Intra-specific and interspecific protein content analysis

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École "Assemblage & Annotation" AVIESAN 2022 - Roscoff

Intra-specific and interspecific protein content analysis

Goals :

- Reduce redondancy (alternative CDS) => **compute representative sequences**
- Build set of repeated sequences or highly conserved families(genes/proteins)
- Compare gene/protein content between
  - assemblies versions
  - individuals of a single species
  - different species

=> Gene loss/gain (toward pangenomics)

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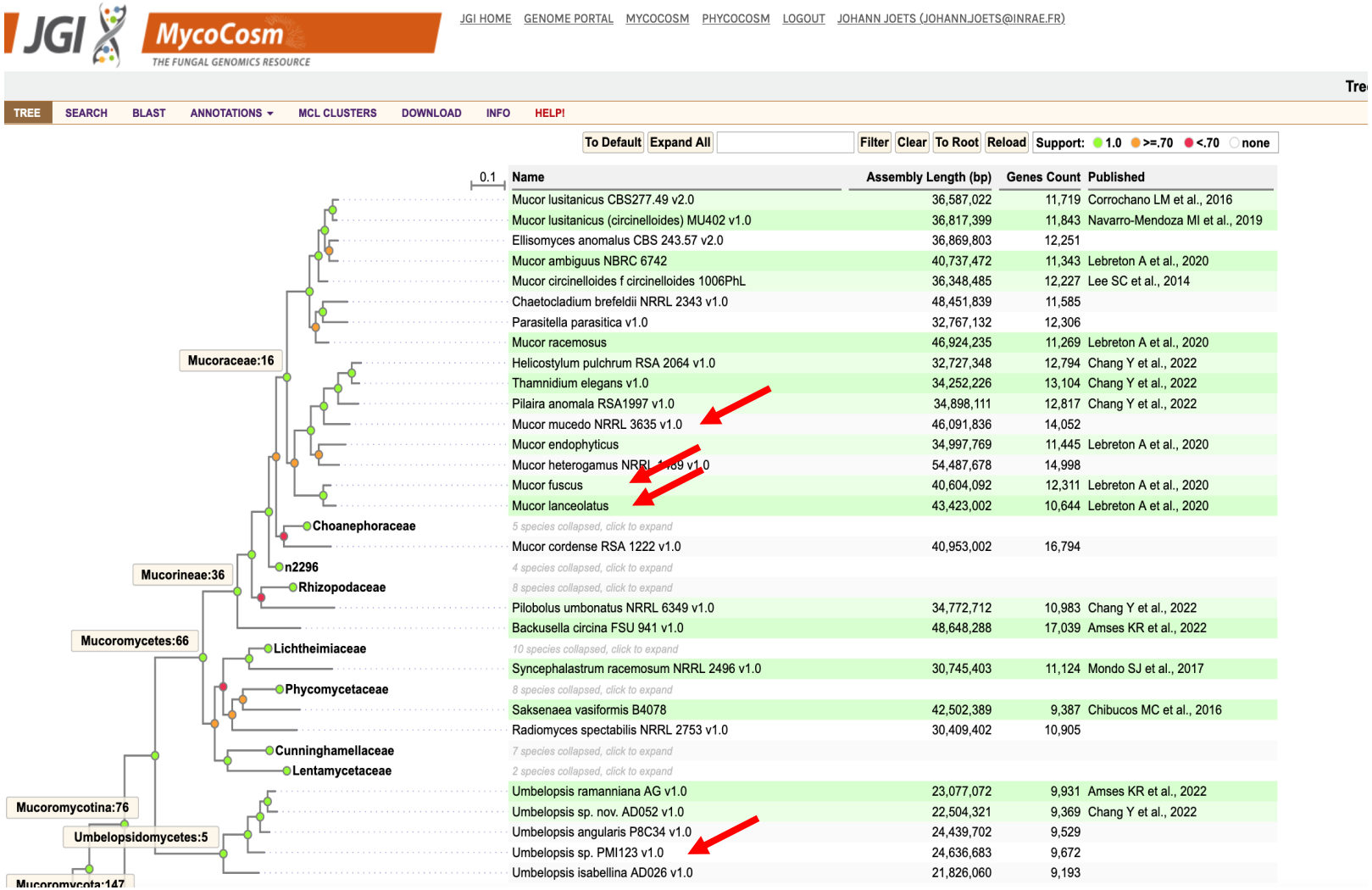
Methods / tools :

- Sequence similarity-based clustering : **CD-HIT** => intra-specific comparaison (*low seq divergence*)
- Phylogeny-based orthology classification : **OrthoFinder** => inter-specific comparaison (*higher seq divergence*)

OrthoFinder. Our dataset:



OrthoFinder. Our dataset:

fungi.prot.fasta

a list with 4 items

- Mmucedo.aa.fasta
- Umbsp.aa.fasta.gz
- Mucfus1.aa.fasta.gz
- Muclan1.aa.fasta.gz

Mycobiology

Research Article

Phylogenetic Status of Two Undescribed Zygomycete Species from Korea: *Actinomucor elegans* and *Mucor minutus*

Thuong T. T. Nguyen[1], Hee-Young Jung[2], Youn Su Lee[3], Kerstin Voigt[4] and Hyang Burm Lee[1,*]

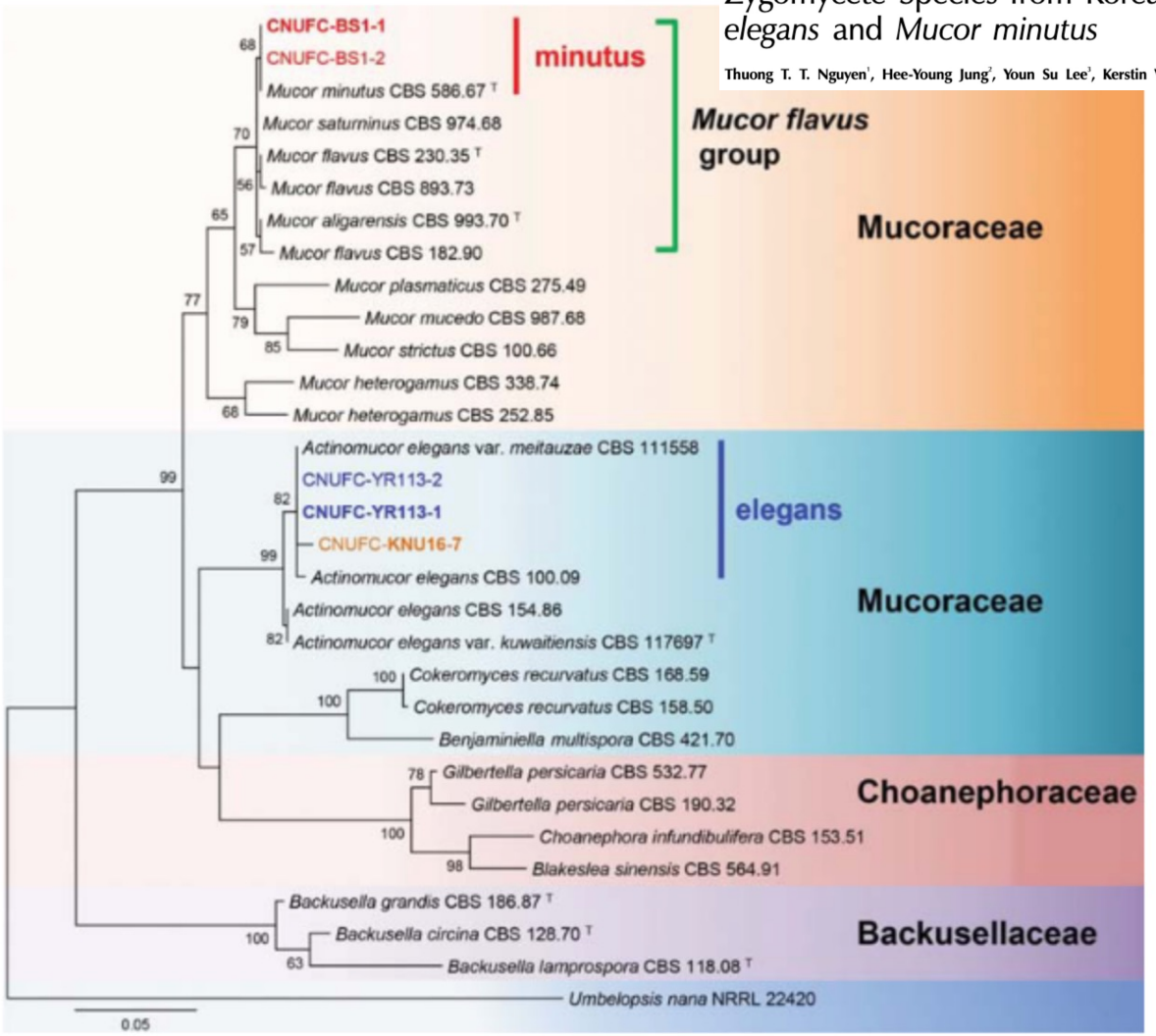
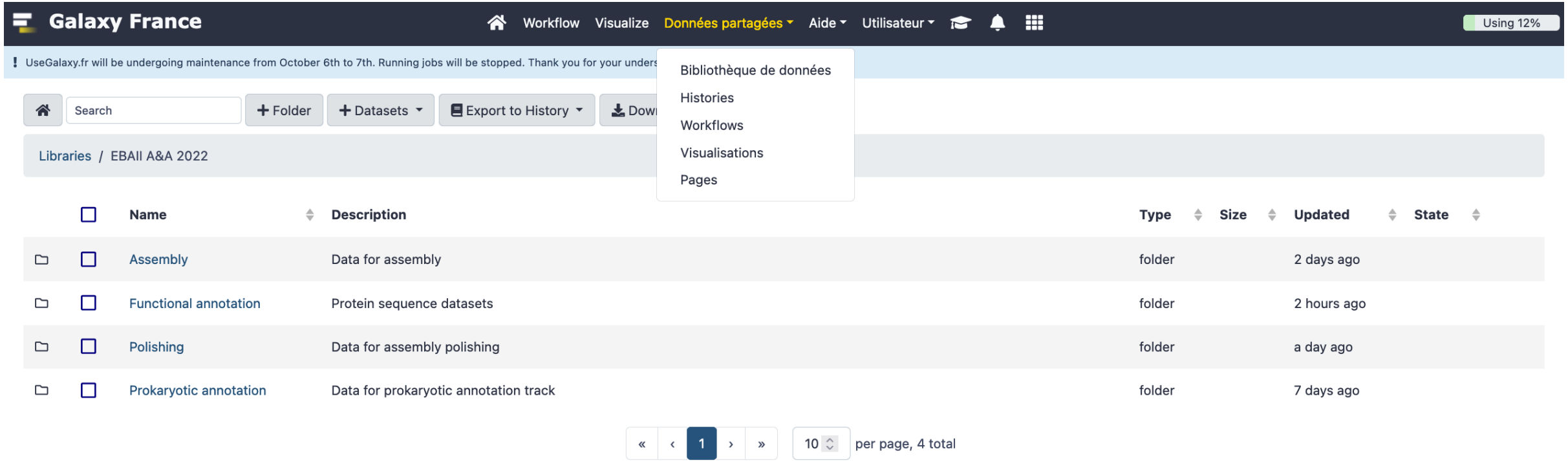


Fig. 2. Phylogenetic tree based on maximum likelihood analysis of 28S rDNA sequences for *Actinomucor elegans* CNUFC-YR113-1, *A. elegans* CNUFC-YR113-2, *A. elegans* CNUFC-KNU16-7, *Mucor minutus* CNUFC-BS1-1, and *M. minutus* CNUFC-BS1-2. *Umbelopsis nana* was used as an outgroup. Bootstrap support values of ≥50% are indicated at the nodes. The bar indicates the number of substitutions per position.

Datasets library



Datasets library

Search | + Folder | + Datasets | Add to History | Download | Details

Libraries / EBAII A&A 2022 / Functional annotation

		Name	Description
	☐	EA1197.default.HQ.prot.fa	uploaded fasta file
	☐	EA1197.default.HQ.prot.fa	uploaded fasta file
	☐	F331.default.HQ.prot.fa	uploaded fasta file
	☐	F331.default.HQ.prot.fa	uploaded fasta file
	☐	GASPE.default.HQ.prot.fa	uploaded fasta file
	☐	GASPE.default.HQ.prot.fa	uploaded fasta file
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	☐	Muclan1.aa.fasta.gz	uploaded fasta.gz file
	☑	Umbsp.aa.fasta.gz	uploaded fasta.gz file

Galaxy France | Workflow | Visualize | Données partagées | Aide | Utilisateur

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- as Datasets
- as a Collection

Libraries / EBAII A&A 2022 / Functional annotation

Name	Description	Type	Size	Updated	State
EA1197.default.HQ.prot.fa	uploaded fasta file	fasta	20.5 MB	over 1 year ago	
EA1197.default.HQ.prot.fa	uploaded fasta file	fasta	20.5 MB	over 1 year ago	
F331.default.HQ.prot.fa	uploaded fasta file	fasta	20.8 MB	over 1 year ago	
F331.default.HQ.prot.fa	uploaded fasta file	fasta	20.8 MB	over 1 year ago	
GASPE.default.HQ.prot.fa	uploaded fasta file	fasta	20.9 MB	over 1 year ago	
GASPE.default.HQ.prot.fa	uploaded fasta file	fasta	20.9 MB	over 1 year ago	
Mmucedo.aa.fasta	uploaded fasta file	fasta	6 MB	over 1 year ago	
Mmucedo.prot.fasta	uploaded fasta file	fasta	6 MB	over 1 year ago	
Mucfus1.aa.fasta.gz	uploaded fasta.gz file	fasta.gz	3.4 MB	over 1 year ago	
Mucfus1.aa.fasta.gz	uploaded fasta.gz file	fasta.gz	3.4 MB	over 1 year ago	
Muclan1.aa.fasta.gz	uploaded fasta.gz file	fasta.gz	3 MB	over 1 year ago	

javascript:void(0)

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Libraries / EBAII A&A 2022 / Functional annotation

- as Datasets
- as a Collection

	Name	Description
	EA1197.default.HQ.prot.fa	uploaded fasta file
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	F331.default.HQ.prot.fa	uploaded fasta file
	F331.default.HQ.prot.fa	uploaded fasta file
	GASPE.default.HQ.prot.fa	uploaded fasta file
	GASPE.default.HQ.prot.fa	uploaded fasta file
☑	Mmucedo.aa.fasta	uploaded fasta file
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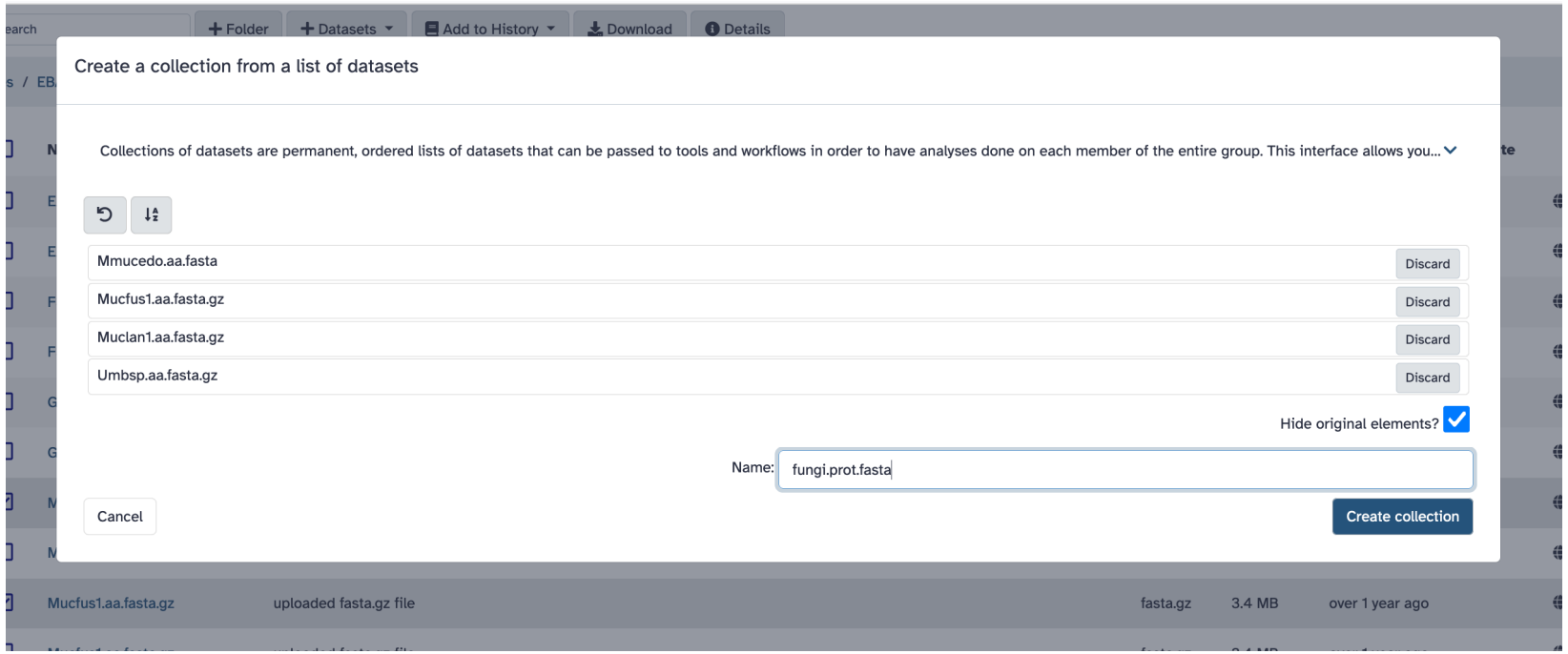
☑	Muclan1.aa.fasta.gz	uploaded fasta.gz file
	Muclan1.aa.fasta.gz	uploaded fasta.gz file
☑	Umbsp.aa.fasta.gz	uploaded fasta.gz file

javascript:void(0)


Folder
Datasets
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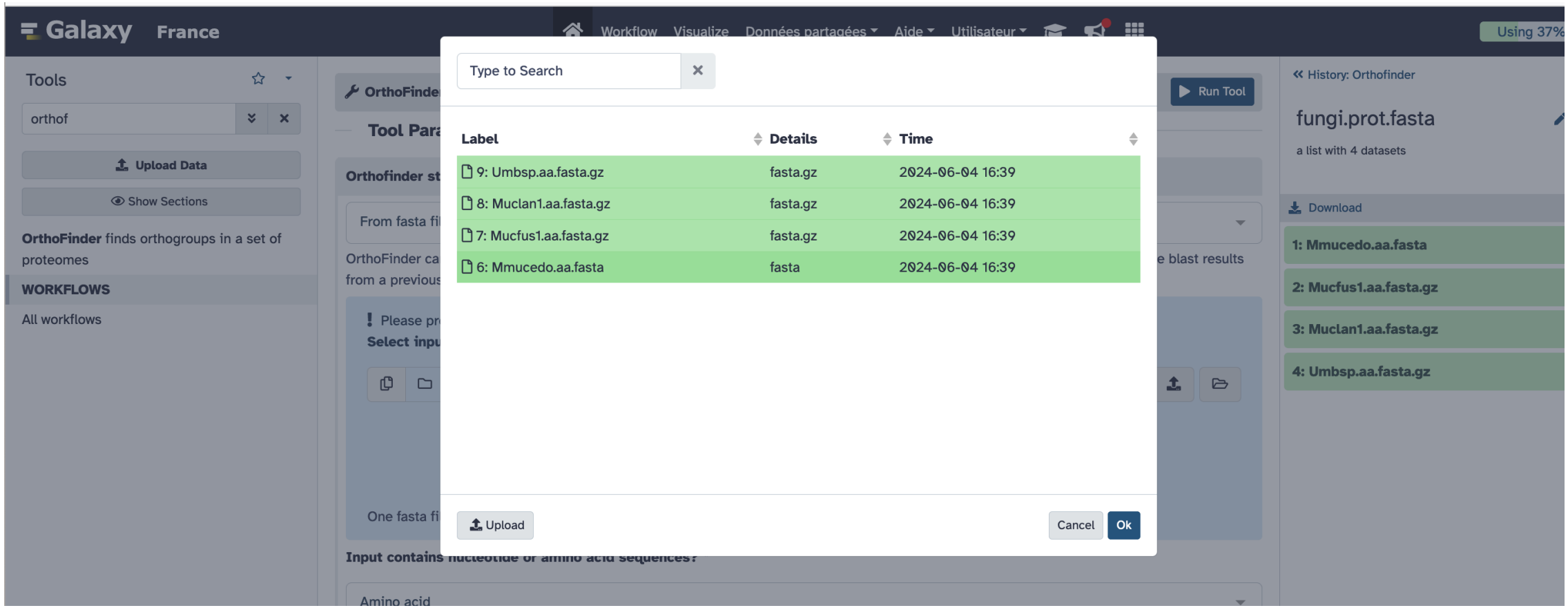
Details
Create a collection from a list of datasets
Collections of datasets are permanent, ordered lists of datasets that can be passed to tools and workflows in order to have analyses done on each member of the entire group. This interface allows you...
Mmucedo.aa.fasta
Discard
Mucfus1.aa.fasta.gz
Discard
Muclan1.aa.fasta.gz
Discard
Umbsp.aa.fasta.gz
Discard
Hide original elements?
Name:
fungi.prot.fasta
Cancel
Create collection
Mucfus1.aa.fasta.gz
uploaded fasta.gz file
fasta.gz
3.4 MB
over 1 year ago


Galaxy France
Workflow
Visualize
Données partagées
Aide
Utilisateur
Using 37%
Tools
orthof
Upload Data
Show Sections
OrthoFinder finds orthogroups in a set of proteomes
WORKFLOWS
All workflows
Run Tool
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9: Umbsp.aa.fasta.gz
fasta.gz
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8: Muclan1.aa.fasta.gz
fasta.gz
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fasta.gz
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6: Mmucedo.aa.fasta
fasta
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Upload
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Ok
History: Orthofinder
fungi.prot.fasta
a list with 4 datasets
Download
1: Mmucedo.aa.fasta
2: Mucfus1.aa.fasta.gz
3: Muclan1.aa.fasta.gz
4: Umbsp.aa.fasta.gz

OrthoFinder: Galaxy

Galaxy France | Workflow | Visualize | Données partagées | Aide | Utilisateur | Using 12%

! UseGalaxy.fr will be undergoing maintenance from October 6th to 7th. Running jobs will be stopped. Thank you for your understanding.

Tools

orthofinder

Upload Data

Show Sections

OrthoFinder finds orthogroups in a set of proteomes

WORKFLOWS

All workflows

Orthofinder starting point

From fasta files

OrthoFinder can be run in 2 steps. Choose 'From fasta files' to run OrthoFinder from scratch or 'From blast results' if you have all the blast results from a previous OrthoFinder run.

Select input fasta files

10: fungi.prot.fasta (with implicit datatype conversion)

8: maize.prot.fasta

One fasta file per species; species and sequence names in the results will remain the same than in the input files.

Input contains nucleotide or amino acid sequences?

Amino acid

Sequence search program

Diamond (faster)

Orthofinder run mode

Full run (including gene trees)

Method for gene tree inference

Dendroblast (faster)

Inflation parameter

1,5

Modify inflation parameter for MCL. Not recommended. (-I)

Generate output about gene duplication events

Yes

Email notification

No

Send an email notification when the job completes.

Execute

History

Back to data

fungi.prot.fasta

a list with 4 items

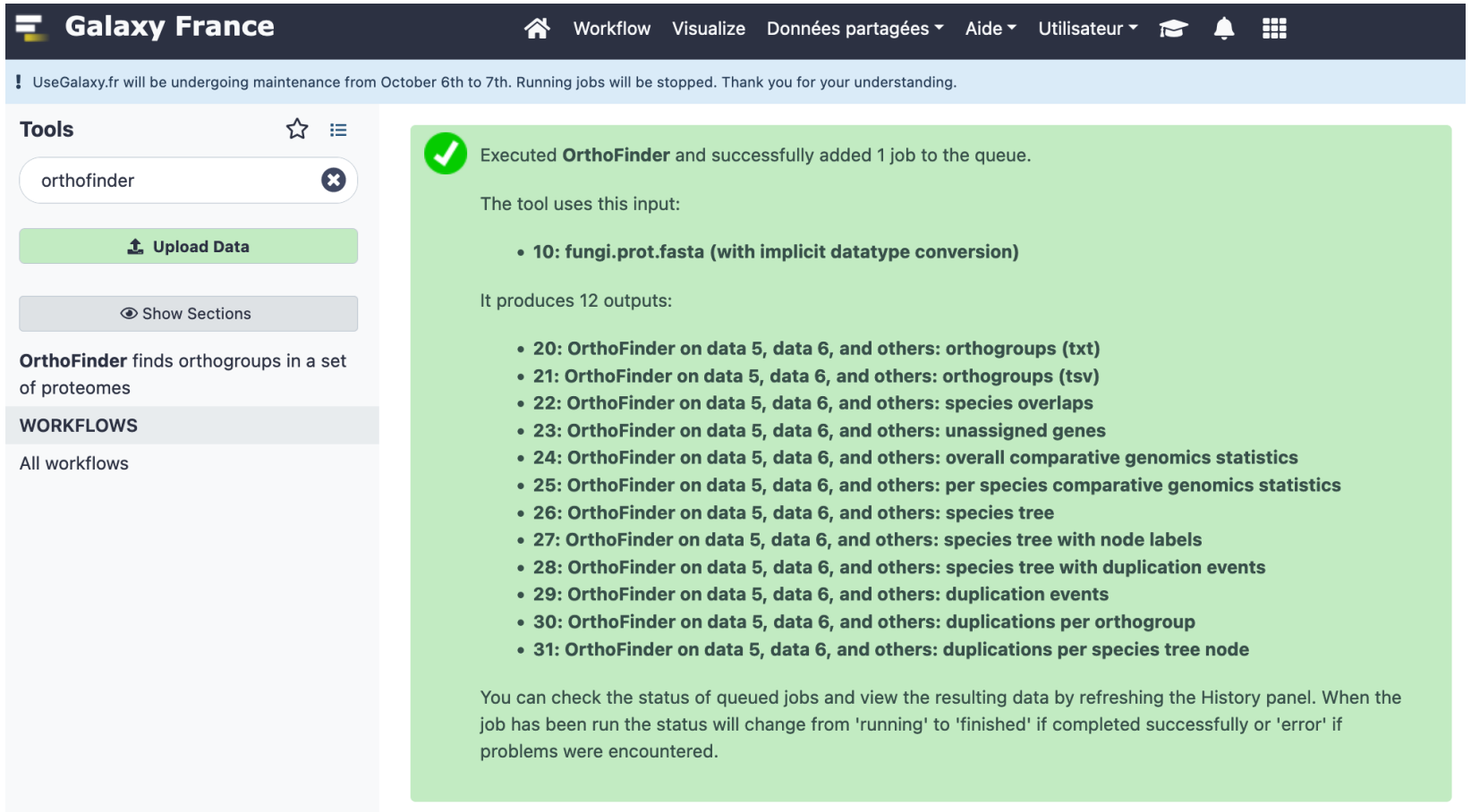
Mmucedo.aa.fasta

Umbsp.aa.fasta.gz

Mucfus1.aa.fasta.gz

Muclan1.aa.fasta.gz

OrthoFinder: Galaxy



CD-HIT a sequence clustering program

Was originaly developed to remove redundancy and select representative sequences at verry high speed

CD-HIT, use incremental clustering algorithm method:

1/ Sequences are sorted in order of decreasing length.

2/ The longest one becomes the representative of the first cluster.

3/ Each remaining sequence is compared to the representatives of existing clusters.

If the similarity with any representative is above a given threshold, it is grouped into that cluster.

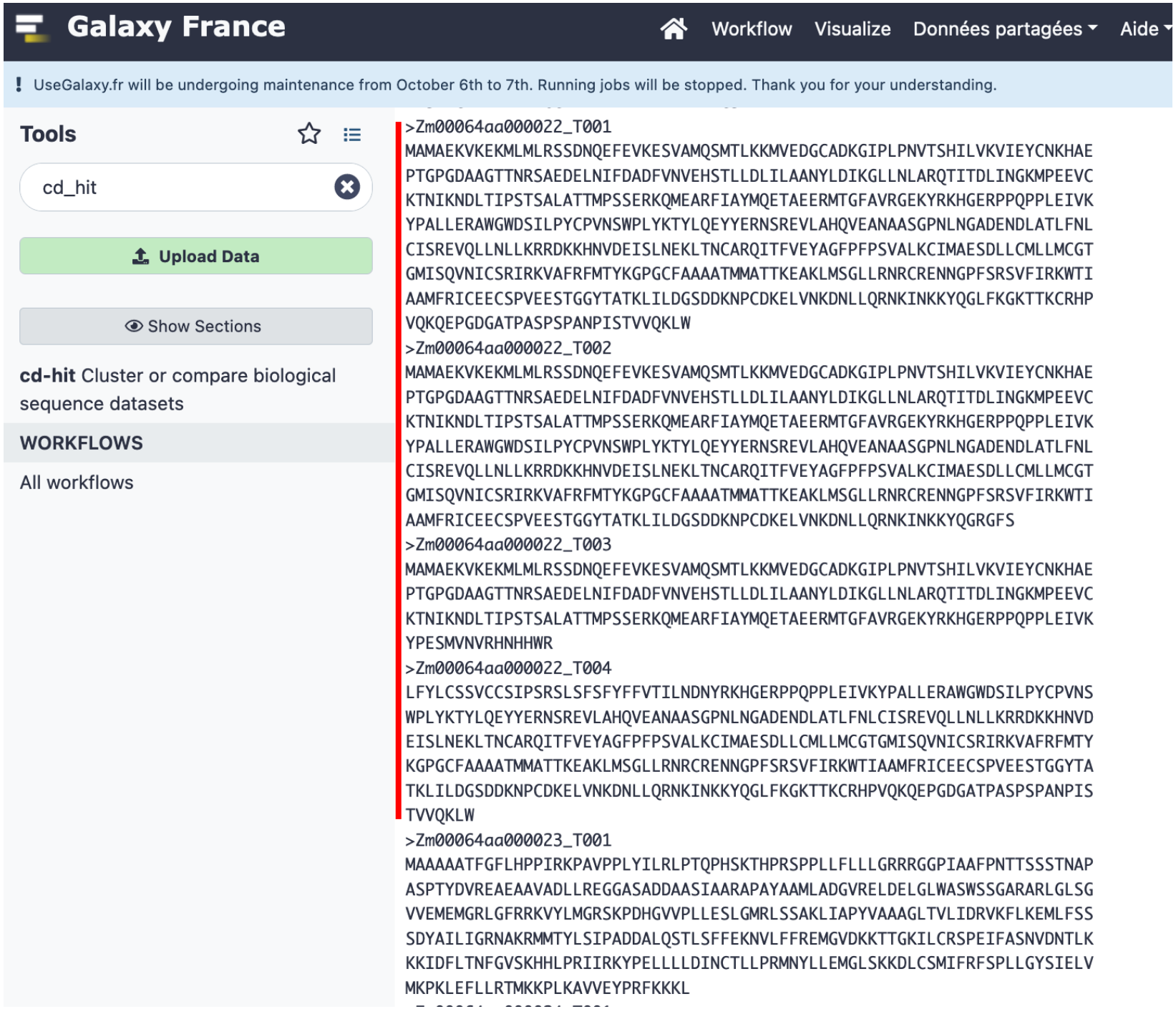
Otherwise, a new cluster is defined with that sequence as the representative.

CD-HIT Use case 1

Alternatives transcripts

Painfull for gene content comparison between genomes.

Try to select a representative sequence per gene.



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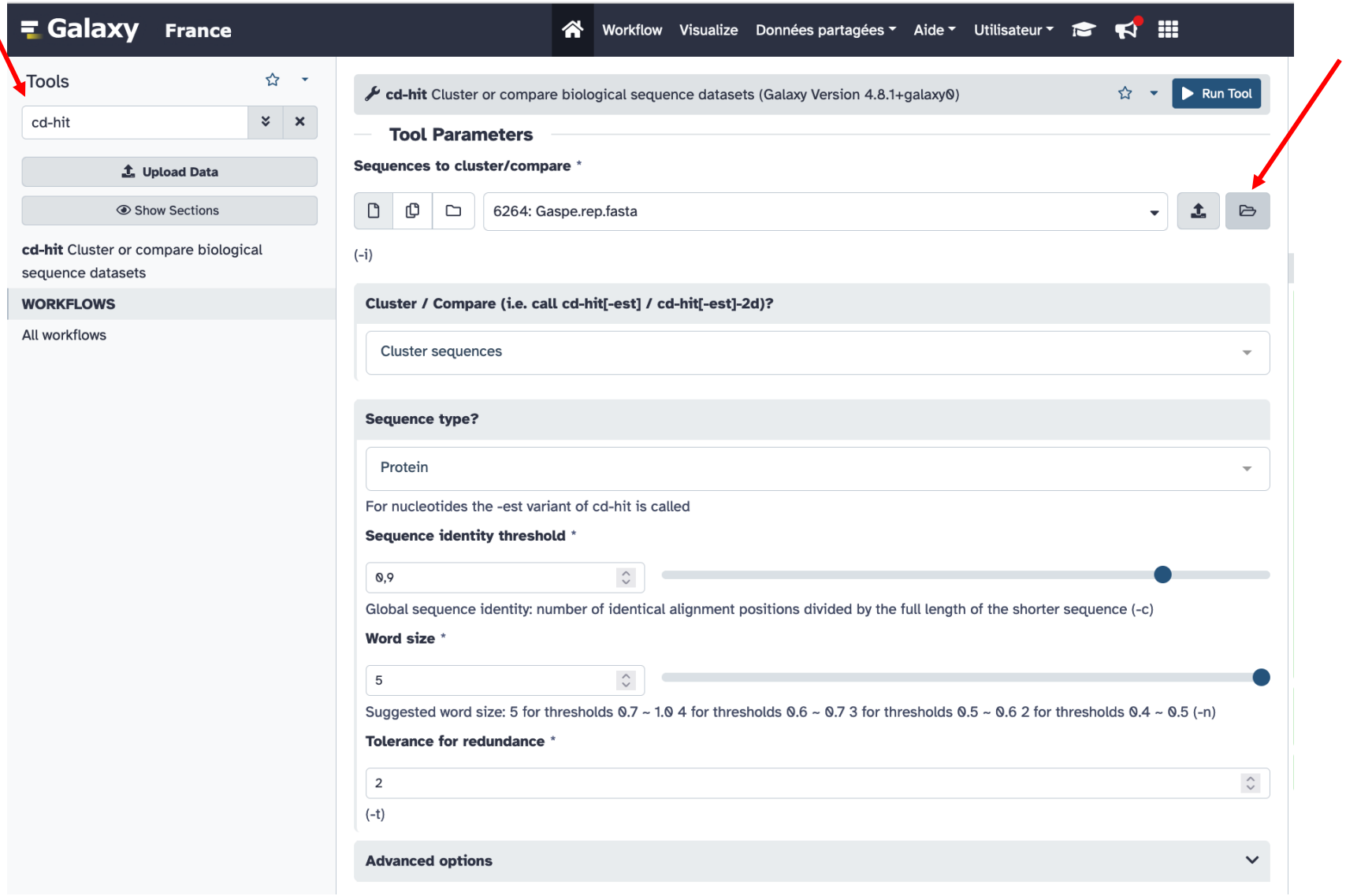

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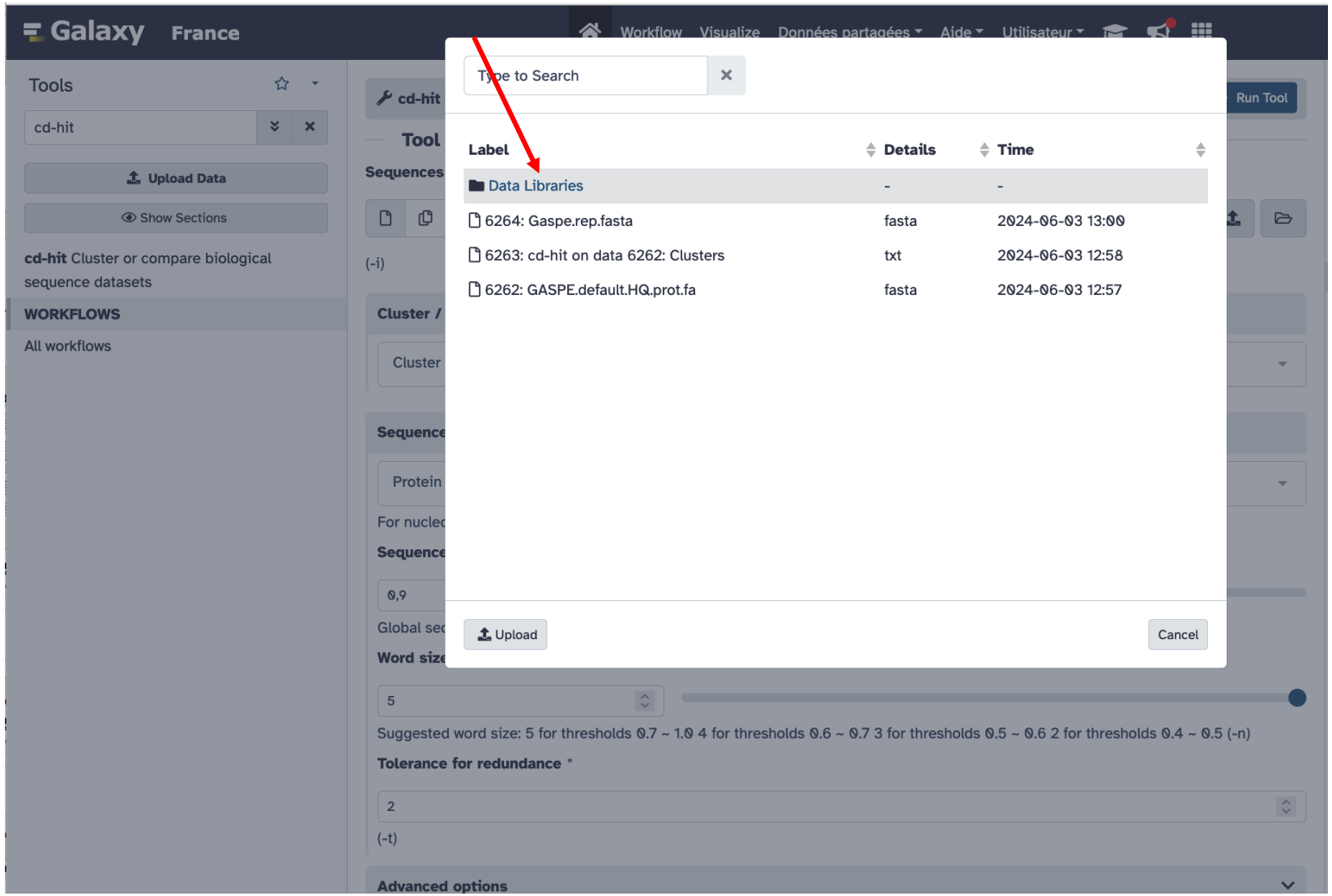

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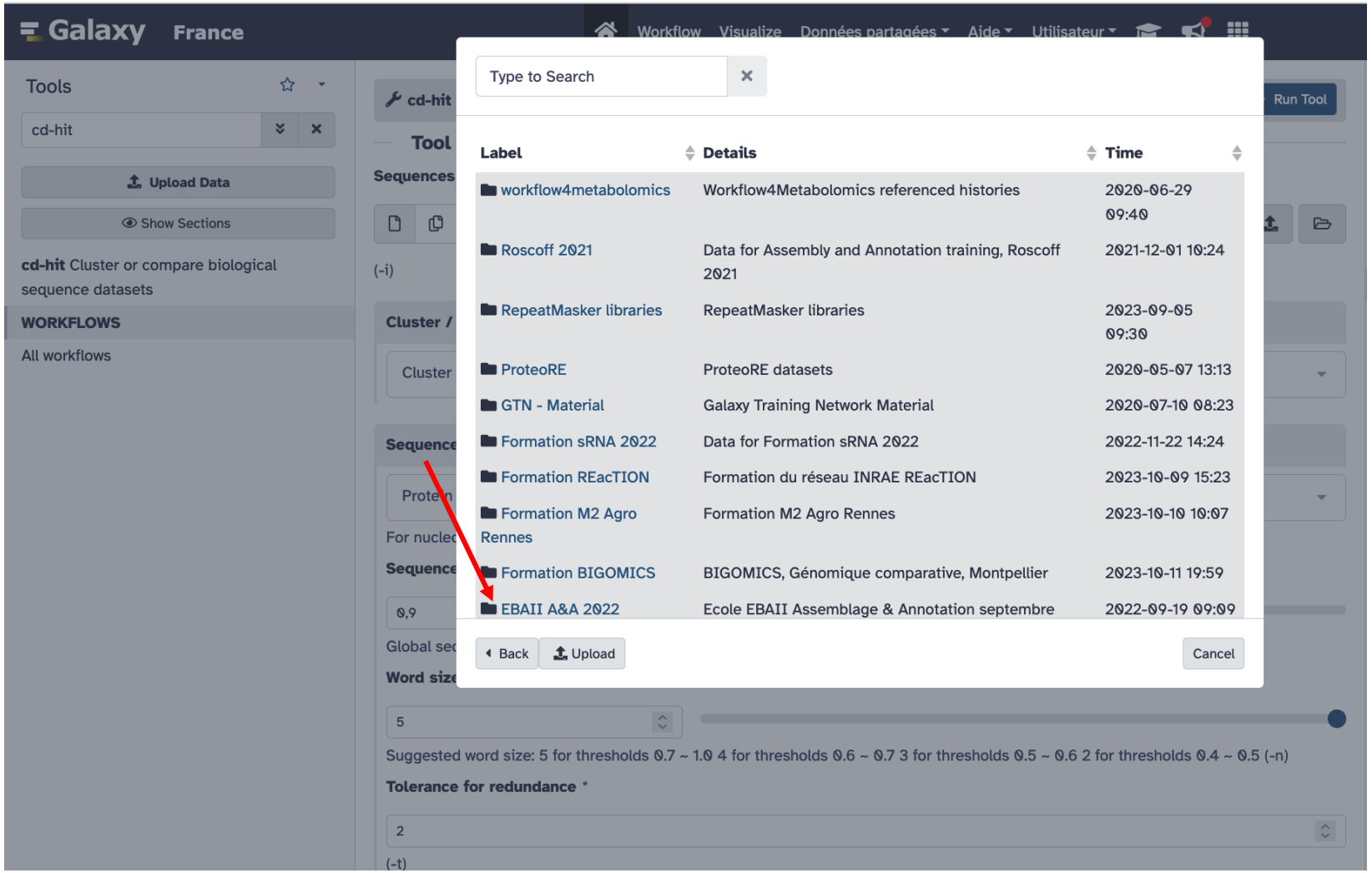

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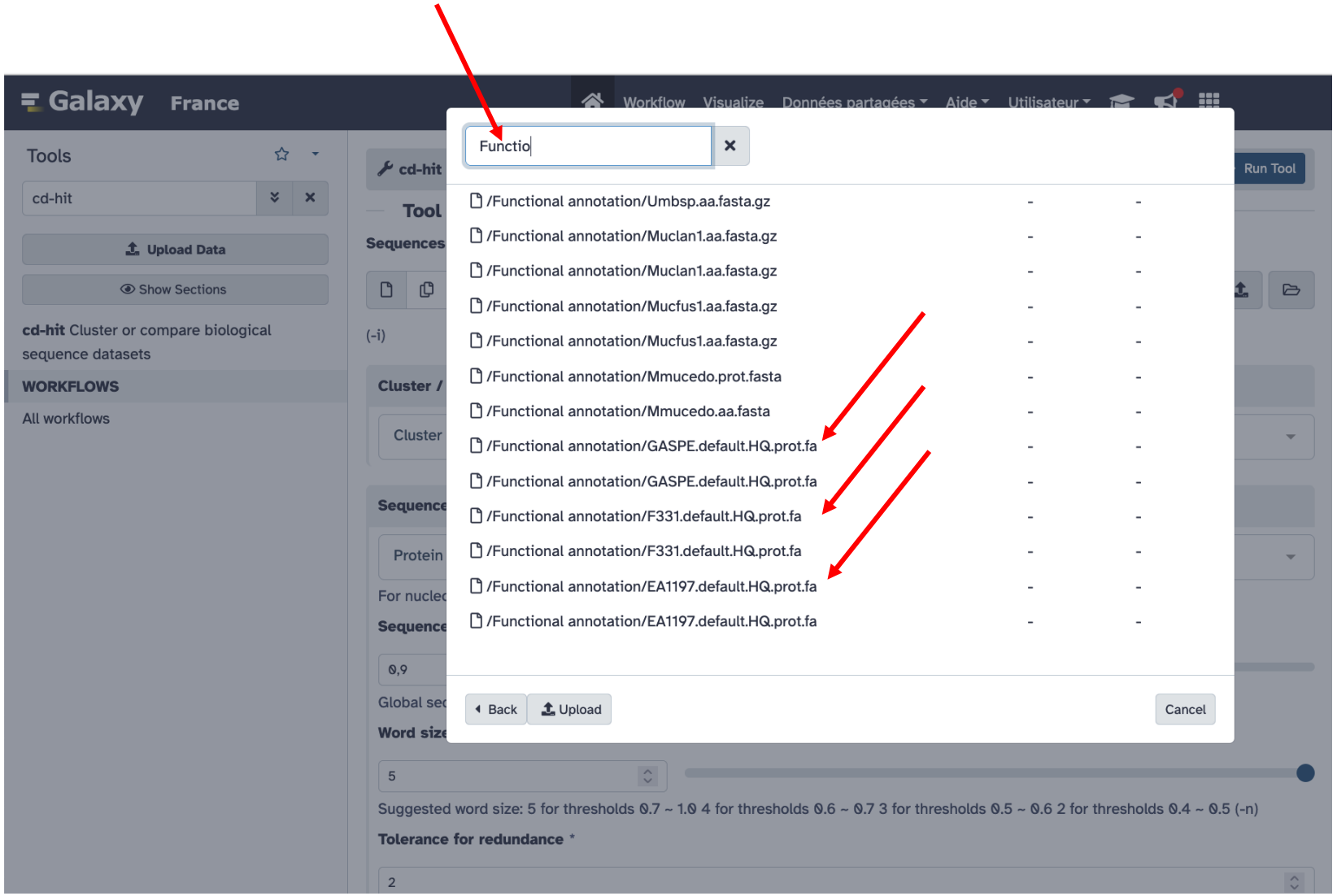

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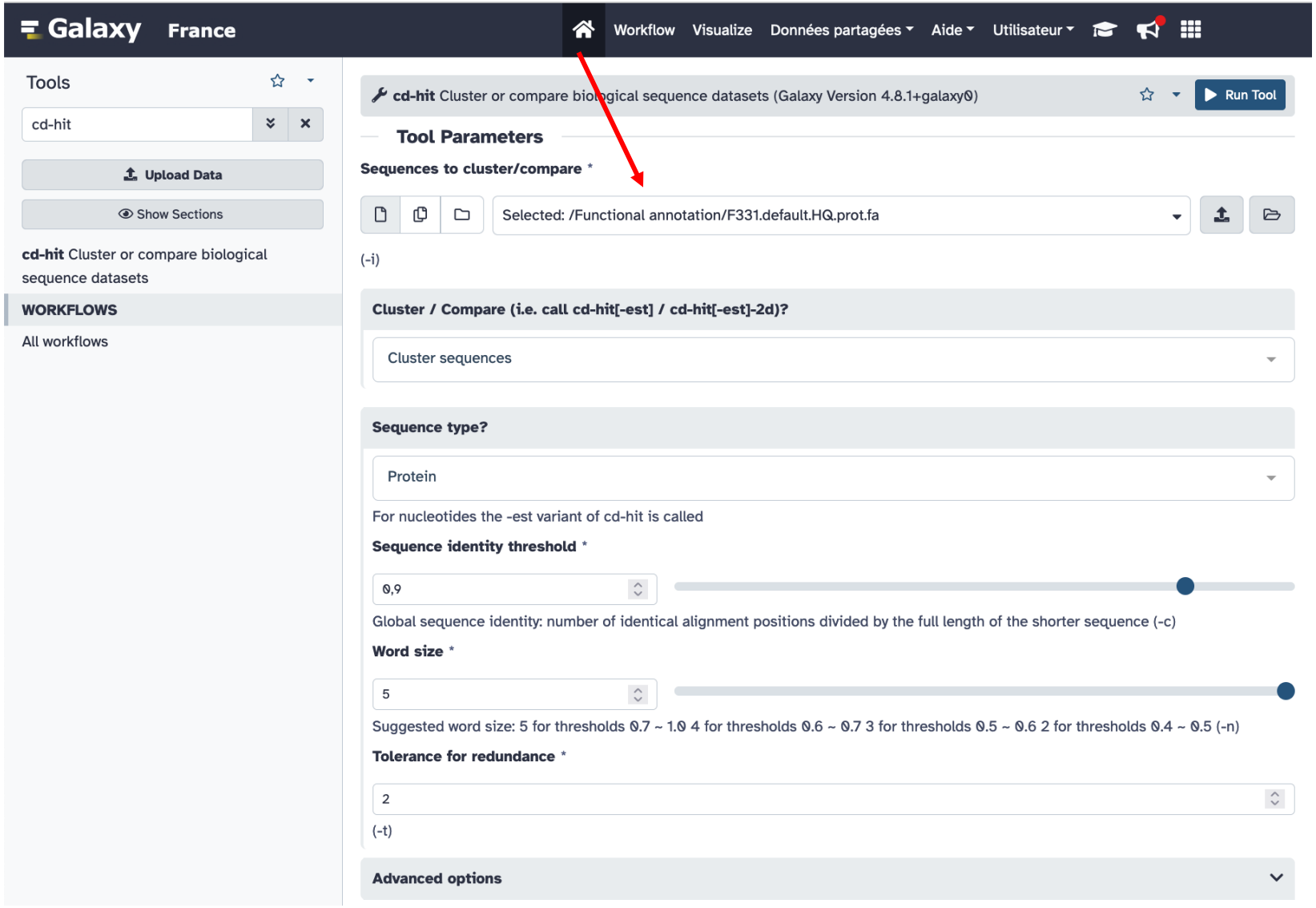

CD-HIT Use case 1

Alternatives transcripts

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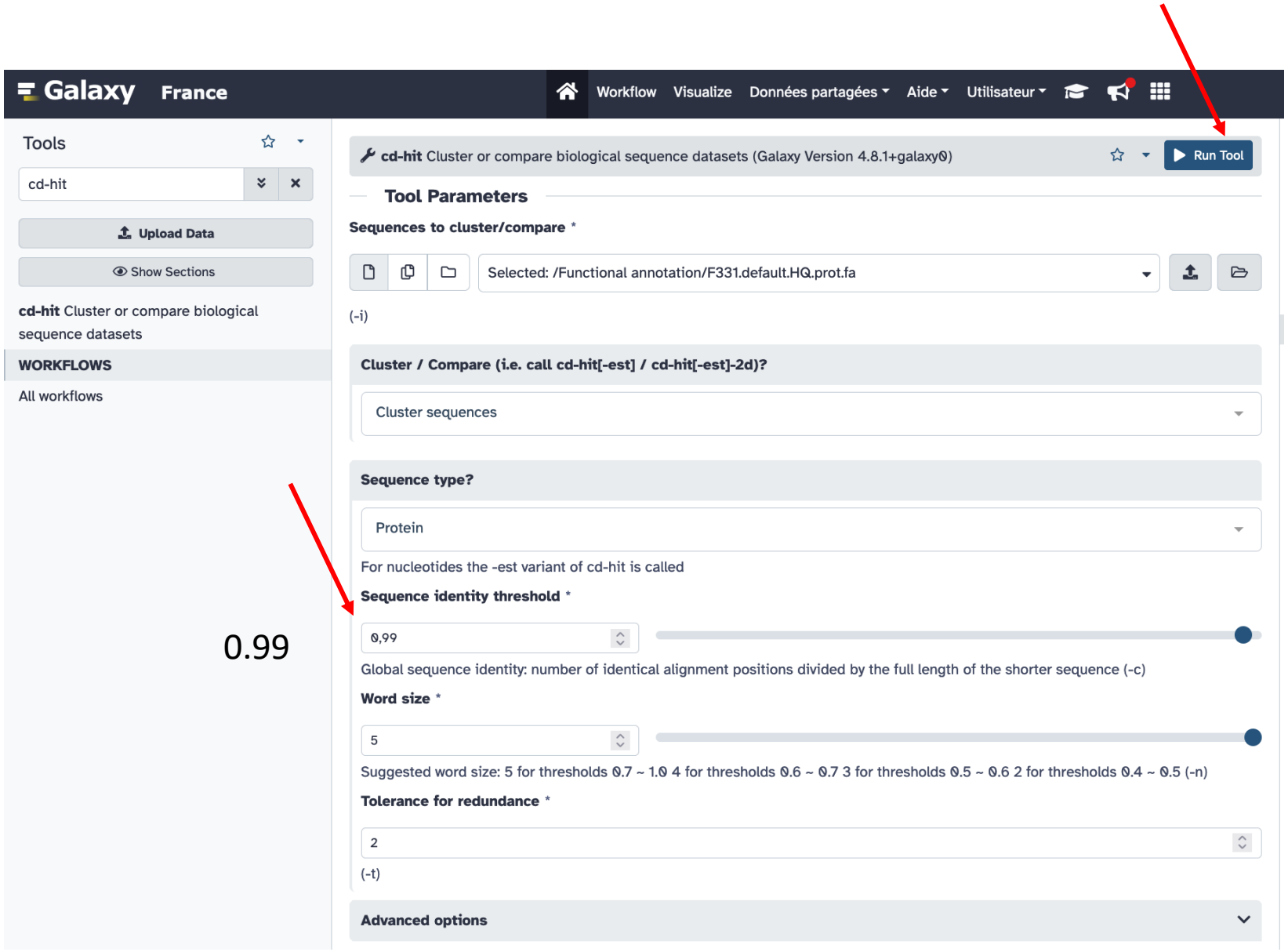

0.99

CD-HIT Use case 1

Alternatives transcripts

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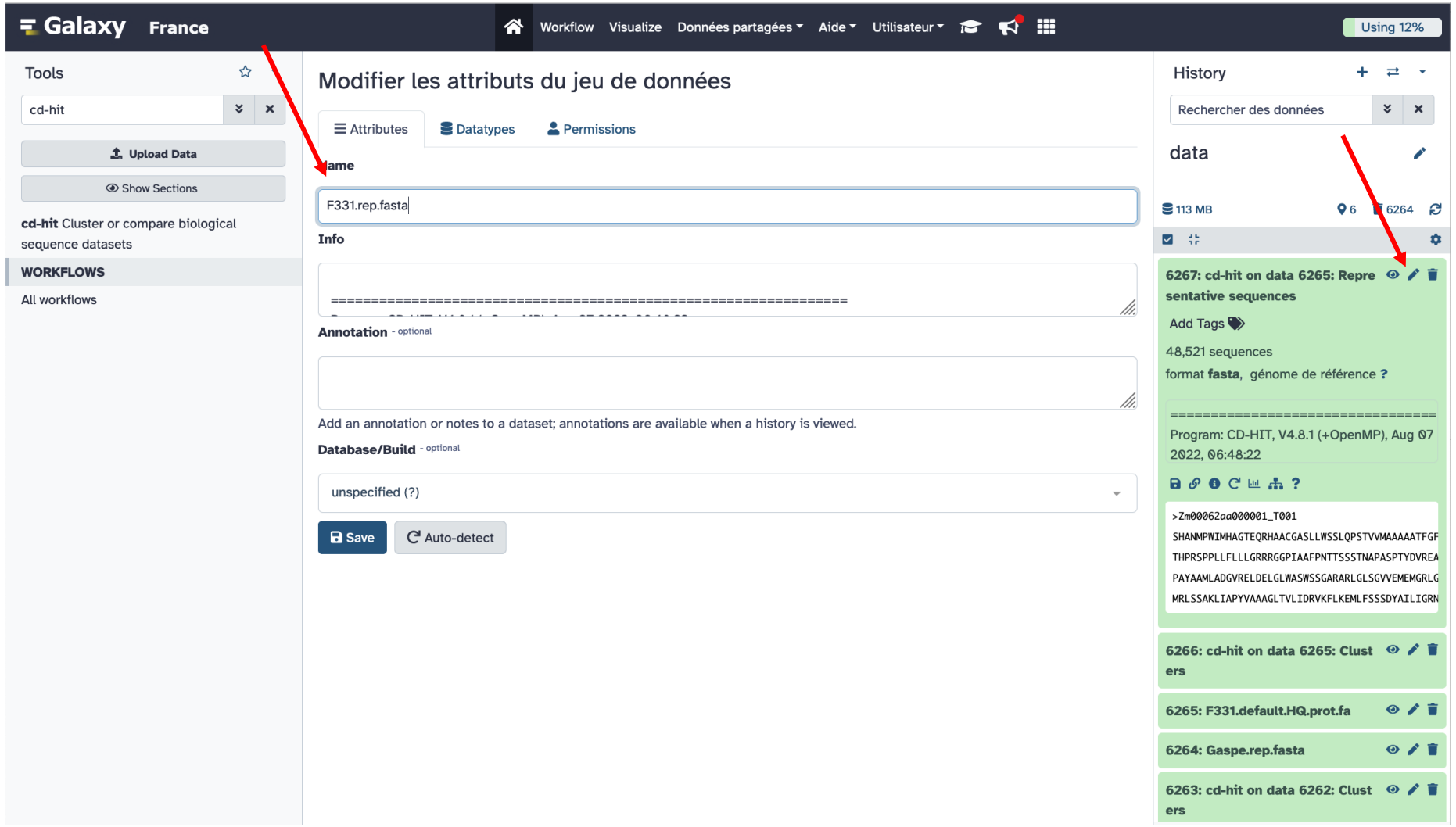
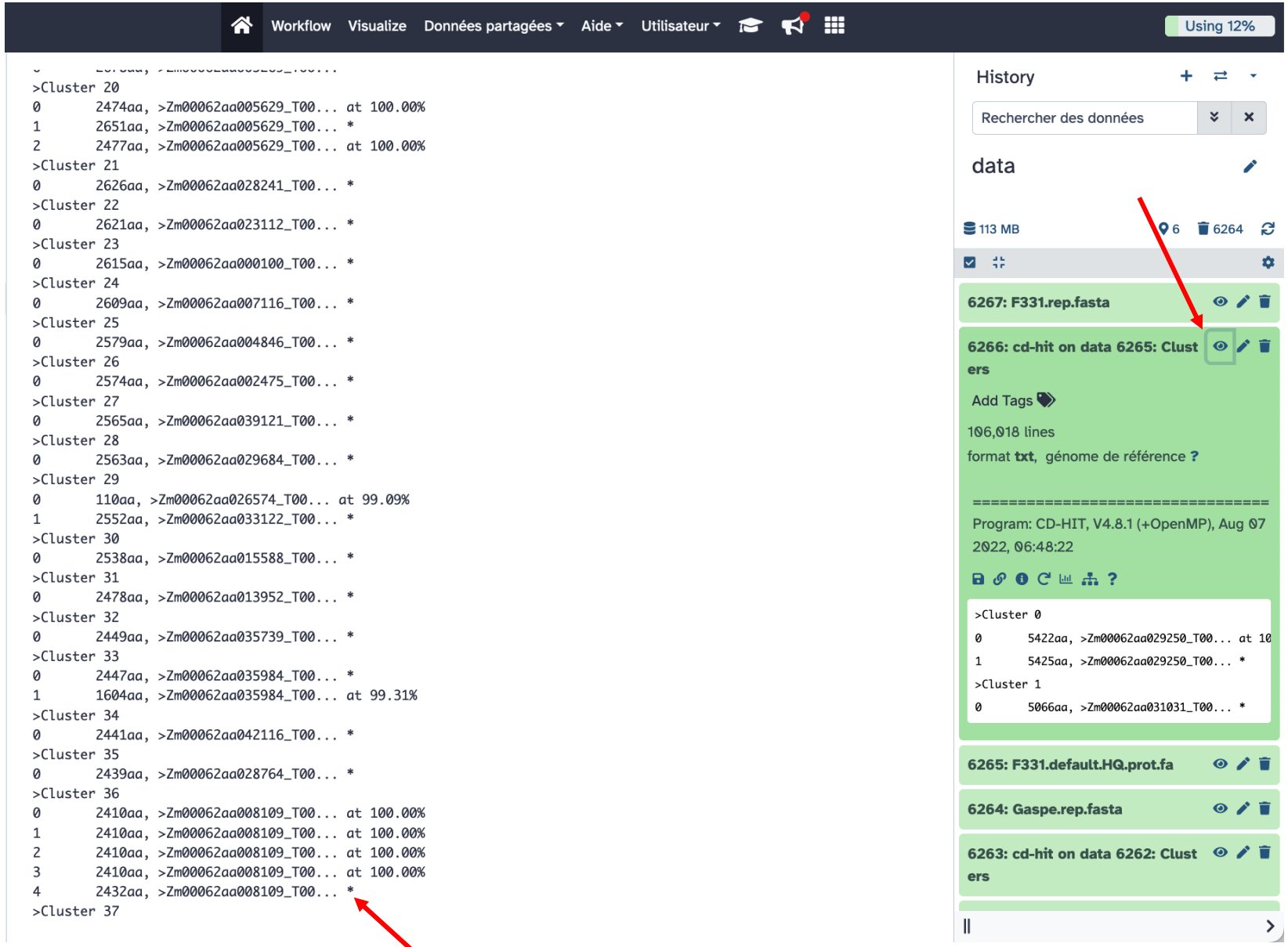


CD-HIT Use case 1

Alternatives transcripts

Painfull for gene content comparison between genomes.

Try to select a representative sequence per gene.



(*) Sequence selected as representative

CD-HIT Use case 1

Alternatives transcripts

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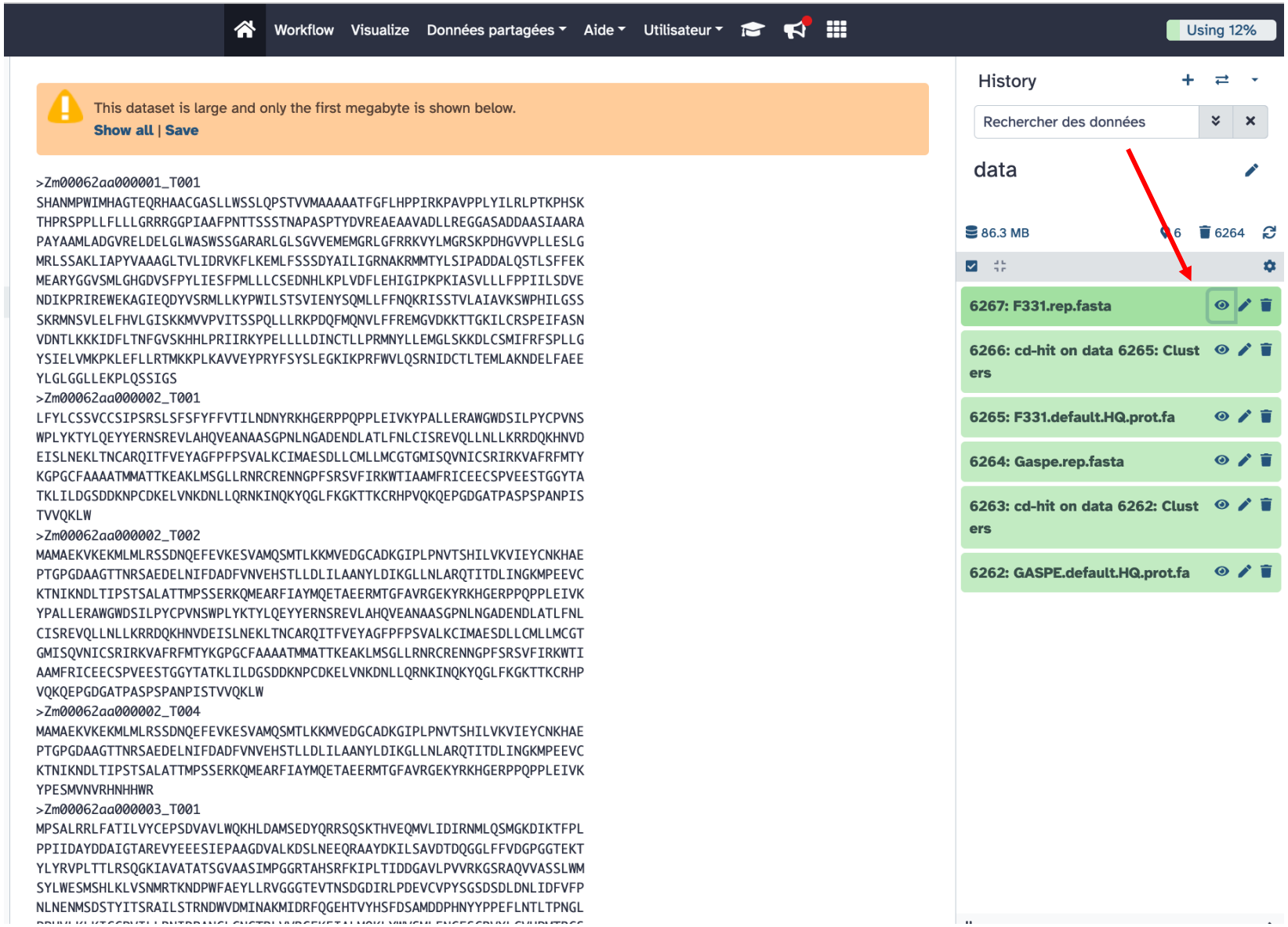
Try to select a representative sequence per gene.



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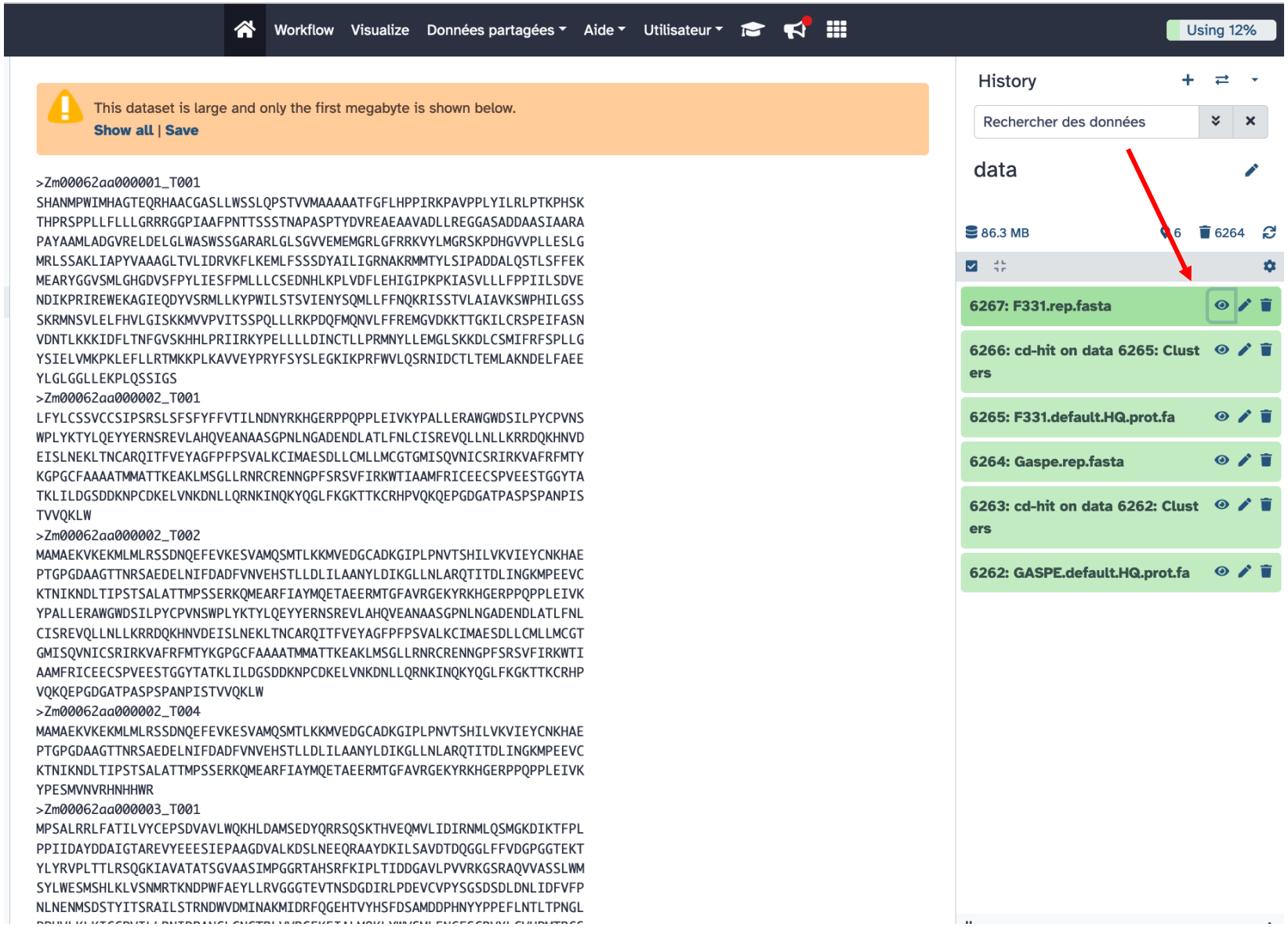
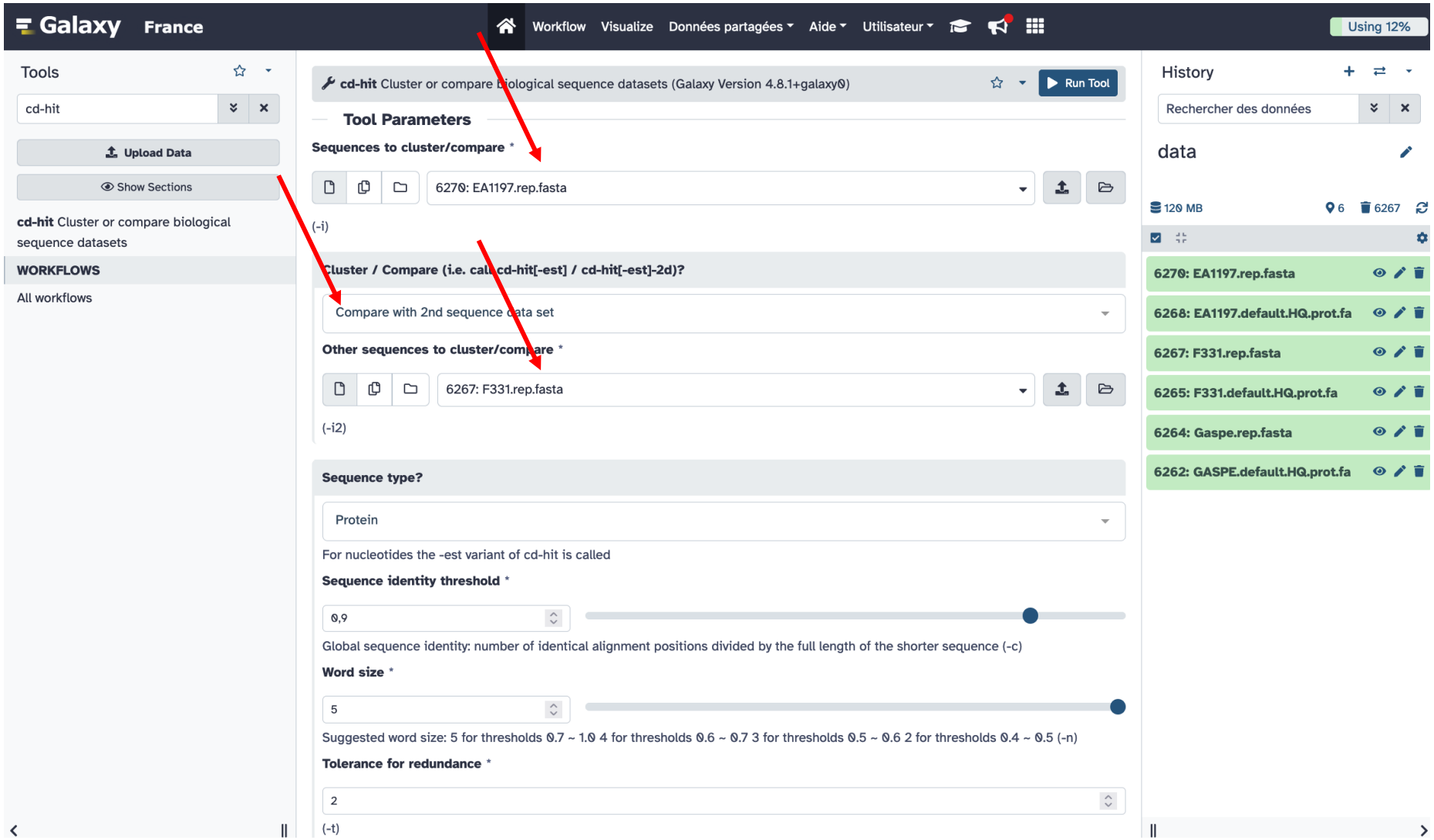


CD-HIT Use case 2

Compare 2 gene/protein dataset

From 2 annotation versions
From 2 individuals (same species)

Input : outputs from use-case 1



CD-HIT Use case 2

Compare 2 gene/protein dataset

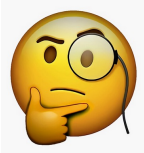
From 2 annotation versions
From 2 individuals (same species)

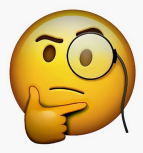
Zm00063 : EA1197
Zm00062 : F331

Workflow Visualize Données partagées Aide Utilisateur Using 12%

This dataset is large and only the first megabyte is shown below.
Show all | **Save**

```
>Cluster 0
0       5425aa, >Zm00063aa018611_T00... *
1       5425aa, >Zm00062aa029250_T00... at 99.83%
>Cluster 1
0       5066aa, >Zm00063aa032449_T00... *
1       5066aa, >Zm00062aa031031_T00... at 99.98%
>Cluster 2
0       4863aa, >Zm00063aa019422_T00... *
1       4863aa, >Zm00062aa006742_T00... at 99.40%
>Cluster 3
0       4210aa, >Zm00063aa003366_T00... *
1       4210aa, >Zm00062aa023384_T00... at 99.95%
>Cluster 4
0       3882aa, >Zm00063aa034457_T00... *
1       3877aa, >Zm00062aa033117_T00... at 99.95%
>Cluster 5
0       3691aa, >Zm00063aa030400_T00... *
1       3691aa, >Zm00062aa005734_T00... at 99.78%
>Cluster 6
0       3650aa, >Zm00063aa035322_T00... *
1       3631aa, >Zm00062aa013354_T00... at 92.29%
2       3642aa, >Zm00062aa041101_T00... at 99.84%
>Cluster 7
0       3631aa, >Zm00063aa007786_T00... *
>Cluster 8
0       3581aa, >Zm00063aa030440_T00... *
1       3581aa, >Zm00062aa005775_T00... at 99.83%
>Cluster 9
0       3287aa, >Zm00063aa002573_T00... *
>Cluster 10
0       3212aa, >Zm00063aa015366_T00... *
>Cluster 11
0       3007aa, >Zm00063aa008396_T00... *
>Cluster 12
0       2872aa, >Zm00063aa020205_T00... *
```





History

Rechercher des données

data

130 MB 8 6267

- 6272: cd-hit on data 6267 and data 6270: Representative sequences
- 6271: cd-hit on data 6267 and data 6270: Clusters
- 6270: EA1197.rep.fasta
- 6268: EA1197.default.HQ.prot.fa
- 6267: F331.rep.fasta
- 6265: F331.default.HQ.prot.fa
- 6264: Gaspe.rep.fasta
- 6262: GASPE.default.HQ.prot.fa

CD-HIT Use case 2

Compare 2 gene/protein dataset

From 2 annotation versions
From 2 individuals (same species)

Zm00063 : EA1197
Zm00062 : F331

Workflow | Visualize | Données partagées | Aide | Utilisateur | Using 12%

This dataset is large and only the first megabyte is shown below.
Show all | **Save**

```
>Cluster 0
0       5425aa, >Zm00063aa018611_T00... *
1       5425aa, >Zm00062aa029250_T00... at 99.83%
>Cluster 1
0       5066aa, >Zm00063aa032449_T00... *
1       5066aa, >Zm00062aa031031_T00... at 99.98%
>Cluster 2
0       4863aa, >Zm00063aa019422_T00... *
1       4863aa, >Zm00062aa006742_T00... at 99.40%
>Cluster 3
0       4210aa, >Zm00063aa003366_T00... *
1       4210aa, >Zm00062aa023384_T00... at 99.95%
>Cluster 4
0       3882aa, >Zm00063aa034457_T00... *
1       3877aa, >Zm00062aa033117_T00... at 99.95%
>Cluster 5
0       3691aa, >Zm00063aa030400_T00... *
1       3691aa, >Zm00062aa005734_T00... at 99.78%
>Cluster 6
0       3650aa, >Zm00063aa035322_T00... *
1       3631aa, >Zm00062aa013354_T00... at 92.29%
2       3642aa, >Zm00062aa041101_T00... at 99.84%
>Cluster 7
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>Cluster 8
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>Cluster 9
0       3287aa, >Zm00063aa002573_T00... *
>Cluster 10
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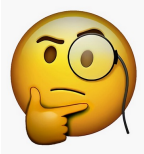
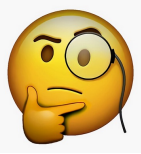
>Cluster 11
0       3007aa, >Zm00063aa008396_T00... *
>Cluster 12
0       2872aa, >Zm00063aa020205_T00... *
```



Orthologous gene to 13354 is missing in EA1197 ?



Orthologous genes missing in F331 ?

History

Rechercher des données

data

130 MB | 8 | 6267

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- 6267: F331.rep.fasta
- 6265: F331.default.HQ.prot.fa
- 6264: Gaspe.rep.fasta
- 6262: GASPE.default.HQ.prot.fa

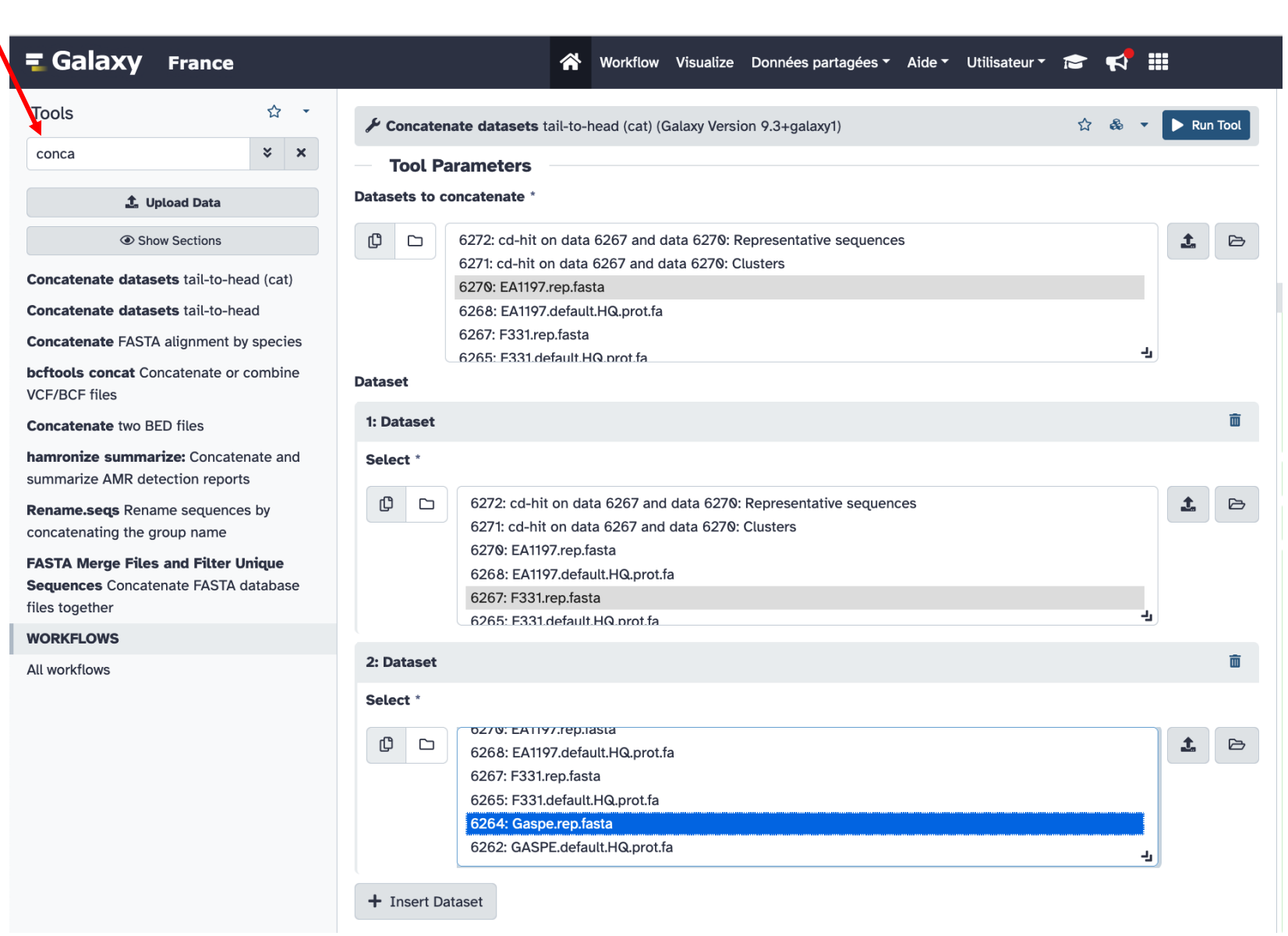
CD-HIT Use case 3 : extand previous use-case to more than 2 sequences sets

Compare n gene/protein dataset

From n annotation versions
From n individuals (same species)

Input : outputs from UC1

Step 1 files concatenation



CD-HIT Use case 3 : extand previous use-case to more than 2 sequences sets

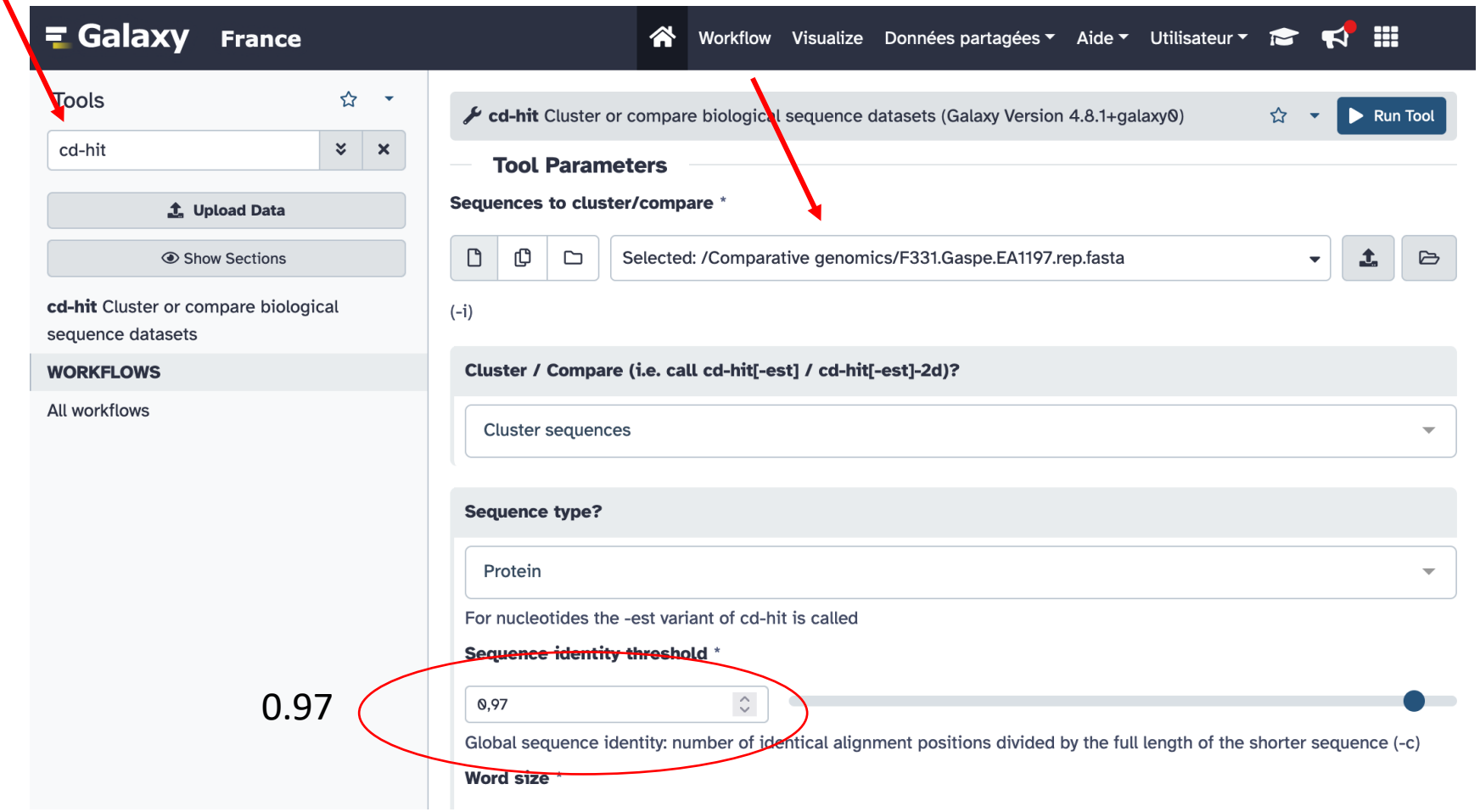
Compare n gene/protein dataset

From n annotation versions
From n individuals (same species)

Input : outputs from UC1

Step 1 files concatenation

Step 2 cluster seq with CD-Hit



0.97

CD-HIT Use case 3 : extand previous use-case to more than 2 sequences sets

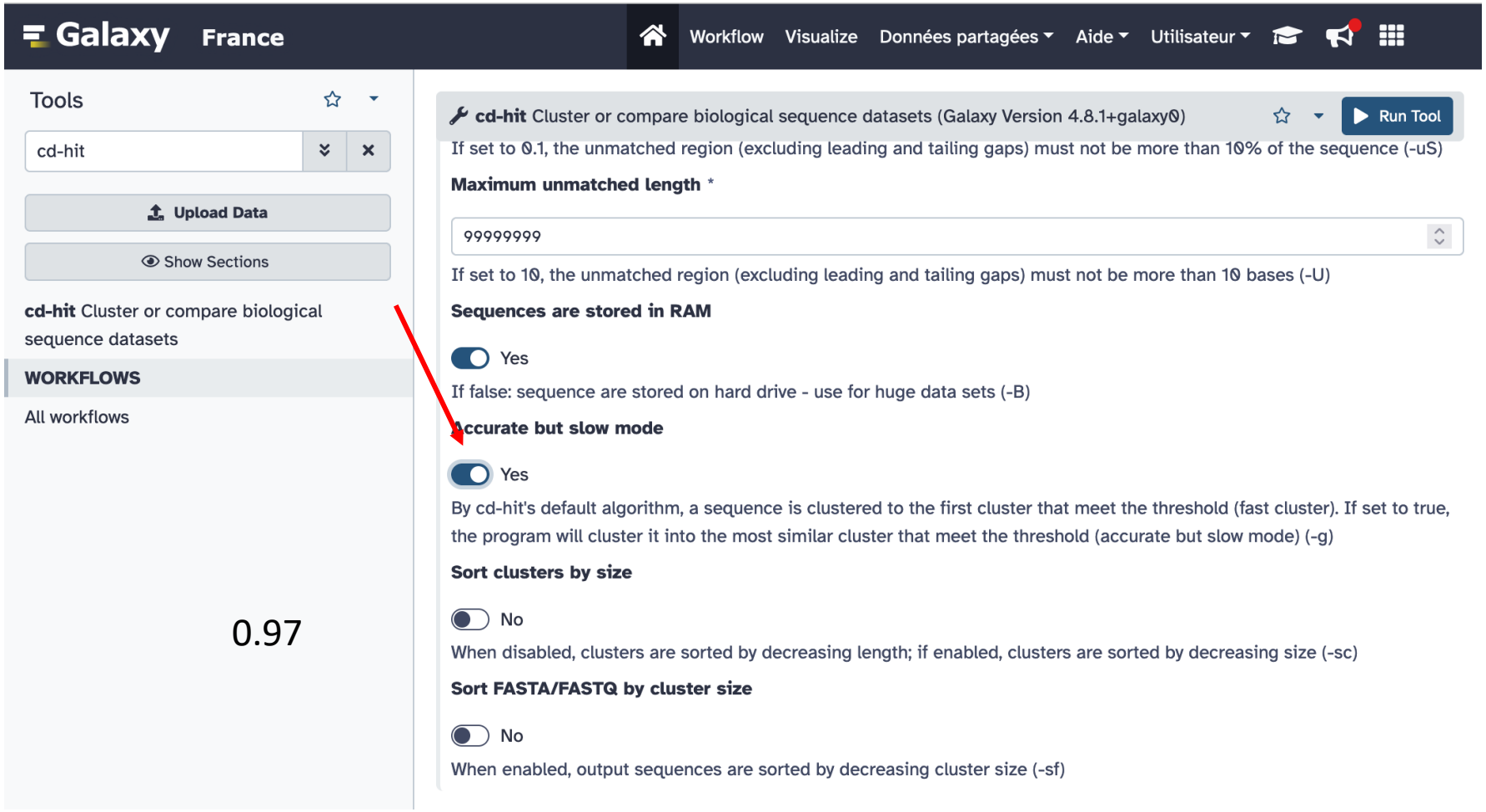
Compare n gene/protein dataset

From n annotation versions
From n individuals (same species)

Input : outputs from UC1

Step 1 files concatenation

Step 2 cluster seq with CD-Hit



CD-HIT Use case 3 : ex

Compare n gene/prot

From n annotation ve
From n individuals (sa

Input : outputs from U

Step 1 files concatena

Step 2 cluster seq wit

Zm00064 : Gaspe
Zm00063 : EA1197
Zm00062 : F331

Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

cd-hit

Upload Data

Show Sections

cd-hit Cluster or compare biological sequence datasets

WORKFLOWS

All workflows

```
0       130aa, >Zm00063aa043711_T00... *
>Cluster 60001
0       130aa, >Zm00063aa044627_T00... *
1       130aa, >Zm00062aa040294_T00... at 100.00%
>Cluster 60002
0       130aa, >Zm00063aa044846_T00... *
>Cluster 60003
0       130aa, >Zm00063aa044897_T00... *
1       130aa, >Zm00062aa040567_T00... at 100.00%
2       130aa, >Zm00064aa040891_T00... at 100.00%
>Cluster 60004
0       130aa, >Zm00062aa000798_T00... *
>Cluster 60005
0       130aa, >Zm00062aa001058_T00... *
1       130aa, >Zm00064aa001104_T00... at 100.00%
>Cluster 60006
0       130aa, >Zm00062aa002134_T00... *
>Cluster 60007
0       130aa, >Zm00062aa004172_T00... *
1       130aa, >Zm00064aa004266_T00... at 100.00%
>Cluster 60008
0       130aa, >Zm00062aa004378_T00... *
1       130aa, >Zm00064aa004472_T00... at 100.00%
>Cluster 60009
0       130aa, >Zm00062aa005951_T00... *
1       130aa, >Zm00064aa006122_T00... at 99.23%
>Cluster 60010
0       130aa, >Zm00062aa006214_T00... *
1       107aa, >Zm00064aa006390_T00... at 100.00%
>Cluster 60011
0       130aa, >Zm00062aa006445_T00... *
>Cluster 60012
0       130aa, >Zm00062aa006531_T00... *
>Cluster 60013
0       130aa, >Zm00062aa007889_T00... *
```

Cluster 60007

Tout surligner | Respecter la casse | Respecter les accents et diacritiques | Mots entiers | Occurrence 1 sur 1

CD-HIT Use case 3 : extand previous use-case to more than 2 sequences sets

Compare n gene/protein dataset

From n annotation versions
From n individuals (same species)

Input : outputs from UC1

Step 1 files concatenation

Step 2 cluster seq with CD-Hit

Zm00064 : Gaspe
Zm00063 : EA1197
Zm00062 : F331

```
>Cluster 60004
0       130aa, >Zm00062aa000798_T00... *
>Cluster 60005
0       130aa, >Zm00062aa001058_T00... *
1       130aa, >Zm00064aa001104_T00... at 100.00%
>Cluster 60006
0       130aa, >Zm00062aa002134_T00... *
>Cluster 60007
0       130aa, >Zm00062aa004172_T00... *
1       130aa, >Zm00064aa004266_T00... at 100.00%
>Cluster 60008
0       130aa, >Zm00062aa004378_T00... *
1       130aa, >Zm00064aa004472_T00... at 100.00%
```

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Workflow Visualize Données partagées Aide Utilisateur

Tools

filter fasta

Upload Data

Show Sections

Filter FASTA on the headers and/or the sequences

Filter fasta to remove sequences based on input criteria (filter_fasta)

WORKFLOWS

All workflows

Filter FASTA on the headers and/or the sequences (Galaxy Version 2.3)

Run Tool

Tool Parameters

FASTA sequences *

1: F331.Gaspe.EA1197.rep.fasta

Criteria for filtering on the headers

Regular expression on the headers

Regular expression pattern the header should match *

Zm00064aa004266

Use the Python regular expression syntax as specified in https://docs.python.org/3/library/re.html

Criteria for filtering on the sequences

No filtering

Remove duplicate sequences

No

Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

miniprot

Upload Data

Show Sections

Miniprot index build a genome index for miniprot

Miniprot align align a protein sequence against a genome with affine gap penalty, splicing and frameshift

WORKFLOWS

All workflows

Miniprot align

Run Tool

align a protein sequence against a genome with affine gap penalty, splicing and frameshift

(Galaxy Version 0.13+galaxy0)

Tool Parameters

Database type

Pre-indexed

Build an index from FASTA or use a pre-indexed database

Pre-indexed genomic database *

4: Zm00064aa004266 (as twobit)

A pre-indexed database built by miniprot

Protein sequence (FASTA) *

4: Zm00064aa004266

Protein sequences to be aligned in FASTA format

Output format *

GFF3

Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

miniprot

Upload Data

Show Sections

Miniprot index build a genome index for miniprot

Miniprot align align a protein sequence against a genome with affine gap penalty, splicing and frameshift

WORKFLOWS

All workflows

compa

/Comparative genomics/Gaspe.genome.fasta.gz - -

/Comparative genomics/F331.rep.fasta - -

/Comparative genomics/F331.genome.fasta.gz - -

/Comparative genomics/F331.Gaspe.EA1197.rep.fasta - -

/Comparative genomics/EA1197Sub.fasta - -

/Comparative genomics/EA1197.rep.fasta - -

/Comparative genomics/EA1197int.bed - -

/Comparative genomics/EA1197.genome.mpi - -

/Comparative genomics/EA1197.genome.fasta.gz - -

Back Upload Cancel

Protein sequences to be aligned in FASTA format

Output format *

GFF3

Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

miniprot

Upload Data

Show Sections

Miniprot index build a genome index for miniprot

Miniprot align align a protein sequence against a genome with affine gap penalty, splicing and frameshift

WORKFLOWS

All workflows

Miniprot align

align a protein sequence against a genome with affine gap penalty, splicing and frameshift

(Galaxy Version 0.13+galaxy0)

Run Tool

Tool Parameters

Database type

Pre-indexed

Build an index from FASTA or use a pre-indexed database

Pre-indexed genomic database *

Selected: /Comparative genomics/EA1197.genome.mpi

A pre-indexed database built by miniprot

Protein sequence (FASTA) *

4: Zm00064aa004266

Protein sequences to be aligned in FASTA format

Output format *

GFF3

Workflow Visualize Données partagées Aide Utilisateur

Seqid	Source	Type	Start	End	Score	Strand	Phase	Attributes
##gff-version 3								
##PAF	Zm00064aa004266_T001	130	0	130	-	chr8	193330780	31199353 31199915 366 390 0 AS:i:536 ms:i:616 np:i:124 fs:i:0 st:i:0 da:i:0 do:i:0 cg:Z:44M83U53M92N32M cs:Z::14*tacC:29*gG~gt80ag-gc:2*ggcS:35*aagT:2*gagk 8*cgcC*cagK~gt92ag:18*cgcS:13
chr8	miniprot	mRNA	31199351	31199915	616	-	.	ID=MP000001;Rank=1;Identity=0.9385;Positive=0.9538;Target=Zm00064aa004 1 130
chr8	miniprot	CDS	31199783	31199915	210	-	0	Parent=MP000001;Rank=1;Identity=0.9778;Target=Zm00064aa004266_T001 1 4
chr8	miniprot	CDS	31199542	31199702	245	-	2	Parent=MP000001;Rank=1;Identity=0.8868;Target=Zm00064aa004266_T001 45
chr8	miniprot	CDS	31199351	31199449	161	-	0	Parent=MP000001;Rank=1;Identity=0.9688;Target=Zm00064aa004266_T001 99
chr8	miniprot	stop_codon	31199351	31199353	0	-	0	Parent=MP000001;Rank=1

Workflow Visualize Données partagées Aide Utilisateur

Seqid	Source	Type	Start	End	Score	Strand	Phase	Attributes
##gff-version 3								
##PAF	Zm00064aa004266_T001	130	0	130	-	chr8	193330780	31199353 31199915 366 390 0 AS:i:536 ms:i:616 np:i:124 fs:i:0 st:i:0 da:i:0 do:i:0 cg:Z:44M83U53M92N32M cs:Z::14*tacC:29*gG~gt80ag-gc:2*ggcS:35*aagT:2*gagk 8*cgcC*cagK~gt92ag:18*cgcS:13
chr8	miniprot	mRNA	31199351	31199915	616	-	.	ID=MP000001;Rank=1;Identity=0.9385;Positive=0.9538;Target=Zm00064aa004 1 130
chr8	miniprot	CDS	31199783	31199915	210	-	0	Parent=MP000001;Rank=1;Identity=0.9778;Target=Zm00064aa004266_T001 1 4
chr8	miniprot	CDS	31199542	31199702	245	-	2	Parent=MP000001;Rank=1;Identity=0.8868;Target=Zm00064aa004266_T001 45
chr8	miniprot	CDS	31199351	31199449	161	-	0	Parent=MP000001;Rank=1;Identity=0.9688;Target=Zm00064aa004266_T001 99
chr8	miniprot	stop_codon	31199351	31199353	0	-	0	Parent=MP000001;Rank=1

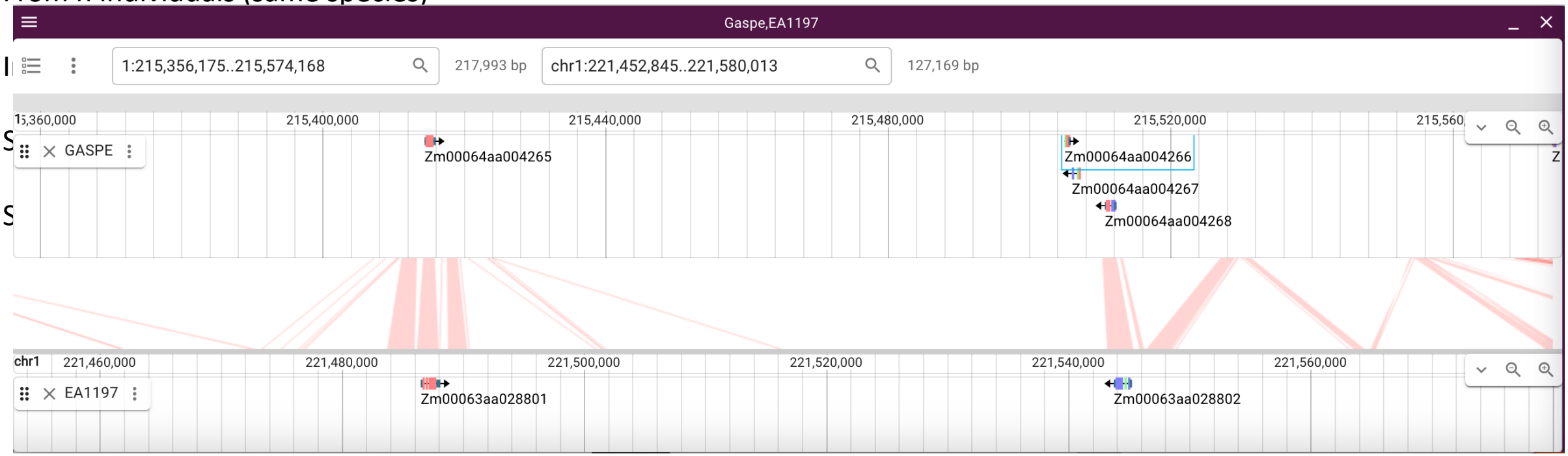
CD-HIT Use case 3 : extand previous use-case to more than 2 sequences sets

Compare n gene/protein dataset

From n annotation versions

From n individuals (same species)

```
>Cluster 60007
0        130aa, >Zm00062aa004172_T00... *
1        130aa, >Zm00064aa004266_T00... at 100.00%
```



Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

getfasta

Upload Data

Show Sections

bedtools getfasta use intervals to extract sequences from a FASTA file

WORKFLOWS

All workflows

bedtools getfasta use intervals to extract sequences from a FASTA file (Galaxy Version 2.31.1+galaxy0)

Run Tool

Tool Parameters

BED/bedGraph/GFF/VCF/EncodePeak file *

Selected: /Comparative genomics/gaspeInt.bed

(-bed)

Choose the source for the FASTA file

History

FASTA file *

Selected: /Comparative genomics/Gaspe.genome.fasta.gz

(-fi)

Use the 'name' column in the BED file and the coordinates for the FASTA headers in the output FASTA file

No

(-name)

Use the 'name' column in the BED file for the FASTA headers in the output FASTA file

No

(-nameOnly)

Report extract sequences in a tab-delimited format instead of in FASTA format

No

(-tab)

Force strandedness

No

If the feature occupies the antisense strand, the sequence will be reverse complemented (-s)

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Workflow Visualize Données partagées Aide Utilisateur

Tools

getfasta

Upload Data

Show Sections

bedtools getfasta use intervals to extract sequences from a FASTA file

WORKFLOWS

All workflows

bedtools getfasta use intervals to extract sequences from a FASTA file (Galaxy Version 2.31.1+galaxy0)

Run Tool

Tool Parameters

BED/bedGraph/GFF/VCF/EncodePeak file *

Selected: /Comparative genomics/EA1197int.bed

(-bed)

Choose the source for the FASTA file

History

FASTA file *

Selected: /Comparative genomics/EA1197.genome.fasta.gz

(-fi)

Use the 'name' column in the BED file and the coordinates for the FASTA headers in the output FASTA file

No

(-name)

Use the 'name' column in the BED file for the FASTA headers in the output FASTA file

No

(-nameOnly)

Report extract sequences in a tab-delimited format instead of in FASTA format

No

(-tab)

Force strandedness

Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

chrom

Upload Data

Show Sections

Chromeister ultra-fast pairwise genome comparisons

SnpEff chromosome-info: list chromosome names/lengths

xcms findChromPeaks (xcmsSet) Chromatographic peak detection

xcms plot chromatogram Plots base peak intensity chromatogram (BPI) and total ion current chromatogram (TIC) from MSnbase or xcms experiment(s)

xcms findChromPeaks Merger Merge xcms findChromPeaks RData into a unique file to be used by group

xcms groupChromPeaks (group) Perform the correspondence, the grouping of chromatographic peaks within and between samples.

xcms refineChromPeaks (refine) Remove or merge chromatographic peaks based on specific criteria.

xcms fillChromPeaks (fillPeaks) Integrate

Chromeister ultra-fast pairwise genome comparisons (Galaxy Version 1.5.a+galaxy1)

Tool Parameters

Query sequence *

12: EA1197_cluster60007

Query sequence file in fasta format

Reference sequence *

9: gaspe_cluster60007

Reference sequence file in fasta format

Output dotplot size *

500

Use around 1000 for chromosome-sized sequences and around 2000 for complete genomes

K-mer seed size *

32

Use 32 as default, and 16 in case no similarities are found

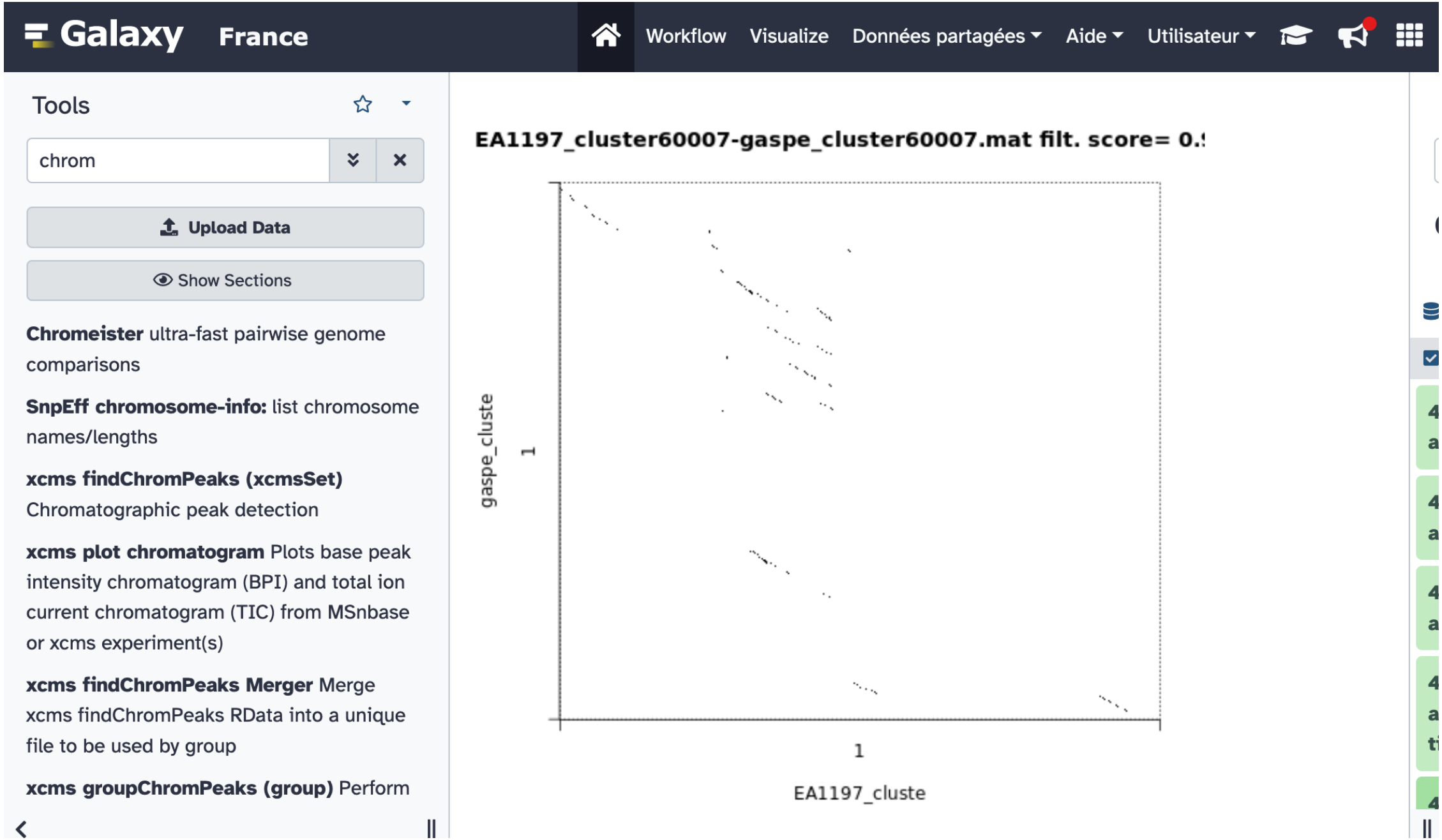
Diffuse value *

1

Level of the heuristic subsampling employed. Change to 1 or 2 if no similarity is found

Add grid to plot for multi-fasta data sets

Yes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Show Sections
Chromeister ultra-fast pairwise genome comparisons
SnpEff chromosome-info: list chromosome names/lengths
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xcms findChromPeaks Merger Merge xcms findChromPeaks RData into a unique file to be used by group
xcms groupChromPeaks (group) Perform
EA1197_cluster60007-gaspe_cluster60007.mat filt. score= 0.
gaspe_cluste
1
1
EA1197_cluste

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Workflow Visualize Données partagées Aide Utilisateur

Tools

chrom

Upload Data

Show Sections

Chromeister ultra-fast pairwise genome comparisons

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xcms fillChromPeaks (fillPeaks) Integrate areas of missing peaks

Chromeister ultra-fast pairwise

Run Tool

Tool Parameters

Query sequence *

4: Zm00064aa

Query sequence file in fasta format

Reference sequence *

4: Zm00064aa

Reference sequence file in fasta forr

Output dotplot size *

1000

Use around 1000 for chromosome-s

K-mer seed size *

32

Use 32 as default, and 16 in case no

Diffuse value *

4

Level of the heuristic subsampling employed. Change to 1 or 2 if no similarity is found

Add grid to plot for multi-fasta data sets

Yes

Do not use grid if your multi-fasta contains more than a hundred sequences (approximately)

compa

Label	Details	Time
/Comparative genomics/gaspeSub.fasta	-	-
/Comparative genomics/Gaspe.rep.fasta	-	-
/Comparative genomics/gaspeInt.bed	-	-
/Comparative genomics/Gaspe.genome.fasta.gz	-	-
/Comparative genomics/F331.rep.fasta	-	-
/Comparative genomics/F331.genome.fasta.gz	-	-
/Comparative genomics/F331.Gaspe.EA1197.rep.fasta	-	-
/Comparative genomics/EA1197Sub.fasta	-	-
/Comparative genomics/EA1197.rep.fasta	-	-
/Comparative genomics/EA1197int.bed	-	-
/Comparative genomics/EA1197.genome.mpi	-	-
/Comparative genomics/EA1197.genome.fasta.gz	-	-

Back Upload Cancel

CD-HIT Use case 3 : extand previous use-c

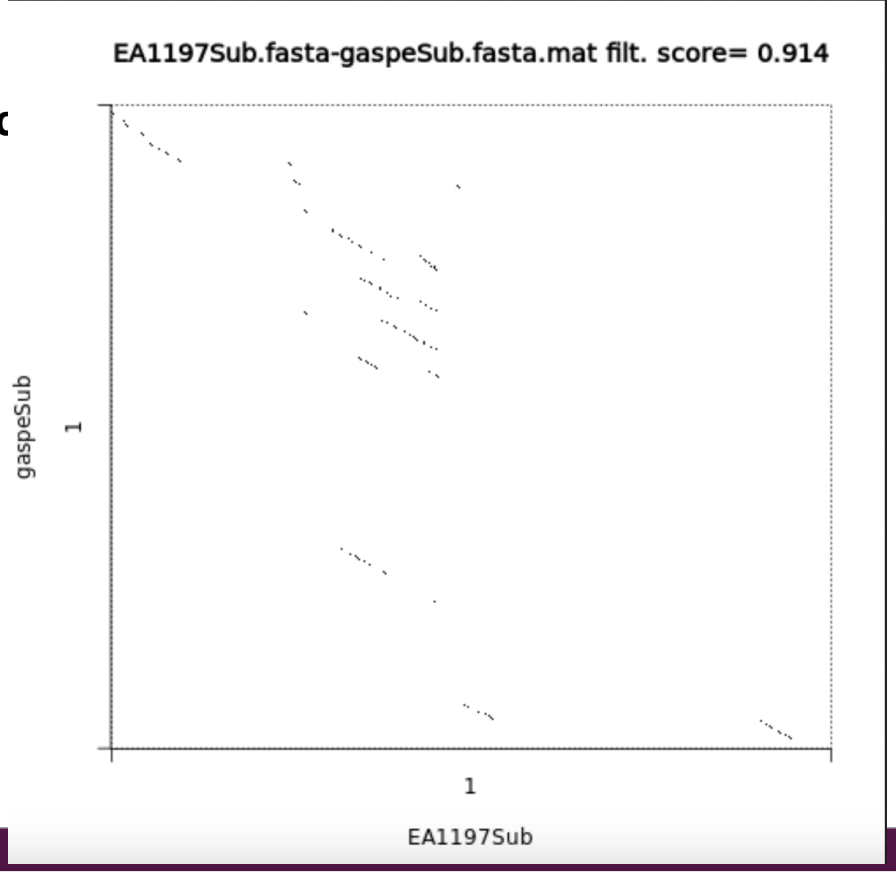
Compare n gene/protein dataset

From n annotation versions
From n individuals (same species)

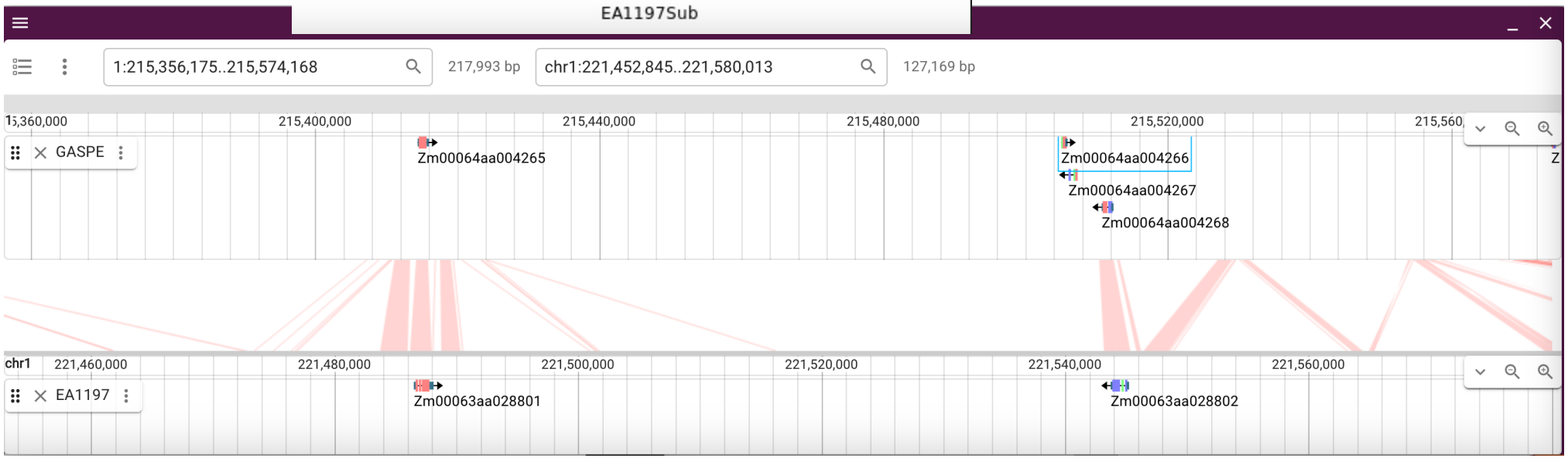
Input : outputs from UC1

Step 1 files concatenation

Step 2 cluster seq with CD-Hit



Zm00064 : Gaspe
Zm00063 : EA1197
Zm00062 : F331



Galaxy France

Workflow Visualize Données partagées Aide Utilis

Tools

chrom

Upload Data

Show Sections

Chromeister ultra-fast pairwise genome comparisons

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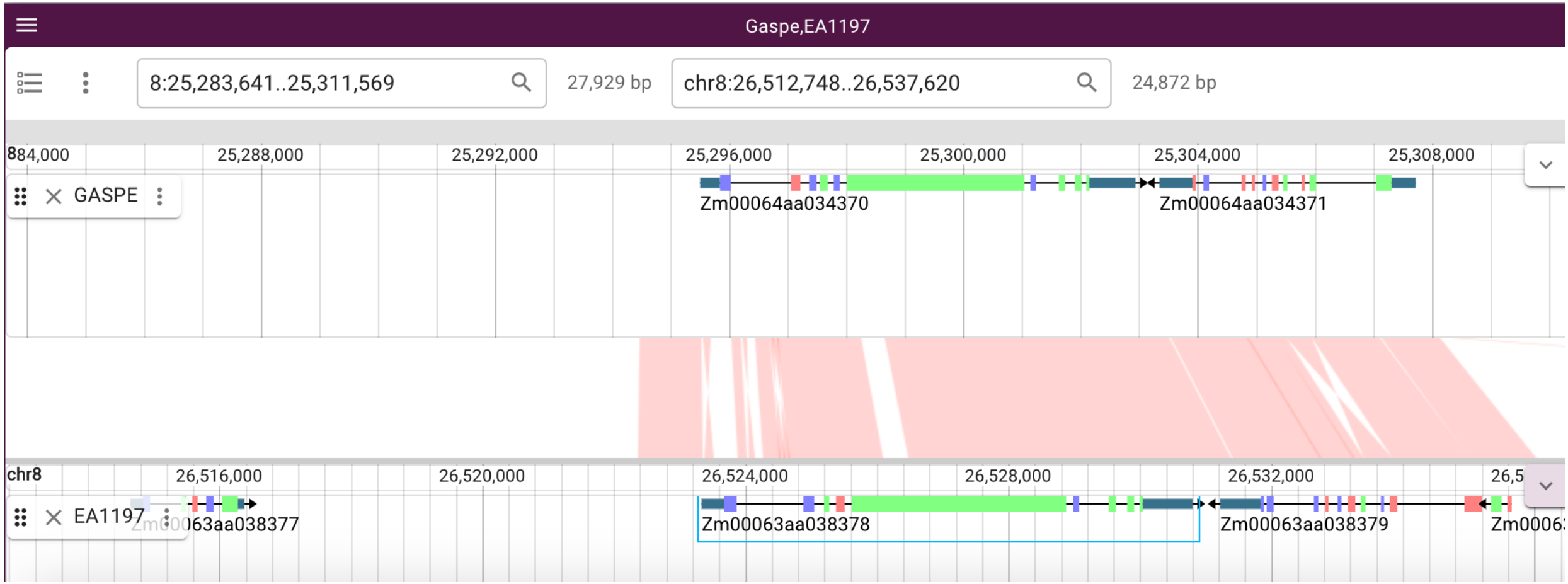
xcms fillChromPeaks (fillPeaks) Integrate areas of missing peaks

bcftools color-chrs plugin Color shared chromosomal segments, requires phased GTs

```
>Cluster 608
0       1394aa, >Zm00063aa013167_T00... at 98.78%
1       1396aa, >Zm00062aa018836_T00... *
2       1396aa, >Zm00064aa019116_T00... at 99.14%
>Cluster 609
0       1396aa, >Zm00064aa026404_T00... *
>Cluster 610
0       1396aa, >Zm00064aa040375_T00... *
>Cluster 611
0       1392aa, >Zm00063aa036892_T00... at 98.20%
1       1262aa, >Zm00062aa042738_T00... at 98.81%
2       1396aa, >Zm00064aa043042_T00... *
>Cluster 612
0       1395aa, >Zm00063aa038378_T00... *
1       1395aa, >Zm00062aa034030_T00... at 99.93%
>Cluster 613
0       1395aa, >Zm00062aa021699_T00... *
>Cluster 614
0       1394aa, >Zm00063aa020662_T00... *
1       1394aa, >Zm00062aa007996_T00... at 99.93%
2       1394aa, >Zm00064aa008223_T00... at 99.93%
>Cluster 615
0       1394aa, >Zm00062aa006093_T00... *
1       147aa, >Zm00062aa020836_T00... at 97.96%
2       147aa, >Zm00064aa021133_T00... at 97.96%
>Cluster 616
0       1392aa, >Zm00063aa014460_T00... *
1       1392aa, >Zm00062aa020118_T00... at 99.93%
2       1392aa, >Zm00064aa020356_T00... at 99.93%
>Cluster 617
0       1392aa, >Zm00063aa031317_T00... *
1       1234aa, >Zm00062aa006621_T00... at 97.97%
>Cluster 618
0       1391aa, >Zm00063aa022626_T00... *
1       1303aa, >Zm00062aa009876_T00... at 98.54%
2       1302aa, >Zm00064aa010183_T00... at 99.77%
>Cluster 619
0       1391aa, >Zm00064aa041061_T00... *
>Cluster 620
0       1146aa, >Zm00063aa013849_T00... at 98.17%
1       1390aa, >Zm00063aa013849_T00... *
2       1039aa, >Zm00063aa013849_T00... at 98.85%
>Cluster 621
0       1390aa, >Zm00063aa044387_T00... *
>Cluster 622
```


Gaspe,EA1197
8:25,283,641..25,311,569
27,929 bp
chr8:26,512,748..26,537,620
24,872 bp
884,000
25,288,000
25,292,000
25,296,000
25,300,000
25,304,000
25,308,000
GASPE
Zm00064aa034370
Zm00064aa034371
chr8
26,516,000
26,520,000
26,524,000
26,528,000
26,532,000
EA1197
63aa038377
Zm00063aa038378
Zm00063aa038379

Galaxy France

Workflow Visualize Données partagées Aide Utilis

Tools

chrom

Upload Data

Show Sections

Chromeister ultra-fast pairwise genome comparisons

SnpEff chromosome-info: list chromosome names/lengths

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bcftools color-chrs plugin Color shared chromosomal segments, requires phased GTs

```
>Cluster 608
0       1394aa, >Zm00063aa013167_T00... at 98.78%
1       1396aa, >Zm00062aa018836_T00... *
2       1396aa, >Zm00064aa019116_T00... at 99.14%
>Cluster 609
0       1396aa, >Zm00064aa026404_T00... *
>Cluster 610
0       1396aa, >Zm00064aa040375_T00... *
>Cluster 611
0       1392aa, >Zm00063aa036892_T00... at 98.20%
1       1262aa, >Zm00062aa042738_T00... at 98.81%
2       1396aa, >Zm00064aa043042_T00... *
>Cluster 612
0       1395aa, >Zm00063aa038378_T00... *
1       1395aa, >Zm00062aa034030_T00... at 99.93%
>Cluster 613
0       1395aa, >Zm00062aa021699_T00... *
>Cluster 614
0       1394aa, >Zm00063aa020662_T00... *
1       1394aa, >Zm00062aa007996_T00... at 99.93%
2       1394aa, >Zm00064aa008223_T00... at 99.93%
2       1368aa, >Zm00064aa012957_T00... at 99.85%
>Cluster 660
0       1368aa, >Zm00064aa034370_T00... *
>Cluster 661
0       1367aa, >Zm00062aa038519_T00... *
2       1392aa, >Zm00064aa020356_T00... at 99.93%
>Cluster 617
0       1392aa, >Zm00063aa031317_T00... *
1       1234aa, >Zm00062aa006621_T00... at 97.97%
>Cluster 618
0       1391aa, >Zm00063aa022626_T00... *
1       1303aa, >Zm00062aa009876_T00... at 98.54%
2       1302aa, >Zm00064aa010183_T00... at 99.77%
>Cluster 619
0       1391aa, >Zm00064aa041061_T00... *
>Cluster 620
0       1146aa, >Zm00063aa013849_T00... at 98.17%
1       1390aa, >Zm00063aa013849_T00... *
2       1039aa, >Zm00063aa013849_T00... at 98.85%
>Cluster 621
0       1390aa, >Zm00063aa044387_T00... *
>Cluster 622
```

Galaxy France

Workflow Visualize Données partagées Aide Utilisateur

Tools

nee

Upload Data

Show Sections

needle Needleman-Wunsch global alignment

RAMClustR define experiment Definition of experimental design used for record keeping and writing spectra data.

Interactive CellXgene Environment

MAGeCK mle - perform maximum-likelihood estimation of gene essentiality scores

featureCounts Measure gene expression in RNA-Seq experiments from SAM or BAM files

xcms get a sampleMetadata file which need to be filled with extra information

xcms get a sampleMetadata file which need to be filled with extra information

WORKFLOWS

All workflows

needle Needleman-Wunsch global alignment (Galaxy Version 5.0.0.1)

Run Tool

Tool Parameters

Sequence 1 *

50: Zm00063aa038378

Sequence 2 *

49: Zm00064aa034370

Gap open penalty *

10.0

Gap extension penalty *

0,5

Brief identity and similarity *

Yes

Output alignment file format *

SRS pair (p)

Additional Options

Email notification

No

Send an email notification when the job completes.

Galaxy France

Workflow Visualize Données partagées Aide Ut

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WORKFLOWS

All workflows

```
#=======================================
#
# Aligned_sequences: 2
# 1: Zm00063aa038378_T001
# 2: Zm00064aa034370_T001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1410
# Identity:    1348/1410 (95.6%)
# Similarity:  1351/1410 (95.8%)
# Gaps:          57/1410 ( 4.0%)
# Score: 6944.5
#
#
#=======================================

Zm00063aa0383      1 MPLVRFEVRNEVGLGDPGLYGGGAAAAAAATAAAGEEEPKALLEGVAVAG     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
Zm00064aa0343      1 MPLVRFEVRNEVGLGDPGLYGGGAAAAAAATAAAGEEEPKALLEGVAVAG     50

Zm00063aa0383     51 LVGILRQLGDLAEFAADVFHDLHEQVIATSARGRKVLTRVQNIEAALPSL    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
Zm00064aa0343     51 LVGILRQLGDLAEFAADVFHDLHEQVIATSARGRKVLTRVQNIEAALPSL    100

Zm00063aa0383    101 EKAVKNQKSHIHFAYVPGSDWHTQLQNEQNHLLATDLPRFMMDS------    144
                     ||||||||||||||||||||||||||||||||||||||||||||
Zm00064aa0343    101 EKAVKNQKSHIHFAYVPGSDWHTQLQNEQNHLLATDLPRFMMDSYEECRD    150

Zm00063aa0383    145 ---------FDNAGAGACVKRYSDPSYFKKAWDTMRADKNANVQREKRSQ    185
                                 ||||||||||||||||||||||||||||||||||||||||
Zm00064aa0343    151 PPRLYLLDKFDNAGAGACVKRYSDPSYFKKAWDTMRADKNANVQREKRSQ    200

Zm00063aa0383    186 KIKRKGSRLREPYHGQAMPRHRGTEFQRSLTAGQLVNRCCTSHTLRYNNF    235
                     |||||||||||||||||||||||||||||||||||||
Zm00064aa0343    201 KIKRKGSRLREPYHGQAMPRHRGTEFQRSLTAGQLVN-------------    237

Zm00063aa0383    236 VSVIILYGCSLLIFEWHIQNSIFNSVFSSRQFASPSNDGQGISEHKSTPD    285
                                                     |||||||||||||||||||||
Zm00064aa0343    238 ------------------------------RQFASPSNDGQGISEHKSTPD    258

Zm00063aa0383    286 ARSNPDNMSRSSSLSSKTQLSSVEQAIDTKPSAVSHENGHGKSLDTKLHK    335
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
Zm00064aa0343    259 ARSNPDNMSRSSSLSSKTQLSSVEQAIDTKPSAVSHENGHGKSLDTKLHK    308
```

OrthoFinder: phylogenetic orthology inference for comparative genomics

Emms and Kelly *Genome Biology* (2019) 20:238
https://doi.org/10.1186/s13059-019-1832-y

Genome Biology

SOFTWARE Open Access

OrthoFinder: phylogenetic orthology inference for comparative genomics

David M. Emms and Steven Kelly*

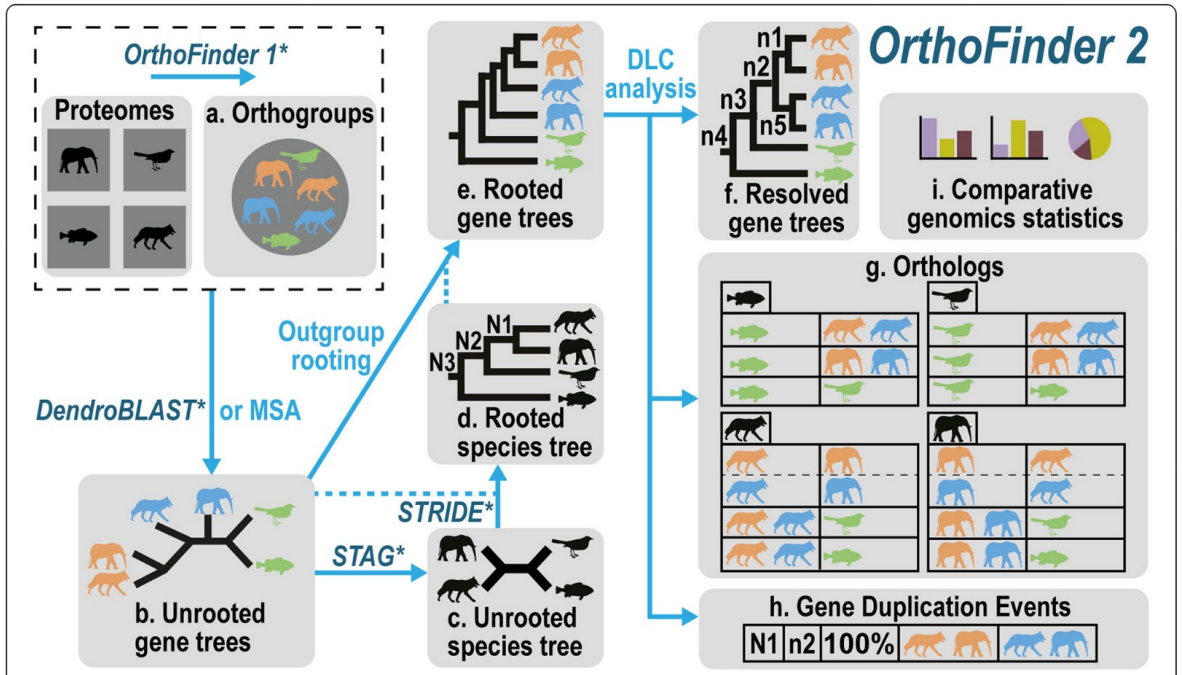


Fig. 2 The OrthoFinder workflow. The method used for each step is shown by the arrow. Published algorithms are shown in italics and are followed by an asterisk. A dotted blue line connecting with a solid arrow indicates additional data that are used in order to carry out the transformation indicated by the solid arrow. MSA, multiple sequence alignment-based tree inference; DLC, duplication-loss-coalescence. (**a**) Orthogroup inference using the original OrthoFinder algorithm (an orthogroup is the set of genes descended from a single gene in the last common ancestor of all the species under consideration). (**b**) Gene tree inference. (**c**) Species tree inference. (**d**) Species tree rooting (**e**) Gene tree rooting (**f**) Hybrid overlap + DLC analysis of rooted gene trees to infer orthologs and gene duplication events. (**g**) Illustration of the ortholog results table for the genes in each input species (four main boxes). The horizontal divisions within these show the orthologs for each individual species pair. (**h**) Illustration of the gene duplication event table showing the location of the gene duplication events mapped to the species tree, the location in the gene tree, the percent retention of the duplicate genes in the sampled species, and the genes descended from the gene duplication event. (**i**) Comparative genomics statistics

OrthoFinder best practices : Selecting which species to include

The first question to ask yourself is what species should you include. The answer to this probably depends on what kind of analysis you want to perform.

Three standard analyses are:

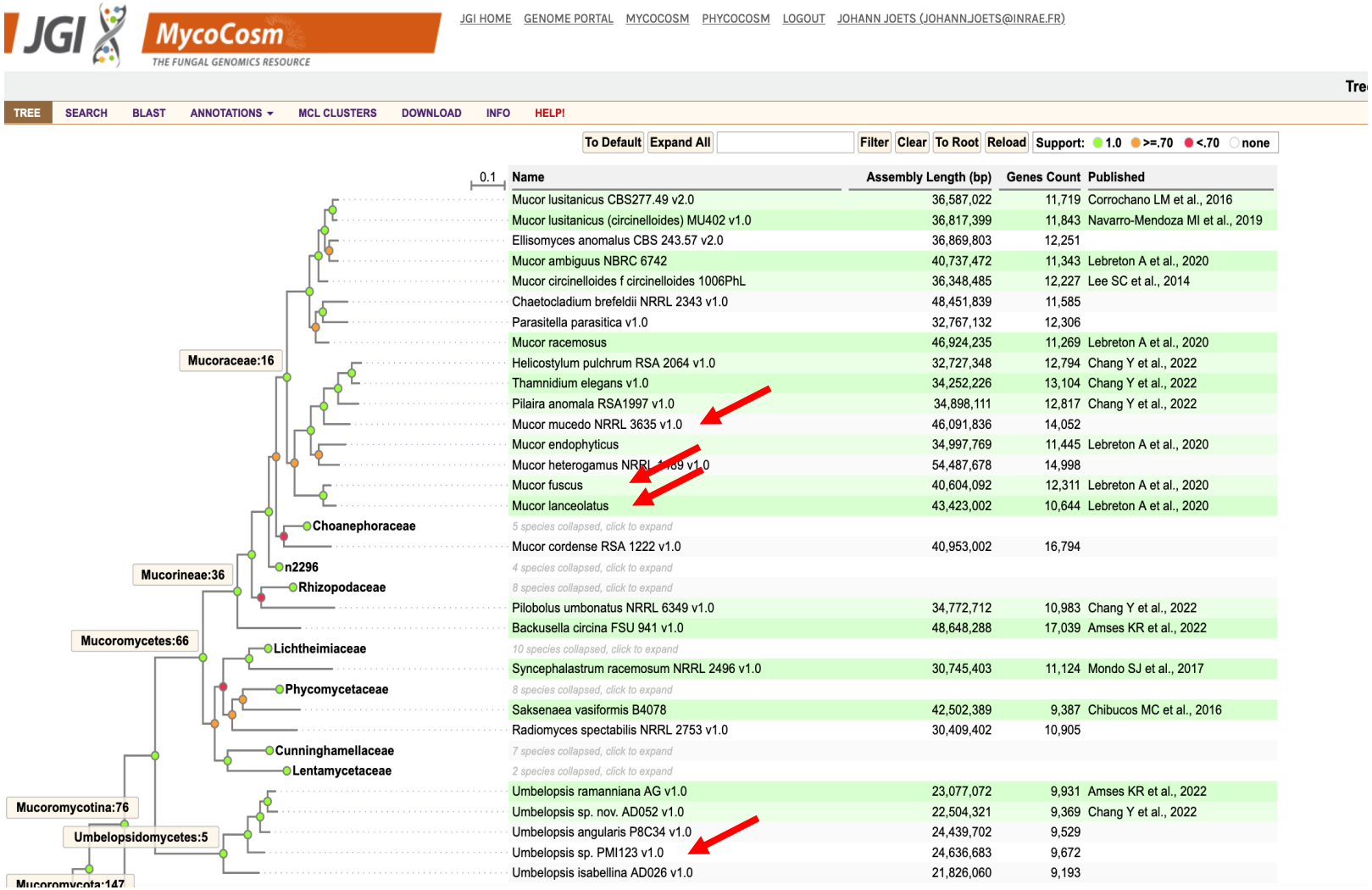
- Performing a comparative analysis across a clade of species
- Identifying orthologs between a pair, or among a small number, of species
- Investigating changes at a particular point in evolutionary history

In the first case just get the proteomes for all the species in your clade that you can. Generally, you don't need to include an outgroup for your clade of interest–in fact, this will push back the point in evolutionary history at which your orthogroups are defined (Orthogroups, Orthologs & Paralogs) and so it's usually better not to since your orthogroups will have lower resolution.

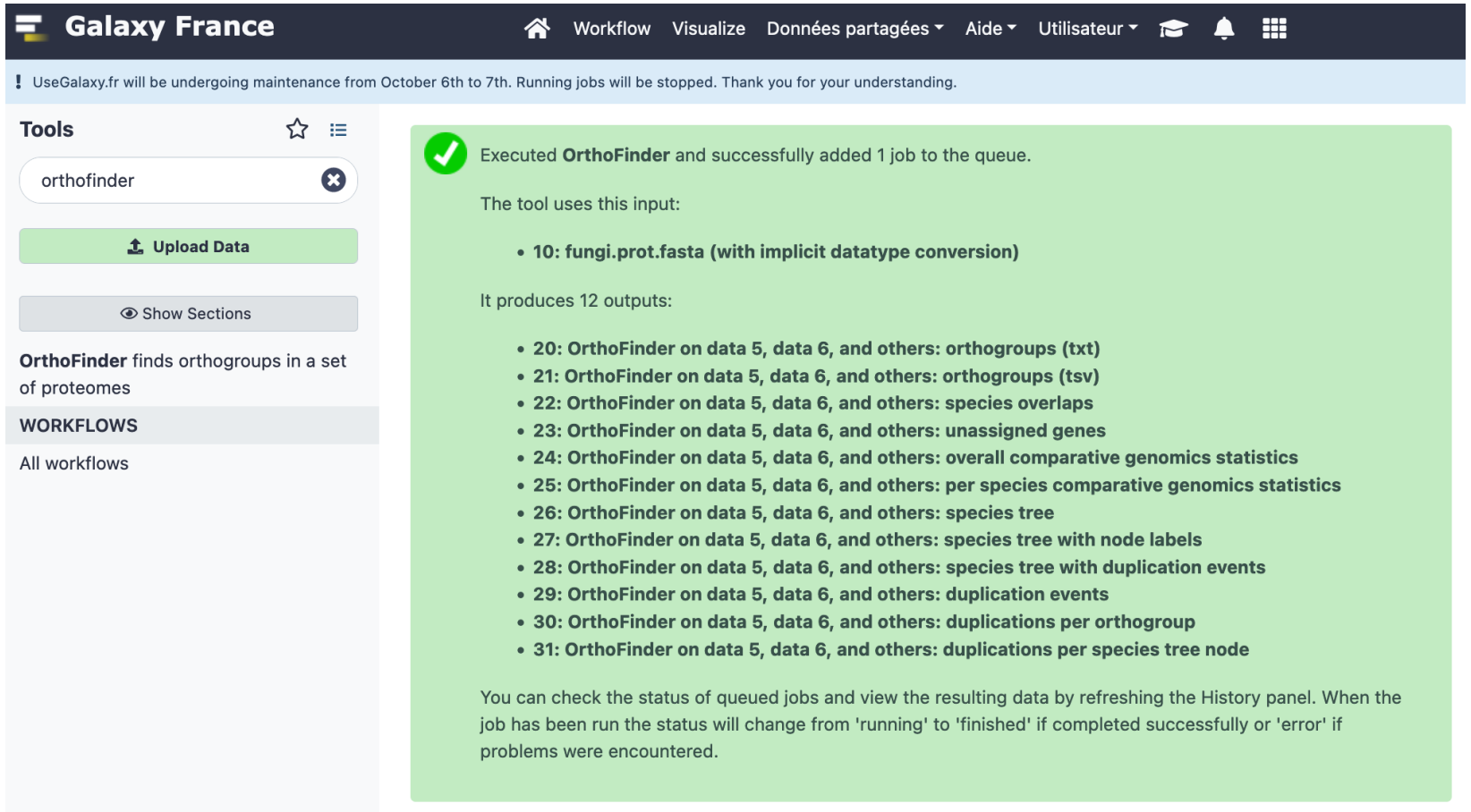
In the second case, it is good to ensure you have sufficient species sampling so as to get the best results. The same rule applies as for inferring a good phylogenetic tree: you should break up long branches with intermediate species. **You want an absolute minimum of 4 species and somewhere between 6-10 is probably optimal.**

If you're interested in what happened on a particular branch of the species tree, then you should likewise ensure good species sampling—ideally at least two species below the branch, at least two species on the closest branch above and two or more species in the outgroup.

OrthoFinder. Our dataset:



OrthoFinder: Galaxy



OrthoFinder: Galaxy

27: OrthoFinder on data 5, data 6, and others: species tree with node labels

1 line

format: **newick**, génome de référence: **?**

```
OrthoFinder version 2.5.4 Copyright
(C) 2014 David Emms

2022-09-28 04:21:27 : Starting
OrthoFinder 2.5.4
1 thread(s) for highly parallel tasks
(BLAST searches etc.)
1 thread(s) for OrthoFinder algorithm

Checking required programs are
installed
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```

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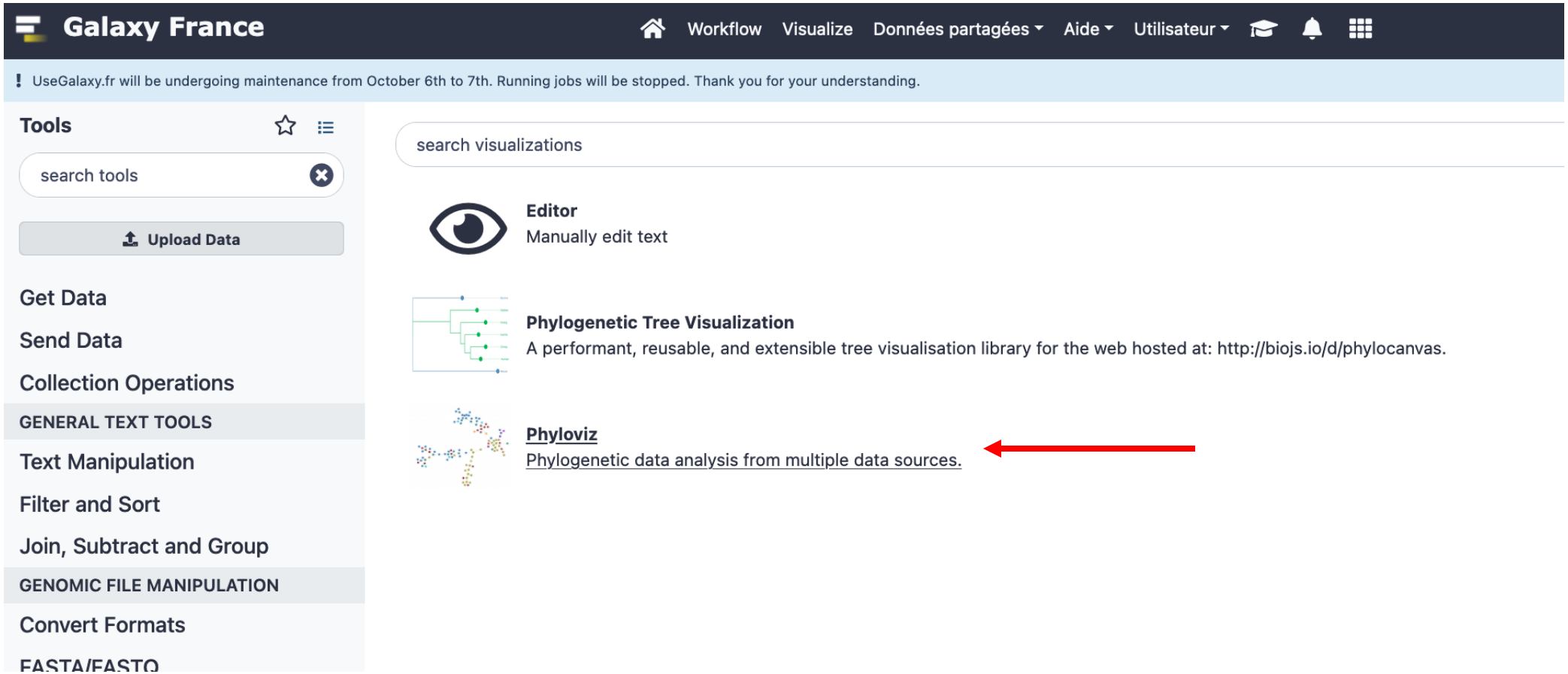
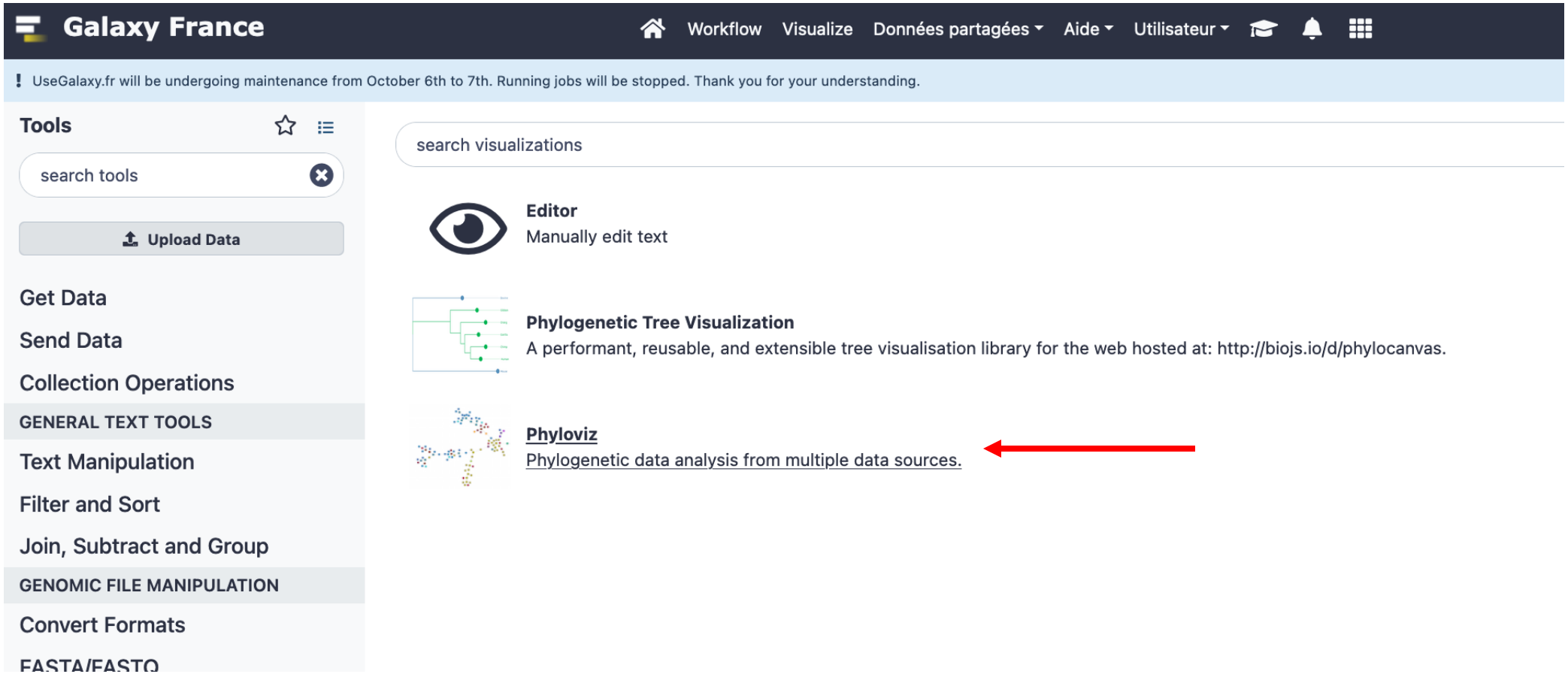
(Umbsp.aa.fasta.gz:0.326289,(Mmucedo.aa.fa
```

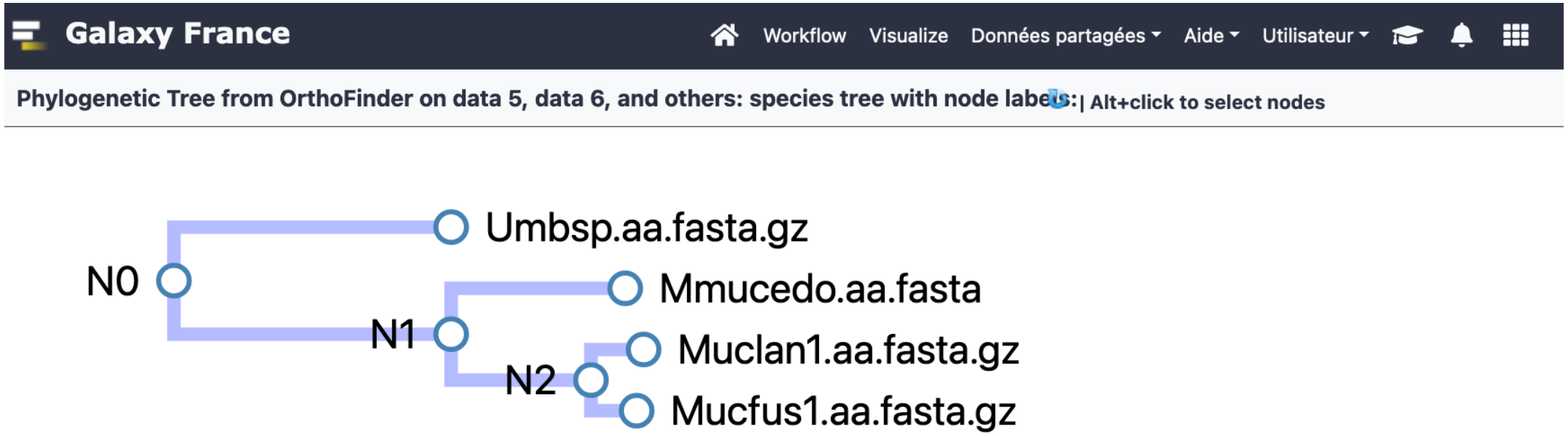
OrthoFinder: Galaxy



OrthoFinder: Galaxy



OrthoFinder: Galaxy



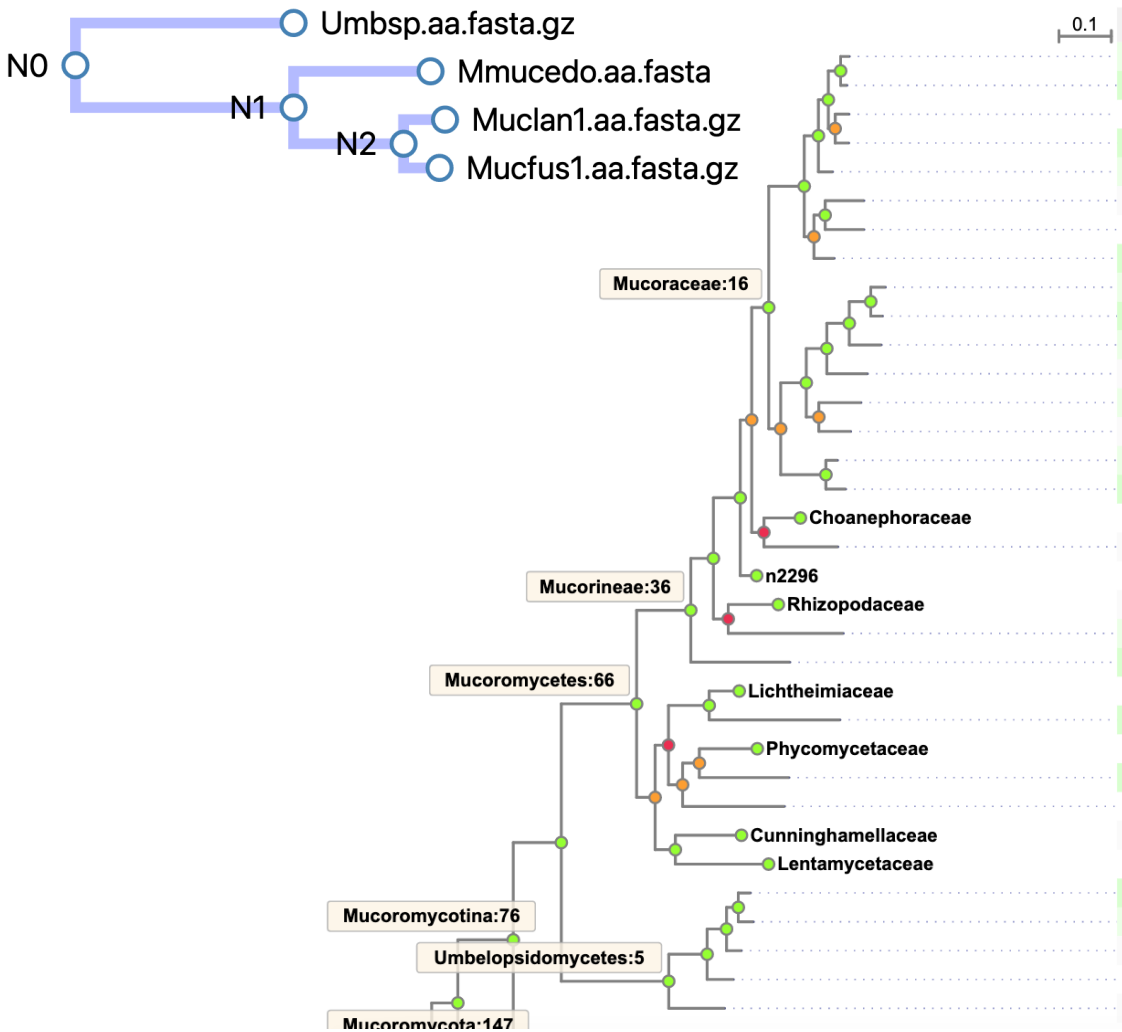
OrthoFinder: Galaxy

JGI MycoCosm THE FUNGAL GENOMICS RESOURCE

JGI HOME | GENOME PORTAL | MYCOCOSM | PHYCOCOSM | LOGOUT | JOHANN JOETS (JOHANNJOETS@INRAE.FR)

TREE | SEARCH | BLAST | ANNOTATIONS | MCL CLUSTERS | DOWNLOAD | INFO | HELP!

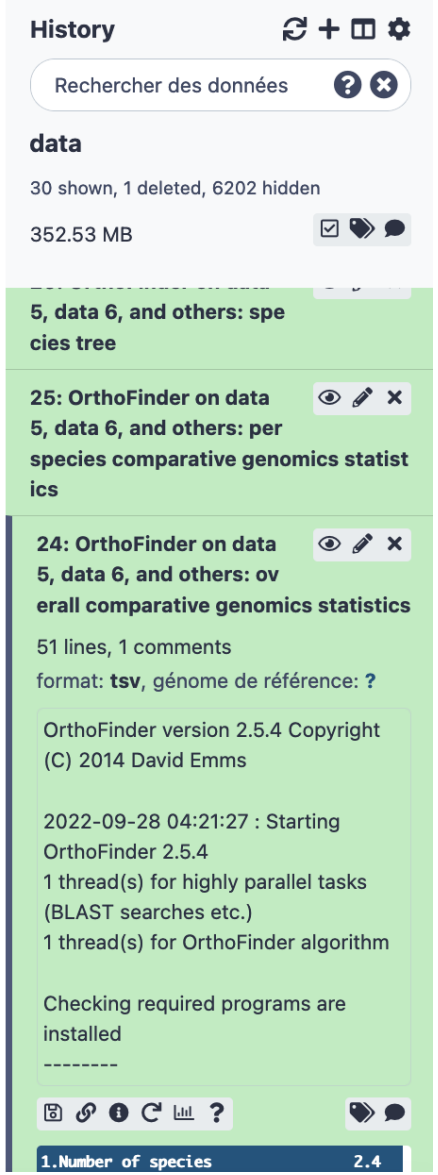
To Default | Expand All | Filter | Clear | To Root | Reload | Support: 1.0 >=.70 <.70 none



Name	Assembly Length (bp)	Genes Count	Published
Mucor lusitanicus CBS277.49 v2.0	36,587,022	11,719	Corrochano LM et al., 2016
Mucor lusitanicus (circinelloides) MU402 v1.0	36,817,399	11,843	Navarro-Mendoza MI et al., 2019
Ellisomyces anomalus CBS 243.57 v2.0	36,869,803	12,251	
Mucor ambiguus NBRC 6742	40,737,472	11,343	Lebreton A et al., 2020
Mucor circinelloides f circinelloides 1006PhL	36,348,485	12,227	Lee SC et al., 2014
Chaetocladium brefeldii NRRL 2343 v1.0	48,451,839	11,585	
Parasitella parasitica v1.0	32,767,132	12,306	
Mucor racemosus	46,924,235	11,269	Lebreton A et al., 2020
Helicostylum pulchrum RSA 2064 v1.0	32,727,348	12,794	Chang Y et al., 2022
Thamnidium elegans v1.0	34,252,226	13,104	Chang Y et al., 2022
Pilaira anomala RSA1997 v1.0	34,898,111	12,817	Chang Y et al., 2022
Mucor mucedo NRRL 3635 v1.0	46,091,836	14,052	
Mucor endophyticus	34,997,769	11,445	Lebreton A et al., 2020
Mucor heterogamus NRRL 1189 v1.0	54,487,678	14,998	
Mucor fuscus	40,604,092	12,311	Lebreton A et al., 2020
Mucor lanceolatus	43,423,002	10,644	Lebreton A et al., 2020
5 species collapsed, click to expand			
Mucor cordense RSA 1222 v1.0	40,953,002	16,794	
4 species collapsed, click to expand			
8 species collapsed, click to expand			
Pilobolus umbonatus NRRL 6349 v1.0	34,772,712	10,983	Chang Y et al., 2022
Backusella circina FSU 941 v1.0	48,648,288	17,039	Amses KR et al., 2022
10 species collapsed, click to expand			
Syncephalastrum racemosum NRRL 2496 v1.0	30,745,403	11,124	Mondo SJ et al., 2017
8 species collapsed, click to expand			
Saksenaea vasiformis B4078	42,502,389	9,387	Chibucos MC et al., 2016
Radiomyces spectabilis NRRL 2753 v1.0	30,409,402	10,905	
7 species collapsed, click to expand			
2 species collapsed, click to expand			
Umbelopsis ramanniana AG v1.0	23,077,072	9,931	Amses KR et al., 2022
Umbelopsis sp. nov. AD052 v1.0	22,504,321	9,369	Chang Y et al., 2022
Umbelopsis angularis P8C34 v1.0	24,439,702	9,529	
Umbelopsis sp. PMI123 v1.0	24,636,683	9,672	
Umbelopsis isabellina AD026 v1.0	21,826,060	9,193	

OrthoFinder: Galaxy

Number of species	4
Number of species	4
Number of genes	45727
Number of genes in orthogroups	42977
Number of unassigned genes	2750
Percentage of genes in orthogroups	94.0
Percentage of unassigned genes	6.0
Number of orthogroups	9227
Number of species-specific orthogroups	707
Number of genes in species-specific orthogroups	3857
Percentage of genes in species-specific orthogroups	8.4
Mean orthogroup size	4.7
Median orthogroup size	4.0
G50 (assigned genes)	4
G50 (all genes)	4
O50 (assigned genes)	2851
O50 (all genes)	3195
Number of orthogroups with all species present	5270
Number of single-copy orthogroups	3448
Date	2022-09-28
Orthogroups file	Orthogroups.tsv
Unassigned genes file	Orthogroups_UnassignedGenes.tsv
Per-species statistics	Statistics_PerSpecies.tsv
Overall statistics	Statistics_Overall.tsv
Orthogroups shared between species	Orthogroups_SpeciesOverlaps.tsv
Average number of genes per-species in orthogroup	Number of orthogroups Percentage of orthogroups Number of genes Percentage of genes
<1	3049 33.0 8180 19.0
'1	5328 57.7 24299 56.5
'2	573 6.2 5160 12.0
'3	141 1.5 1855 4.3
'4	63 0.7 1089 2.5
'5	20 0.2 428 1.0



OrthoFinder: Galaxy

	Mmucedo.aa.fasta	Mucfus1.aa.fasta.gz	Muclan1.aa.fasta.gz	Umbsp.aa.fasta.gz
	Mmucedo.aa.fasta	Mucfus1.aa.fasta.gz	Muclan1.aa.fasta.gz	Umbsp.aa.fasta.gz
Number of genes	13403	12311	10644	9369
Number of genes in orthogroups	12626	11987	10268	8096
Number of unassigned genes	777	324	376	1273
Percentage of genes in orthogroups	94.2	97.4	96.5	86.4
Percentage of unassigned genes	5.8	2.6	3.5	13.6
Number of orthogroups containing species	7814	8339	8153	6236
Percentage of orthogroups containing species	84.7	90.4	88.4	67.6
Number of species-specific orthogroups	330	130	58	189
Number of genes in species-specific orthogroups	2454	567	198	638
Percentage of genes in species-specific orthogroups	18.3	4.6	1.9	6.8
Number of genes per-species in orthogroup	Number of orthogroups	Number of orthogroups	Number of orthogroups	Number of orthogroups
'0	1413	888	1074	2991
'1	6076	6705	6686	5002
'2	1119	1110	1114	907
'3	269	241	225	202
'4	97	93	68	66
'5	59	55	22	29
'6	42	34	19	12
'7	22	12	10	3
'8	14	15	2	3
'9	18	6	1	1
'10	6	7	2	3
11-15	35	33	2	5
16-20	24	10	1	3
21-50	27	17	1	0
51-100	5	1	0	0
101-150	1	0	0	0
151-200	0	0	0	0
201-500	0	0	0	0
501-1000	0	0	0	0
'1001+	0	0	0	0
Number of genes per-species in orthogroup	Percentage of orthogroups	Percentage of orthogroups	Percentage of orthogroups	Percentage of orthogroups
'0	15.3	9.6	11.6	32.4
'1	65.9	72.7	72.5	54.2
'2	12.1	12.0	12.1	9.8
'3	2.9	2.6	2.4	2.2

History

Rechercher des données

data

30 shown, 1 deleted, 6202 hidden

352.53 MB

25: OrthoFinder on data 5, data 6, and others: per species comparative genomics statistics

99 lines, 1 comments

format: **tsv**, génome de référence: **?**

OrthoFinder version 2.5.4 Copyright (C) 2014 David Emms

2022-09-28 04:21:27 : Starting OrthoFinder 2.5.4
1 thread(s) for highly parallel tasks (BLAST searches etc.)
1 thread(s) for OrthoFinder algorithm

Checking required programs are installed

1.	2.Mmuc
	Mmucedo
Number of genes	13403
Number of genes in orthogroups	12626
Number of unassigned genes	777
Percentage of genes in orthogroups	94.2

24: OrthoFinder on data 5, data 6, and others: overall comparative genomics statistics

23: OrthoFinder on data 5, data 6, and others: unassigned genes

OrthoFinder: Galaxy

Number of genes per-species in orthogroup	Percentage of genes	Percentage of genes	Percentage of genes	Percentage of genes
'0	0.0	0.0	0.0	0.0
'1	45.3	54.5	62.8	53.4
'2	16.7	18.0	20.9	19.4
'3	6.0	5.9	6.3	6.5
'4	2.9	3.0	2.6	2.8
'5	2.2	2.2	1.0	1.5
'6	1.9	1.7	1.1	0.8
'7	1.1	0.7	0.7	0.2
'8	0.8	1.0	0.2	0.3
'9	1.2	0.4	0.1	0.1
'10	0.4	0.6	0.2	0.3
11-15	3.2	3.4	0.2	0.7
16-20	3.2	1.4	0.2	0.5

25: OrthoFinder on data 5, data 6, and others: per species comparative genomics statistics

99 lines, 1 comments

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```
OrthoFinder version 2.5.4 Copyright
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2022-09-28 04:21:27 : Starting
OrthoFinder 2.5.4
1 thread(s) for highly parallel tasks
(BLAST searches etc.)
1 thread(s) for OrthoFinder algorithm
```

OrthoFinder: Galaxy

Classeur3

Accueil | Insertion | Dessin | Mise en page | Formules | Données | Révision | Affichage

Ouvrir des classeurs récupérés ? Vos modifications récentes ont été enregistrées. Voulez-vous continuer à travailler là où vous vous étiez arrêté ?

A6042 | OG0006040

	A	B	C	D	
5818	OG0005816	FUN_011186-T1	jgi|Mucfus1|369267|Mf11816.m_SAM50-like	jgi|Muclan1|1369|SAM50-like	jgi|Umbsp_AD052
5819	OG0005817	FUN_011187-T1	jgi|Mucfus1|358331|Mf86363.m_Unknown	jgi|Muclan1|2915|Ml92955.m_Unknown	jgi|Umbsp_AD052
5820	OG0005818	FUN_011190-T1	jgi|Mucfus1|358334|Guanosine-diphosphatase	jgi|Muclan1|2918|Guanosine-diphosphatase	jgi|Umbsp_AD052
5821	OG0005819	FUN_011197-T1	jgi|Mucfus1|357467|Pirin	jgi|Muclan1|3538|Pirin	jgi|Umbsp_AD052
5822	OG0005820	FUN_011202-T1	jgi|Mucfus1|357463|Signal	jgi|Muclan1|3534|Signal	jgi|Umbsp_AD052
5823	OG0005821	FUN_011209-T1	jgi|Mucfus1|358899|Bloom, jgi|Mucfus1|360777|ATP-dependent,	jgi|Mucfus1|368146|Mf43602.m_ATP-dependent	
5824	OG0005822	FUN_011213-T1	jgi|Mucfus1|368705|Mf96070.m_SH3	jgi|Muclan1|7256|Ml07161.m_SH3	jgi|Umbsp_AD052
5825	OG0005823	FUN_011216-T1	jgi|Mucfus1|358055|Gamma-secretase	jgi|Muclan1|2952|Gamma-secretase	jgi|Umbsp_AD052
5826	OG0005824	FUN_011221-T1	jgi|Mucfus1|365074|Mf10441.m_Unknown	jgi|Muclan1|7773|Ml56041.m_Unknown	jgi|Umbsp_AD052
5827	OG0005825	FUN_011222-T1	jgi|Mucfus1|366442|Multiprotein-bridging	jgi|Muclan1|9299|Multiprotein-bridging	jgi|Umbsp_AD052
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5829	OG0005827	FUN_011314-T1	jgi|Mucfus1|359380|Mf62724.m_Unknown	jgi|Muclan1|3091|Ml44294.m_Unknown	jgi|Umbsp_AD052
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5832	OG0005830	FUN_011318-T1	jgi|Mucfus1|359384|L-lactate	jgi|Muclan1|1368|L-lactate	jgi|Umbsp_AD052
5833	OG0005831	FUN_011322-T1	jgi|Mucfus1|367884|Uracil-regulated	jgi|Muclan1|1627|Uracil-regulated	jgi|Umbsp_AD052
5834	OG0005832	FUN_011323-T1	jgi|Mucfus1|367885|Uracil	jgi|Muclan1|1626|Uracil	jgi|Umbsp_AD052
5835	OG0005833	FUN_011324-T1	jgi|Mucfus1|367887|Mf08238.m_Unknown	jgi|Muclan1|1625|Ml25463.m_Unknown	jgi|Umbsp_AD052
5836	OG0005834	FUN_011331-T1	jgi|Mucfus1|367888|Mf25101.m_ATP-dependent	jgi|Muclan1|1621|Ml24741.m_ATP-dependent	jgi|Umbsp_AD052
5837	OG0005835	FUN_011344-T1	jgi|Mucfus1|367677|Ubiquitin-conjugating	jgi|Muclan1|4994|Ubiquitin-conjugating	jgi|Umbsp_AD052
5838	OG0005836	FUN_011346-T1	jgi|Mucfus1|360540|Ribosomal	jgi|Muclan1|10260|Ribosomal	jgi|Umbsp_AD052
5839	OG0005837	FUN_011347-T1	jgi|Mucfus1|357212|Cell	jgi|Muclan1|4975|Septin	jgi|Umbsp_AD052
5840	OG0005838	FUN_011353-T1	jgi|Mucfus1|359874|Mf15169.m_Unknown	jgi|Muclan1|318|Ml56381.m_Unknown	jgi|Umbsp_AD052
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5842	OG0005840	FUN_011356-T1	jgi|Mucfus1|367678|Mf26248.m_Unknown	jgi|Muclan1|322|Ml09600.m_Unknown	jgi|Umbsp_AD052
5843	OG0005841	FUN_011384-T1	jgi|Mucfus1|365938|Haloacid	jgi|Muclan1|5842|Haloacid	jgi|Umbsp_AD052
5844	OG0005842	FUN_011386-T1	jgi|Mucfus1|365936|Carbamoyl-phosphate	jgi|Muclan1|5840|Carbamoyl-phosphate	jgi|Umbsp_AD052
5845	OG0005843	FUN_011390-T1	jgi|Mucfus1|366173|FKBP12-associated	jgi|Muclan1|4245|FKBP12-associated	jgi|Umbsp_AD052
5846	OG0005844	FUN_011392-T1	jgi|Mucfus1|367157|Cytoplasmic	jgi|Muclan1|6507|Cytoplasmic	jgi|Umbsp_AD052_1|312247|estExt_Genewise1Plus.
5847	OG0005845	FUN_011394-T1	jgi|Mucfus1|365803|Transcription	jgi|Muclan1|7889|Transcription	jgi|Umbsp_AD052_1|361134|gm1.5473_g
5848	OG0005846	FUN_011396-T1	jgi|Mucfus1|365804|Mf89779.m_Unknown	jgi|Muclan1|7890|Ml16212.m_Unknown	jgi|Umbsp_AD052_1|325631|fgenesh1_kg.18_#_70_#
5849	OG0005847	FUN_011442-T1	jgi|Mucfus1|359948|NudC	jgi|Muclan1|4879|NudC	jgi|Umbsp_AD052_1|313267|fgenesh1_kg.1_#_570_#

Feuil1

Modifier | Accessibilité : vérification terminée | 100 %

21: OrthoFinder on data 5, data 6, and others: ort hogroups (tsv)

9,227 lines, 1 comments

format: **tsv**, génome de référence: **?**

```
OrthoFinder version 2.5.4 Copyright
(C) 2014 David Emms

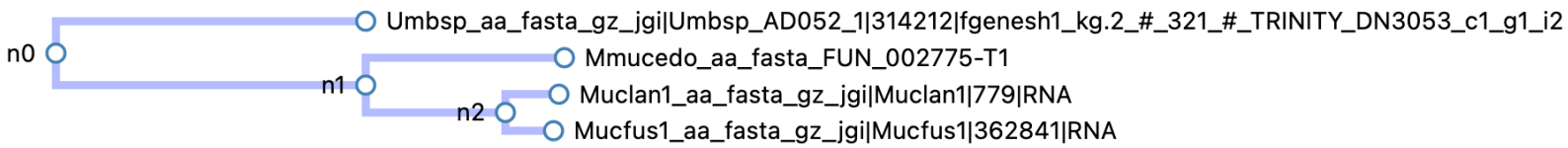
2022-09-28 04:21:27 : Starting
OrthoFinder 2.5.4
1 thread(s) for highly parallel tasks
(BLAST searches etc.)
1 thread(s) for OrthoFinder algorithm

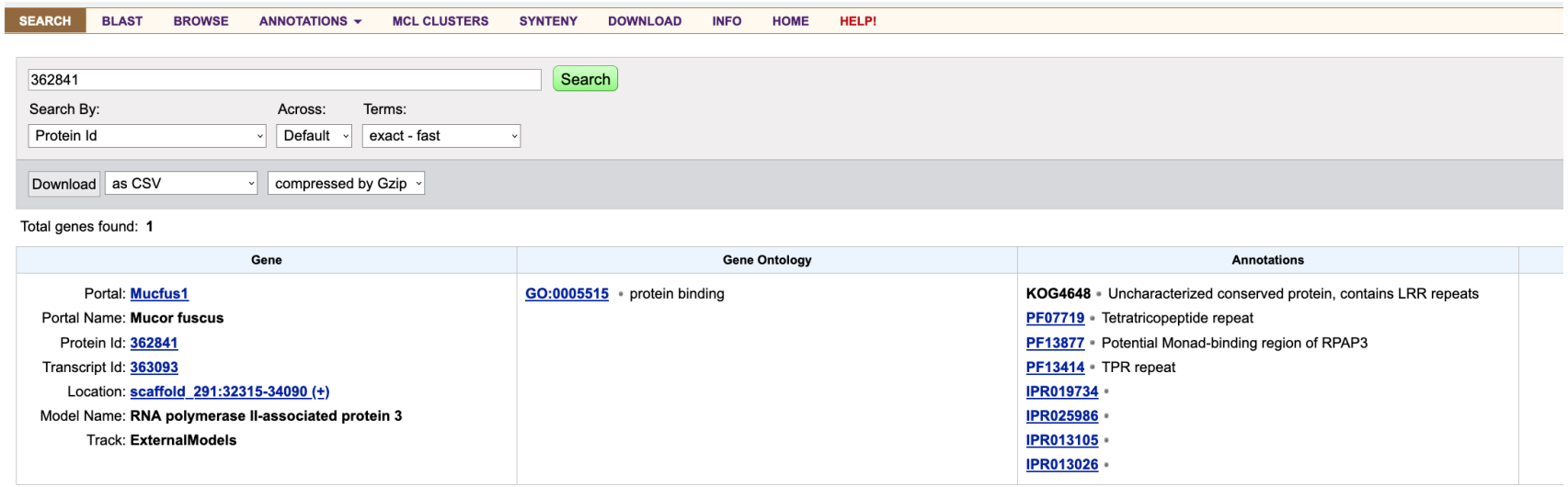
Checking required programs are
installed
--------
```

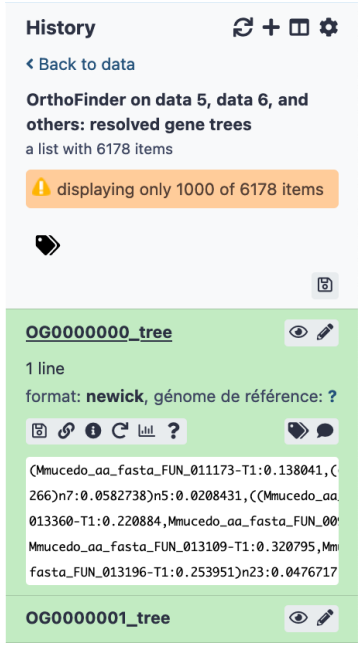
1.Orthogroup 2.Mmucedo.aa.fasta

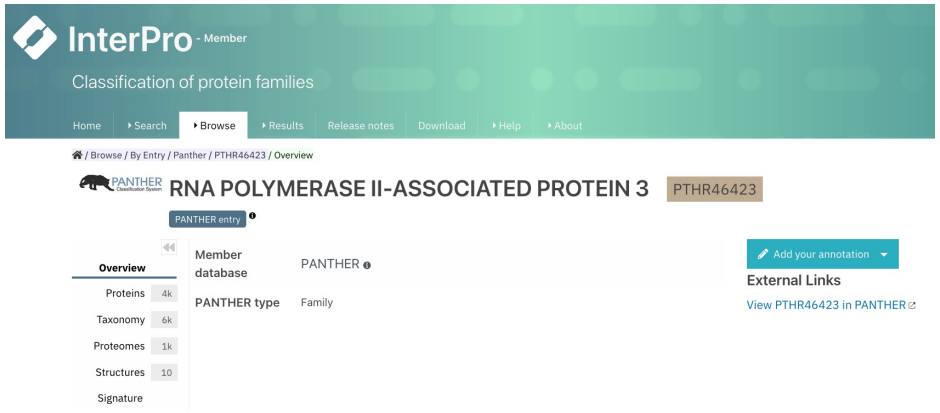
Orthogroup	Mmucedo.aa.fasta
OG0000000	FUN_000055-T1, FUN_000056-T1,
OG0000001	FUN_000167-T1, FUN_000491-T1,
OG0000002	FUN_000685-T1, FUN_000919-T1,
OG0000003	FUN_002416-T1, FUN_002419-T1,

OrthoFinder: Galaxy









OrthoFinder: Galaxy

October 6th to 7th. Running jobs will be stopped. Thank you for your understanding.

Orthogroup	Mmucedo.aa.fasta	Mucfus1.aa.fasta.gz	Muclan1.aa.fasta.gz
Orthogroup	Mmucedo.aa.fasta	Mucfus1.aa.fasta.gz	Muclan1.aa.fasta.gz
OG0009227	FUN_000003-T1		
OG0009228	FUN_000045-T1		
OG0009229	FUN_000085-T1		
OG0009230	FUN_000089-T1		
OG0009231	FUN_000101-T1		
OG0009232	FUN_000124-T1		
OG0009233	FUN_000125-T1		
OG0009234	FUN_000126-T1		
OG0009235	FUN_000131-T1		
OG0009236	FUN_000132-T1		
OG0009237	FUN_000133-T1		
OG0009238	FUN_000134-T1		
OG0009239	FUN_000135-T1		
OG0009240	FUN_000152-T1		
OG0009241	FUN_000157-T1		
OG0009242	FUN_000159-T1		
OG0009243	FUN_000176-T1		
OG0009244	FUN_000180-T1		
OG0009245	FUN_000187-T1		
OG0009246	FUN_000243-T1		
OG0009247	FUN_000254-T1		
OG0009248	FUN_000290-T1		
OG0009249	FUN_000292-T1		
OG0009250	FUN_000326-T1		
OG0009251	FUN_000337-T1		
OG0009252	FUN_000340-T1		
OG0009253	FUN_000450-T1		
OG0009254	FUN_000474-T1		
OG0009255	FUN_000498-T1		
OG0009256	FUN_000515-T1		

History

Rechercher des données

data

30 shown, 1 deleted, 6202 hidden

352.53 MB

25: OrthoFinder on data 5, data 6, and others: per species comparative genomics statistics

24: OrthoFinder on data 5, data 6, and others: overall comparative genomics statistics

23: OrthoFinder on data 5, data 6, and others: unassigned genes

2,750 lines, 1 comments

format: **tsv**, génome de référence: **?**

```
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2022-09-28 04:21:27 : Starting
OrthoFinder 2.5.4
1 thread(s) for highly parallel tasks
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1 thread(s) for OrthoFinder algorithm

Checking required programs are
installed
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```