: start..end bt4\_SupSuperContig\_110r\_56\_1: 219664..222044  
cds\_length 1854  
quality regular

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

**Gene - BofuT4\_P014290.1**  
**GnpArray: Gene card**

**Gene details**

Name : BofuT4\_P014290.1  
Associated sequences : BofuT4\_P014290.1

**Associated gene lists**

- Bc1 - In planta Up (Botrytis-B0510 - in vitro vs in planta[sunflower] 48h)

**Associated reporters**

- botrytisP00047432
- botrytisP00047435
- botrytisP00047436
- botrytisP00047437
- botrytisP00047438
- botrytisP00047439
- botrytisP00047440
- botrytisP00047433
- botrytisP00047441

**Normalized data**

Gene list	FOLD CHANGE	Normalized_Variance	pVALUE
Bc1 - In planta Up (Botrytis-B0510 - in vitro vs in planta[sunflower] 48h)	6.8	0.92	2.97187E-6

**Genome Report System**

- Gene Identifier
- Protein
- 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

**Gbrowse: functional domains**

Landmark or Region: Lma\_P123290.1 Search  
Data Source: Leprosiphonia musculus (P0) automated functional gene annotation...  
ScrollZoom: 100% Show 443 bp + - Flip

**Details**

- General info
- Targeting
- Protein
- Domain
- Localization
- Function
- Structure
- Genome
- Ortholog
- Swissprot 10 best hits (Blastx)
- Protein 10 best hits (Blastx)
- CDs 10 best hits (Eugene)
- King 10 best hits (Blastx)
- COG 10 best hits (Eugene)
- King 10 best hits (Blastx)

# Gbrowse\_syn: *Botrytis* T4 & B0510 / *Sclerotinia*

landmark

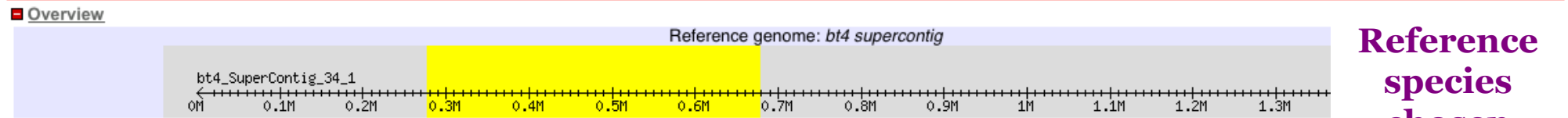
Species to align with the reference

Reference species

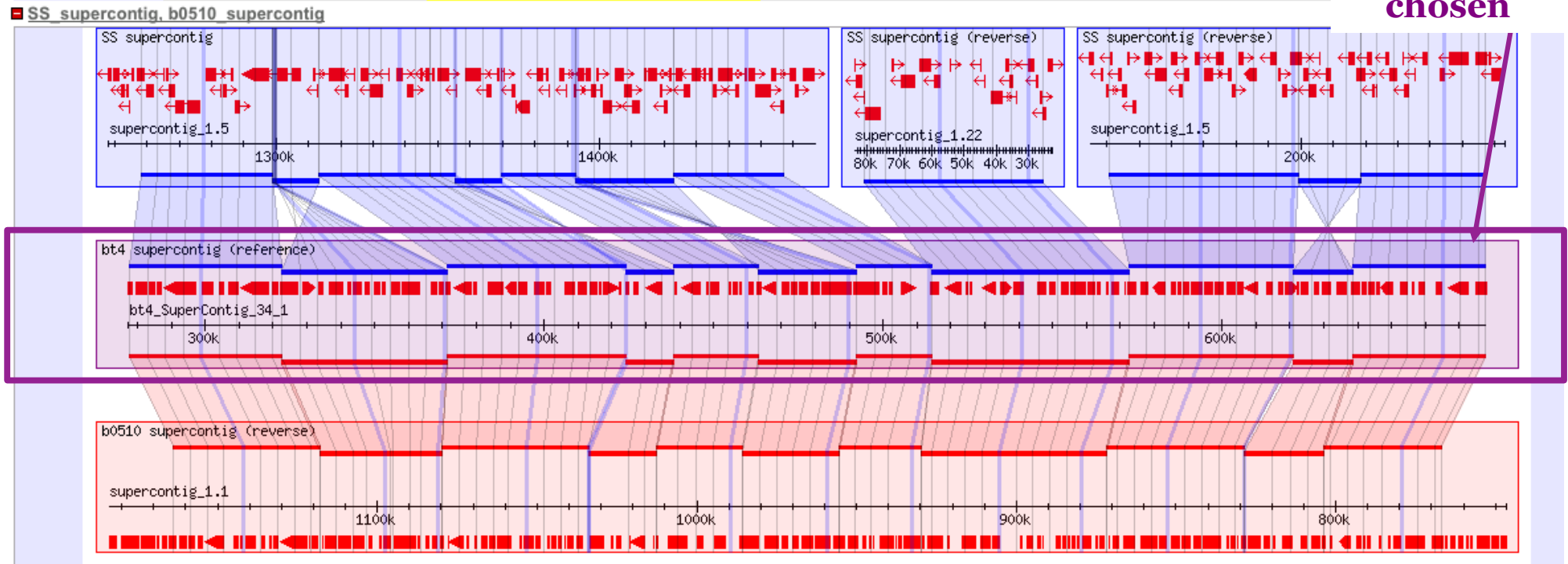
Zoom

**Search**  
Landmark:  Search Reset  
Genome to Search:

**Aligned Species:**  
 b0510 supercontig  SS supercontig  
MERCATOR/MAVID *Botrytis Cinerea* *Sclerotinia sclerotiorum*  
Alignment



Reference species chosen



**Display settings**

Image widths:  640  768  800  1024  1280

Image options:  
Chain alignments  on  off  
Flip minus strand panels  on  off  
Grid lines  on  off  
Edges  on  off  
Shading  on  off

## Genome Report System

■ Access to Reports

*Leptosphaeria maculans*

*Botrytis cinerea T4*

*Sclerotinia sclerotiorum*

*Botrytis cinerea B0510*



Genome Report System - copyright INRA 2009

## Botrytis cinerea T4 GRS

### Functional annotation

BofuT4\_P000210.1

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

More in the next  
Nicolas' talk

**Analysis tracks**

**Gene models**

The screenshot shows the Apollo genome browser interface for *Botrytis fuckeliana*. The top track displays transcripts such as `bt4_SuperContig_10_1_bt4ctg_0222_fgenesh_Botrytis_transcript_0010`. Below this, gene models are represented by colored bars with labels like `BofuT4_T016120.1` and `egN5_BofuT4_T016120.1`. A zoomed-in view of a specific feature is shown at the bottom, with a table of genomic data.

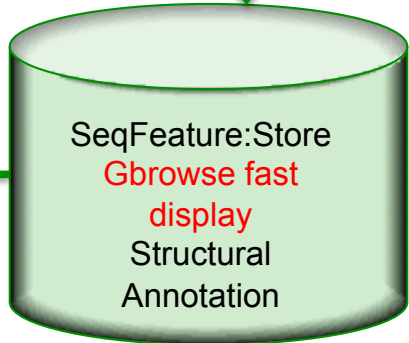
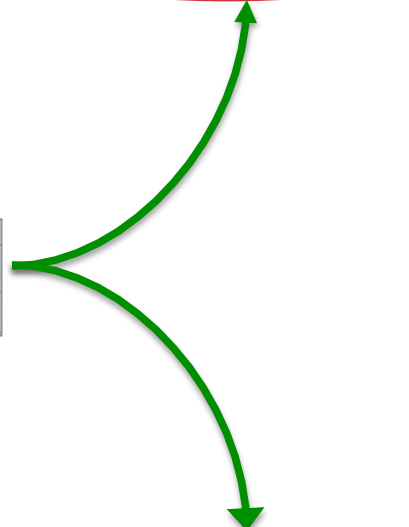
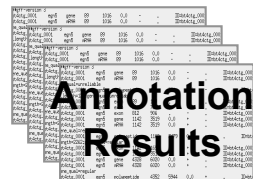
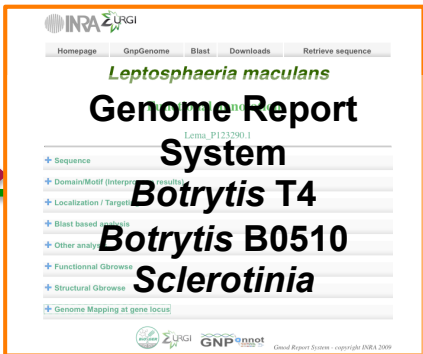
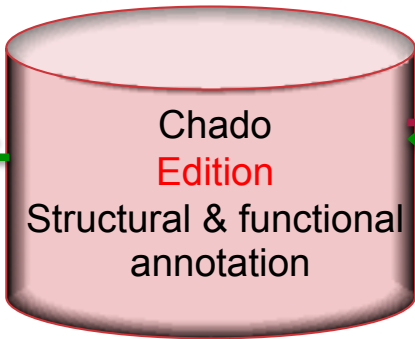
Type	Name	Range	Score
Eugene	egN5_BofuT4_T01...	274210-275265	96.0

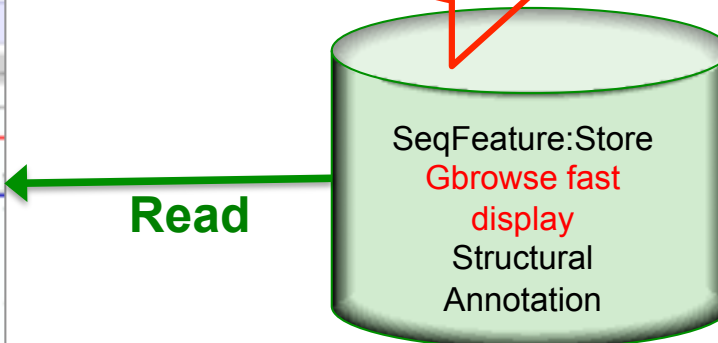
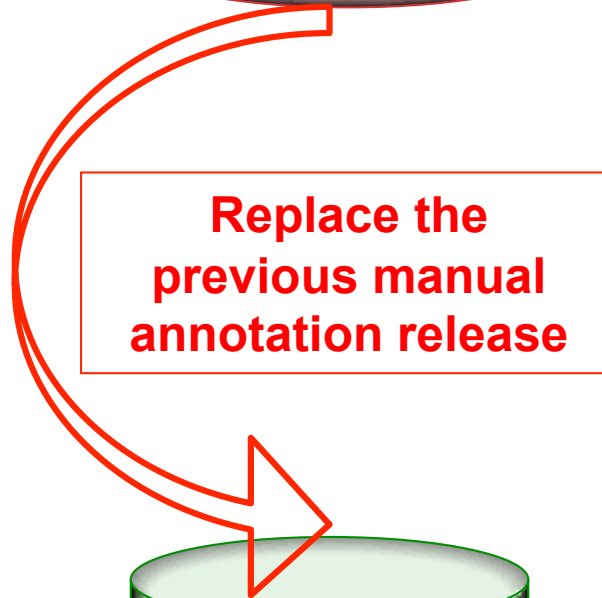
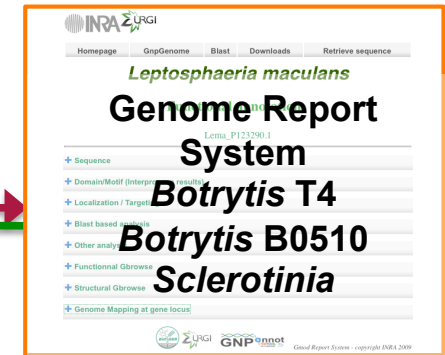
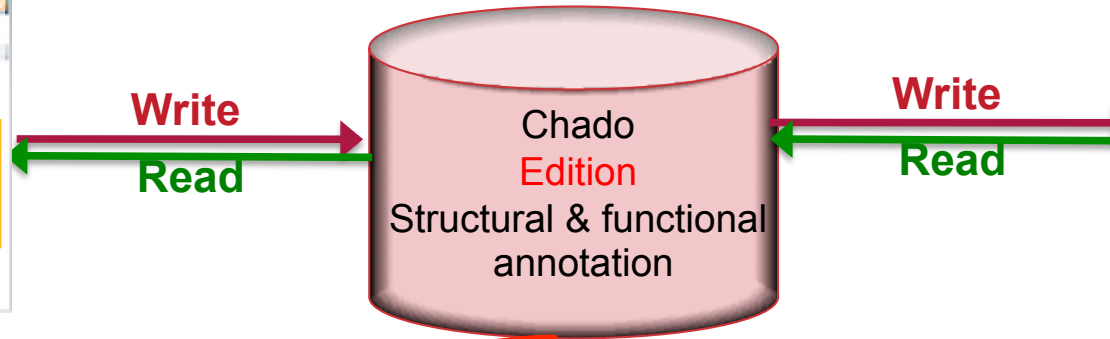
  

Genomic Range	Genomic Length	Score	query_frame
274210-274315	106	96.0	2
274381-274510	130	96.0	2
274570-274647	78	96.0	2
274746-275265	520	96.0	1

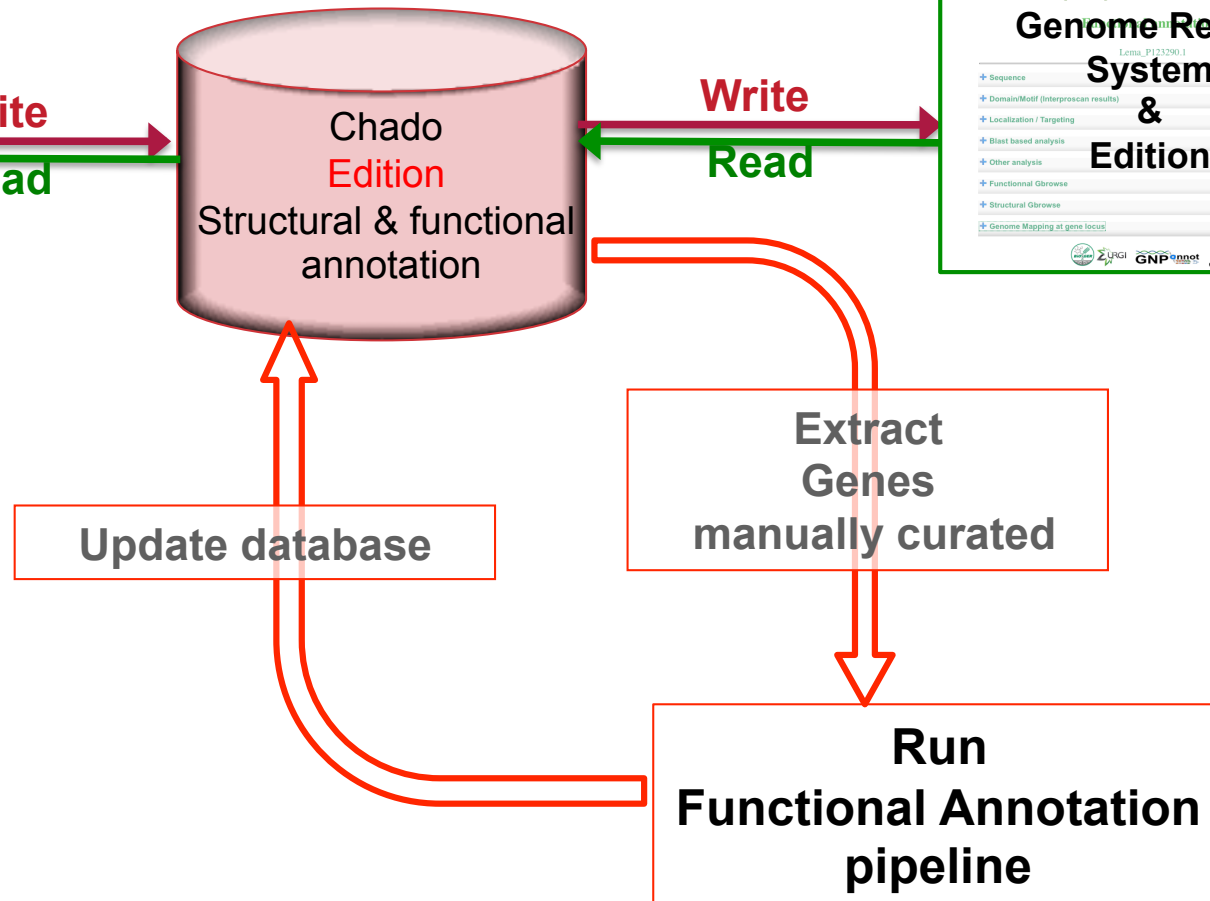
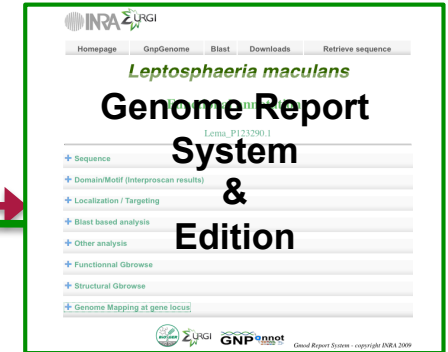
**Zoom**

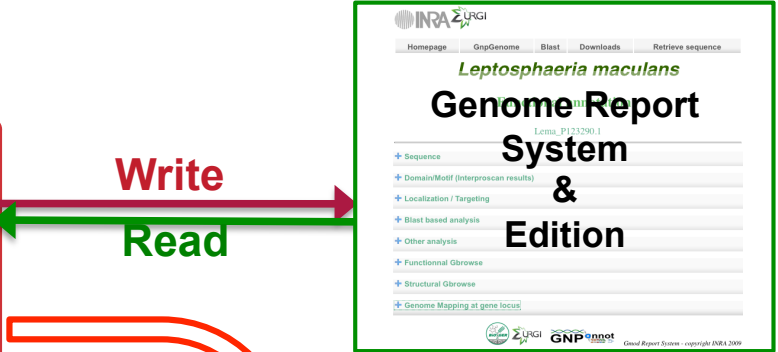
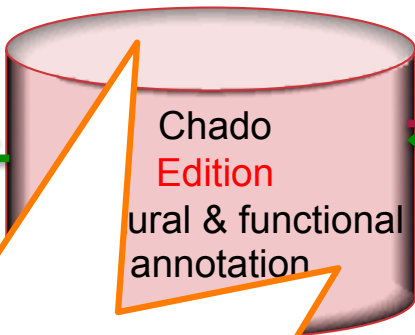
**Selected feature information**











**> 1200 genes manually validated/curated**  
**+**  
**Functional automated re-annotation**

**Extract Genes manually curated**

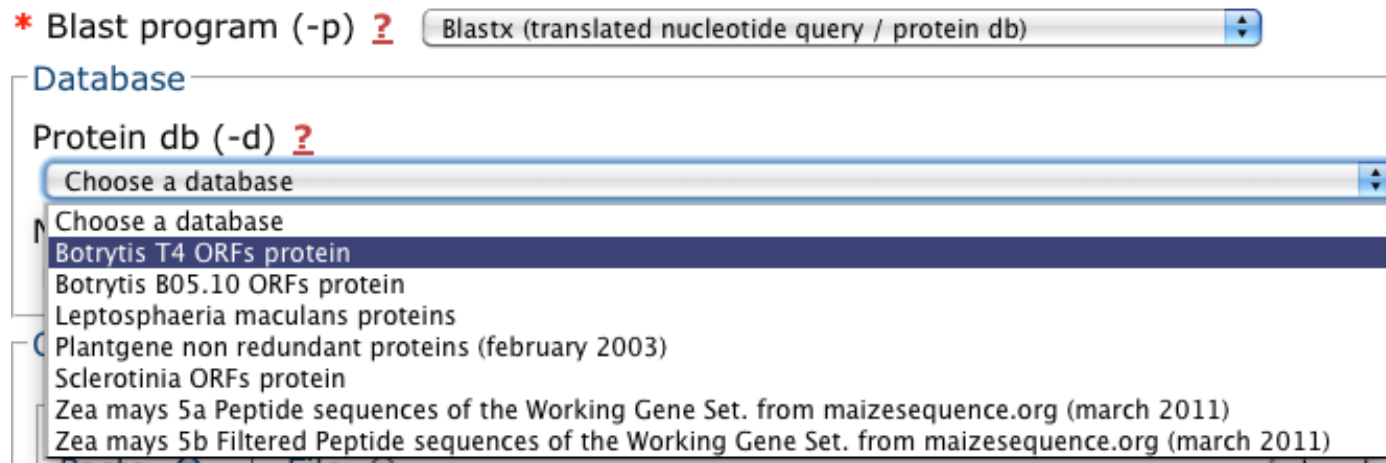
**Run Functional Annotation pipeline**



# Annotation Workflow tutorial

# Annotation workflow 1

- Start from fasta sequence
- Blast it
  - ◆ <http://urgi.versailles.inra.fr/index.php/urgi/Species/Botrytis/>
  - ◆ → Sequences & Databases → Blast



\* Blast program (-p) ?

Database

Protein db (-d) ?

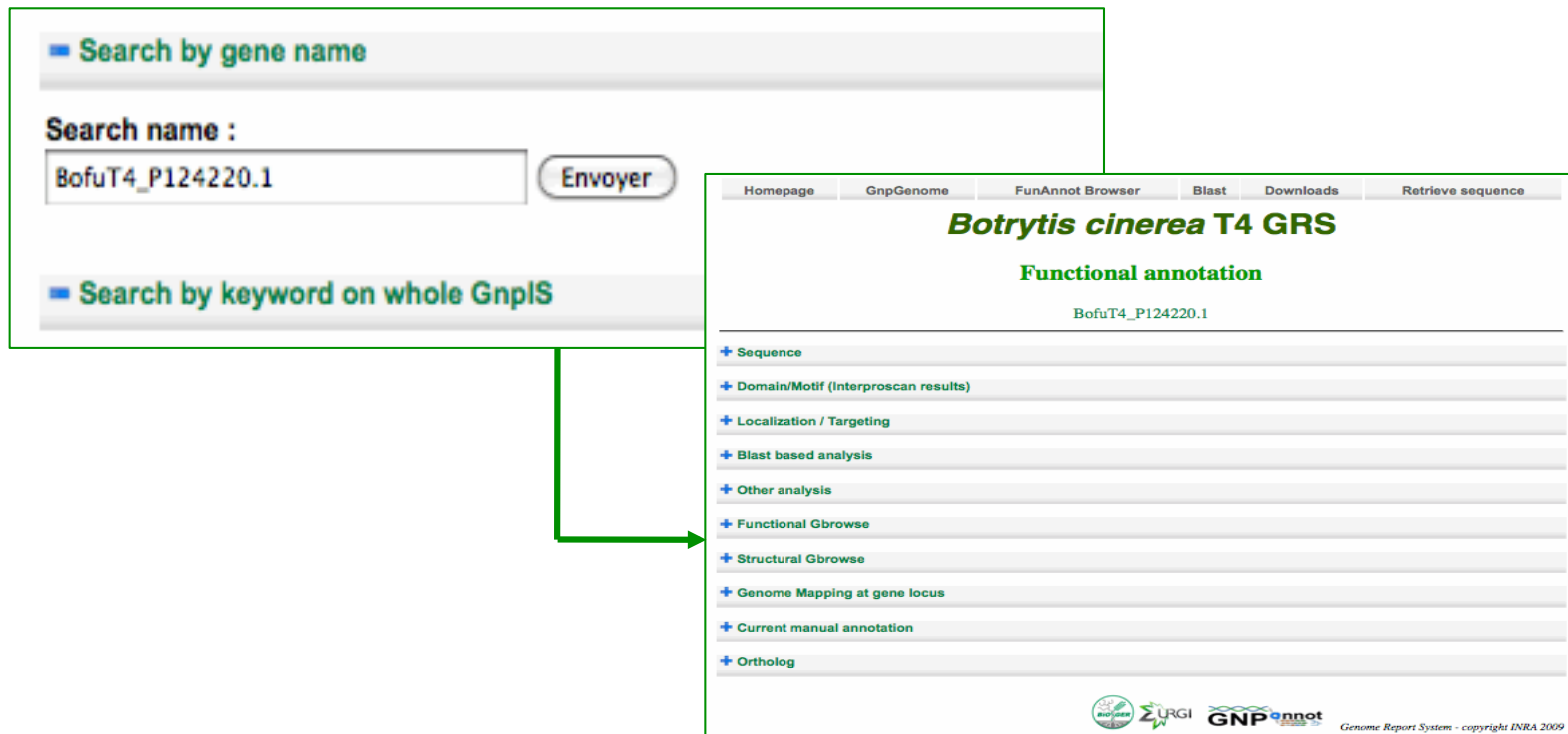
Choose a database

- Choose a database
- Botrytis T4 ORFs protein
- Botrytis B05.10 ORFs protein
- Leptosphaeria maculans proteins
- Plantgene non redundant proteins (february 2003)
- Sclerotinia ORFs protein
- Zea mays 5a Peptide sequences of the Working Gene Set. from maizesequence.org (march 2011)
- Zea mays 5b Filtered Peptide sequences of the Working Gene Set. from maizesequence.org (march 2011)

- ◆ Get the list of genes IDs in Botrytis T4/B0510 or *Sclerotinia* genome

# Annotation workflow 1

- Start from fasta sequence
- Blast it
- Retrieve whole BT4 annotation (structural & functional) for each gene in Genome Report System
  - ◆ <http://urgi.versailles.inra.fr/grs/index.html>



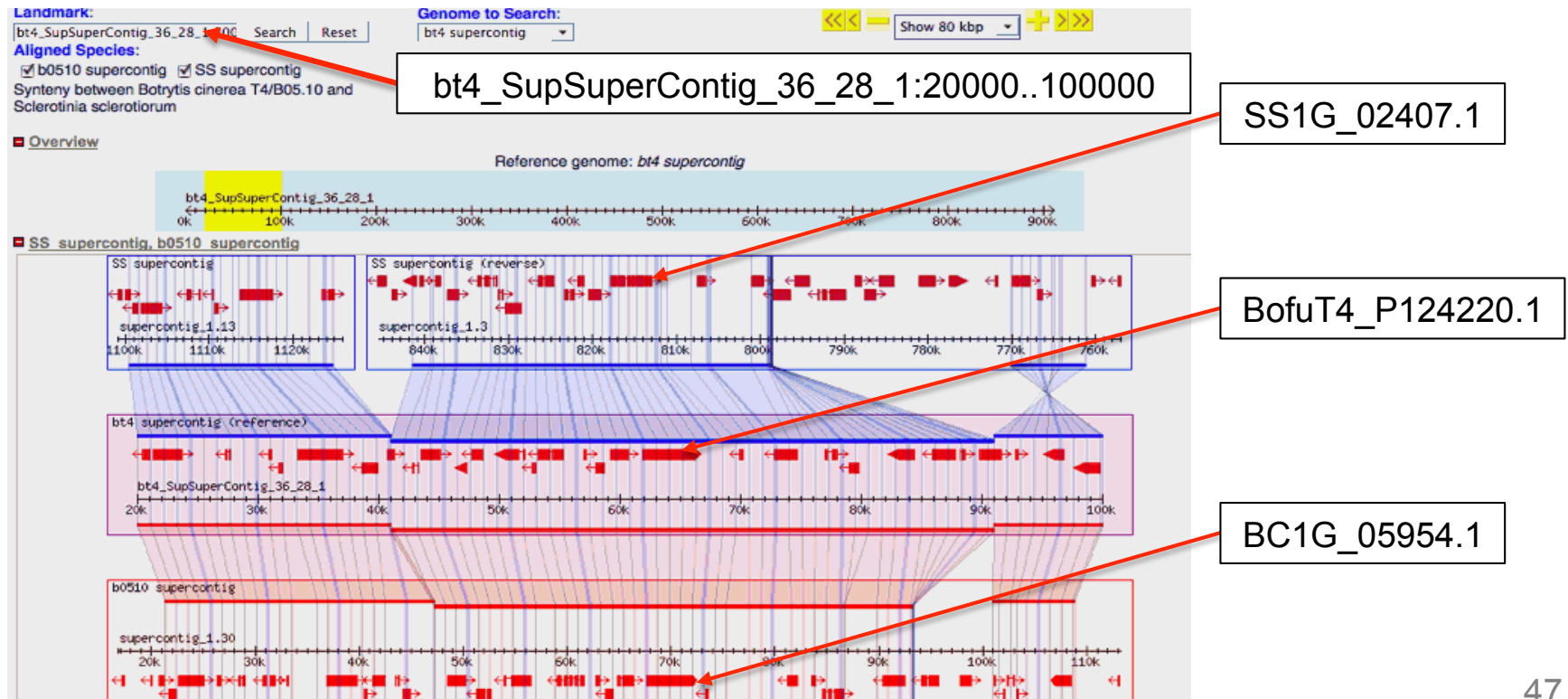
The screenshot illustrates the workflow from a search form to a detailed gene annotation page. On the left, a search form titled "Search by gene name" contains a text input field with "BofuT4\_P124220.1" and an "Envoyer" button. Below it is a "Search by keyword on whole GnpIS" option. A green arrow points from the search form to the right-hand page. The right-hand page is titled "Botrytis cinerea T4 GRS" and "Functional annotation" for the gene "BofuT4\_P124220.1". It features a navigation menu with options: "Homepage", "GnpGenome", "FunAnnot Browser", "Blast", "Downloads", and "Retrieve sequence". The main content area lists various analysis options, each with a plus sign: "Sequence", "Domain/Motif (Interproscan results)", "Localization / Targeting", "Blast based analysis", "Other analysis", "Functional Gbrowse", "Structural Gbrowse", "Genome Mapping at gene locus", "Current manual annotation", and "Ortholog". The footer includes logos for INRA, ZURGI, and GNPannot, along with the text "Genome Report System - copyright INRA 2009".

# Annotation workflow 1

- Start from fasta sequence
- Blast it
- Retrieve whole BT4 annotation (structural & functional) for each gene in Genome Report System
  - ◆ What does the conserved domains indicate about the protein function?
  - ◆ How many Botrytis ESTs match to the gene? What does it indicate about the expression pattern?
  - ◆ Does the BDBH program indicate putative orthologs in B05-10 strain and in Sclerotinia?
  - ◆ Which T4 SuperContig contain the gene?
  - ◆ Select the ESTs tracks. Are they in accordance with the predicted annotation from Eugene (and/or Fgenesh)? How many exons are detected?

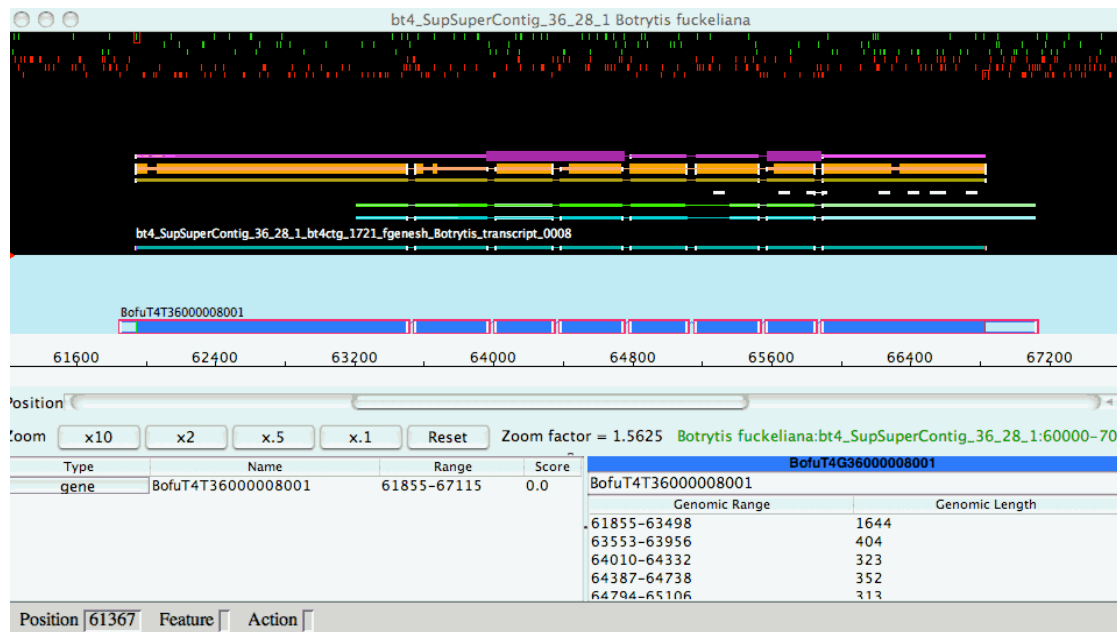
# Annotation workflow 1

- Start from fasta sequence
- Blast it
- Retrieve whole BT4 annotation (structural & functional) for each gene in Genome Report System
- Look at the orthologs genes in the three genomes.
- Is there a synteny between *Botrytis* and *Sclerotinia* around the gene
  - ◆ [http://gpi.versailles.inra.fr/cgi-bin/gbrowse\\_syn/botrytis](http://gpi.versailles.inra.fr/cgi-bin/gbrowse_syn/botrytis)



# Annotation workflow 1

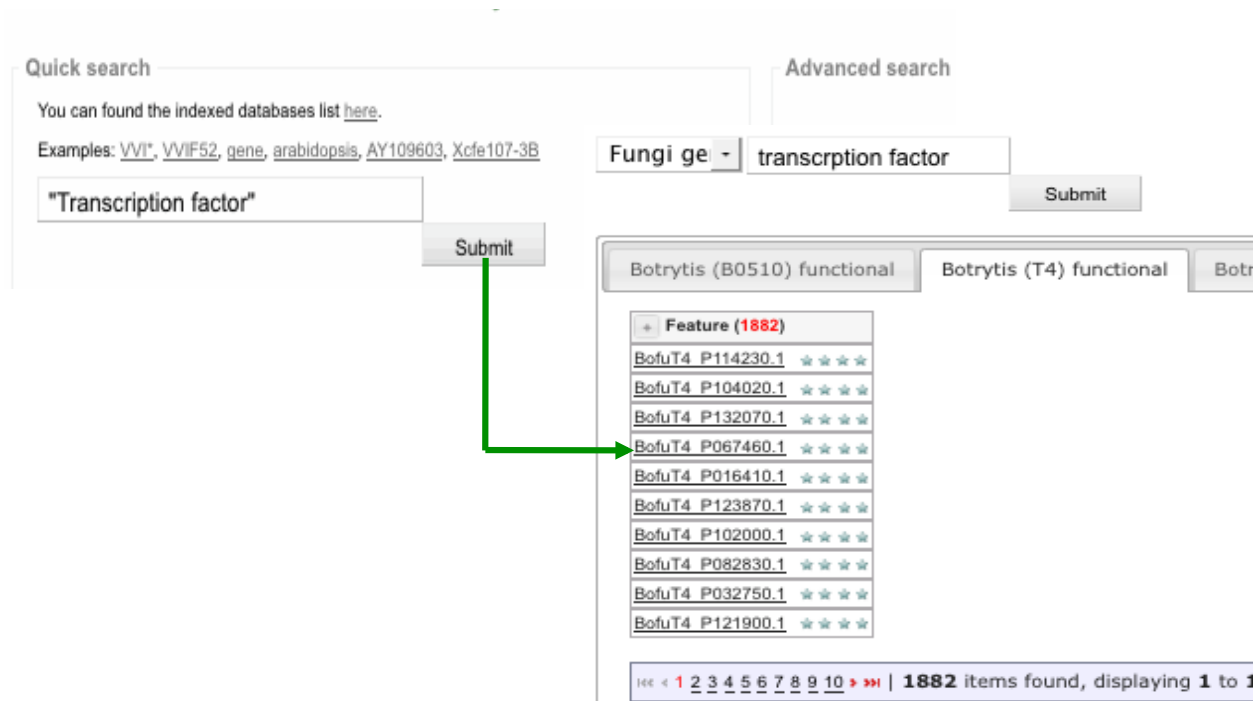
- Start from fasta sequence
- Blast it
- Retrieve whole BT4 annotation (structural & functional) for each gene in Genome Report System
- Look at the orthologs genes in the three genomes.
- Is there a synteny between Botrytis and Sclerotinia around the gene
- **Get coordinates from GnpGenome then open apollo to check curate/validate the gene**
  - ◆ <http://urgi.versailles.inra.fr/Tools/Apollo>





## Annotation workflow 2

- Search for a gene family. Ex: "transcription factor"
  - ◆ No fasta sequence provided
  - ◆ Search by keyword
  - ◆ <http://urgi.versailles.inra.fr/gnpis>



The screenshot shows the URGIS search interface. On the left, there is a 'Quick search' section with a text input field containing '"Transcription factor"' and a 'Submit' button. Below this, it says 'You can find the indexed databases list [here](#). Examples: [VVI\\*](#), [VVIF52](#), [gene](#), [arabidopsis](#), [AY109603](#), [Xcfe107-3B](#)'. On the right, there is an 'Advanced search' section with a dropdown menu set to 'Fungi ge' and a text input field containing 'transcription factor', followed by a 'Submit' button. Below the search results, there are tabs for 'Botrytis (B0510) functional', 'Botrytis (T4) functional', and 'Botr'. A green arrow points from the 'Submit' button in the 'Quick search' section to the search results. The results are displayed in a table with a header 'Feature (1882)' and a list of items, each with a link and a star rating. The items listed are:

Feature (1882)
<a href="#">BofuT4 P114230.1</a> ★★★★★
<a href="#">BofuT4 P104020.1</a> ★★★★★
<a href="#">BofuT4 P132070.1</a> ★★★★★
<a href="#">BofuT4 P067460.1</a> ★★★★★
<a href="#">BofuT4 P016410.1</a> ★★★★★
<a href="#">BofuT4 P123870.1</a> ★★★★★
<a href="#">BofuT4 P102000.1</a> ★★★★★
<a href="#">BofuT4 P082830.1</a> ★★★★★
<a href="#">BofuT4 P032750.1</a> ★★★★★
<a href="#">BofuT4 P121900.1</a> ★★★★★

At the bottom of the results, there is a pagination bar: '1882 items found, displaying 1 to 1'.

## Annotation workflow 2

- Search for a gene family. Ex: "transcription factor"
- Display the Genome report for these genes

Fungi ge - transcription factor

Botrytis (B0510) functional Botrytis (T4) functional Botr

**+ Feature (1882)**

- [BofuT4\\_P114230.1](#) ★★★★★
- [BofuT4\\_P104020.1](#) ★★★★★
- [BofuT4\\_P132070.1](#) ★★★★★
- [BofuT4\\_P067460.1](#) ★★★★★
- [BofuT4\\_P016410.1](#) ★★★★★
- [BofuT4\\_P123870.1](#) ★★★★★
- [BofuT4\\_P102000.1](#) ★★★★★
- [BofuT4\\_P082830.1](#) ★★★★★
- [BofuT4\\_P032750.1](#) ★★★★★
- [BofuT4\\_P121900.1](#) ★★★★★

[BofuT4\\_P104020.1](#)

**+ Gene Identifier**

**+ DbXrefs**

**Domain/Motif (Interproscan results)**

Analysis	Domains	Begin	End	Length	Gene Ontology	Cross Ref	InterPro
HMMPfam	<a href="#">PF05091</a>	13	554	542	<a href="#">GO:0003743</a> translation initiation factor activity	<a href="#">---</a>	<a href="#">IPR007783</a>
					<a href="#">GO:0006413</a> translational initiation	<a href="#">---</a>	
HMMSmart	no results						
HMMTigr	no results						
HMMPanther	<a href="#">PTHR12399</a>	4	576	573	<a href="#">GO:0003743</a> translation initiation factor activity	<a href="#">---</a>	none
					<a href="#">GO:0006413</a> translational initiation	<a href="#">---</a>	

- Get list of gene sharing the same GeneOntology ID

## Annotation workflow 2

- Search for a gene family. Ex: "transcription factor"
- Display the Genome report for these genes
- Get list of gene sharing the same GeneOntology ID
- **Get the orthologs in B0510 & *Sclerotinia***
  - ◆ From GRS using Ortholog category
  - ◆ From GRS, get gene coordinates and look for syntenic region using Gbrowse\_syn



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- Adeline Simon
- Muriel Viaud

Thanks to ...

### Botrytis / Sclerotinia Genome project consortium

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PLOS GENETICS

## Genomic Analysis of the Necrotrophic Fungal Pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*

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