

Galaxy: ressource pour le calcul en bioinformatique

Alexis Dereeper, Jean-François Dufayard, Marilyne Summo, Gautier Sarah, Manuel Ruiz

avec l'aide des formateurs précédents: Félix Homa, Stéphanie Pointet, Cédric Farcy

La bioinformatique sans Galaxy

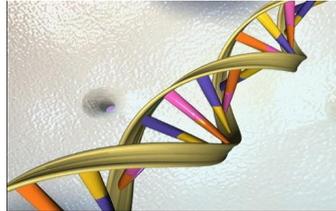


Problématique relevant de la bioinformatique





Problématique relevant de la bioinformatique



Je dispose d'un bioinformaticien sur place





Problématique relevant de la bioinformatique



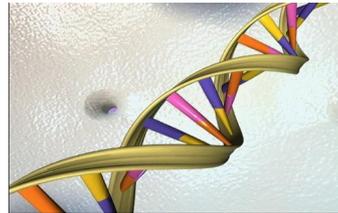
Je dispose d'un bioinformaticien sur place



- Il n'est pas omniscient.
- Il n'est pas omnipotent.
- Il ne dispose que d'un temps limité.
- Il est dépendant d'une structure pour le calcul intensif.



Problématique relevant de la bioinformatique



Je dispose d'une plateforme



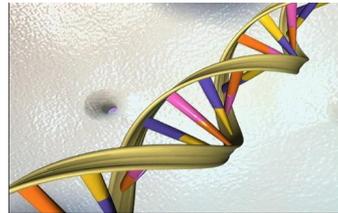
Je dispose d'un bioinformaticien sur place



- Il n'est pas omniscient.
- Il n'est pas omnipotent.
- Il ne dispose que d'un temps limité.
- Il est dépendant d'une structure pour le calcul intensif.



Problématique relevant de la bioinformatique



Je dispose d'une plateforme

- Identifier le bon interlocuteur est délicat.
- Le temps de réaction peut varier.



Je dispose d'un bioinformaticien sur place



- Il n'est pas omniscient.
- Il n'est pas omnipotent.
- Il ne dispose que d'un temps limité.
- Il est dépendant d'une structure pour le calcul intensif.

Parfois, l'analyse est "simple", et consiste à employer des outils connus...

La technique du "Je Le Fais Moi-Même"

Dans cette situation, la solution la plus fréquemment employée est le

JLF2M: Je le fais moi-même !

La technique du "Je Le Fais Moi-Même"

Dans cette situation, la solution la plus fréquemment employée est le

JLF2M: Je le fais moi-même !

```
simmons@earth:~/work/xterm/orig/xterm-XF86-4.3.0$ ls
256colres.h      error.h          misc.c           Tekparse.h      VTPrsTbl.c
256colres.pl    fontutils.c     mkdirs.sh       Tekproc.c       xctest.h
88colres.h      fontutils.h     os2main.c       TekPrsTbl.c     wwidth.c
88colres.pl    Imakefile       piink.sh        testrects      wwidth.h
AAA_README_VMS.txt input.c         precompose.c    termcap         xcharmouse.h
aclocal.m4      INSTALL        precompose.h    terminfo       xstrings.c
button.c        install.sh      print.c         Tests           xstrings.h
charclass.c     keySYM2ucs.c   proto.h         testxmc.c       XTerm.ad
charclass.h     keySYM2ucs.h   ptydata.c      trace.c         xterm_arp.opt
charproc.c     link_arp.com   ptYx.h         trace.h         xtermcfg.hin
charsets.c     main.c         README         vtermcap       XTerm-col.ad
config.guess    main.h         README.os390   util.c          xterm.dat
config.sub      make.com       resize.c       uxterm         xterm.h
configure       Makefile       resize.man     UXTerm.ad      xterm_io.h
configure.in    Makefile.in   screen.c      version.h      xterm_log.html
cursor.c        MANIFEST      scrollbar.c    vms.c          xterm.man
data.c          menu.c         sinstall.sh    vms.h          xutf8.c
data.h          menu.h         tabs.c         VTparse.def    xutf8.h
doublechr.c    mininstall.sh  Tekparse.def  VTparse.h
```

Une invite de commandes



Un cluster de calcul

La technique du "Je Le Fais Moi-Même"

```
simmons@earth:~/work/xterm/orig/xterm-XF86-4.3.0
[simmons@earth xterm-XF86-4.3.0]$ ls
256colres.h      error.h          misc.c           Tekparse.h      VTPrsTbl.c
256colres.pl    fontutils.c     mkdirs.sh       Tekproc.c       xutf8.c
88colres.h      fontutils.h     os2main.c       TekPrsTbl.c     xwidth.c
88colres.pl     Inakefile       plink.sh        testests        xwidth.h
AAA_README_VMS.txt input.c         precompose.c    termcap         xcharmouse.h
aclocal.m4      INSTALL        precompose.h    terminfo       xstrings.c
button.c        install.sh      print.c         Tests           xstrings.h
charclass.c     keySYM2ucs.c   proto.h         testxmc.c       XTerm.ad
charclass.h     keySYM2ucs.h   ptydata.c      trace.c         xterm_arp.opt
charproc.c      link_axp.com   ptvx.h         trace.h         xtermcfg.hin
charsets.c      main.c         README         unicode        XTerm-col.ad
config.guess    main.h         README.os390   util.c         xterm.dat
config.sub      make.com       resize.c       uxterm         xterm.h
configure       Makefile       resize.man     UXTerm.ad     xterm_io.h
configure.in    Makefile.in   screen.c      version.h     xterm.log.html
cursor.c        MANIFEST      scrollbar.c   vms.c         xterm.man
data.c          menu.c        sinstall.sh   vms.h         xutf8.c
data.h          menu.h        tabs.c        VTparse.def   xutf8.h
doublechr.c     ninstall.sh   Tekparse.def  VTparse.h
[simmons@earth xterm-XF86-4.3.0]$
```



- Apprendre les commandes Linux de base.
- Apprendre les commandes spécifiques à la communication avec un cluster de calcul.

La technique du "Je Le Fais Moi-Même"



Utiliser les logiciels en ligne de commande, les manuels en ligne ou en interface texte.

Command line parameters

All program parameters can be entered in the command line. The first parameter must always be the name of the alignment file or the pathnames file. If this is the only given parameter, the menu of the program is activated. For example:

Gblocks nad3.pir

The next parameters are entered according to the letter of the corresponding menu item. They can be entered in any order. The list of all parameters is:

PARAMETER NAME	MEANING (Default)	ALLOWED VALUES
(None)	Filename (No default)	Alignment or pathnames file
-t=	Type Of Sequence (Protein, DNA, Codons)	p, d, c
-b1=	Minimum Number Of Sequences For A Conserved Position (50% of the number of sequences + 1)	Any integer bigger than half the number of sequences and smaller or equal than the total number of sequences
-b2=	Minimum Number Of Sequences For A Flank Position (85% of the number of sequences)	Any integer equal or bigger than Minimum Number Of Sequences For A Conserved Position
	Maximum Number Of Contiguous	

```
dufayard@marmadais:/home/dufayard/tmp
New Info Customize Close Execute Bookmarks
dufayard@marmadais: dufayard@marmadais: dufayard@marmadais: dufayard@marmadais: Local
The support threshold for gene tree branch collapse (optional, default 80.0)
-st species_threshold
The length threshold for species tree branch collapse (optional, default 10.0)
-pt polymorphism_threshold
The length depth threshold to deduce to polymorphism, allelism ... (optional,
default 0.05)
-k k_level
The k-level of the subtree-neighbor measure (optional, default 2)
-idupw i_duplication_weight
The weight of intersection duplication in functional orthology scoring (0.0 for
maximum weight, 1.0 for no weight, optional, default 0.90)
-tdupw t_duplication_weight
The weight of topological duplication in functional orthology scoring (0.0 for
maximum weight, 1.0 for no weight, optional, default 0.95)
-specw speciation_weight
The weight of speciation in functional orthology scoring (0.0 for maximum weig
ht, 1.0 for no weight, optional, default 0.99)
-ultraw ultraparalogy_weight
The weight of an ultraparalogy node in functional orthology scoring (0.0 for m
aximum weight, 1.0 for no weight, optional, default 0.99)
-distw distance_weight
The weight of evolutionary distance in functional orthology scoring (0.0 for m
aximum weight, 1.0 for no weight, optional, default 0.10)
[root@marmadais tmp]#
```


Galaxy, rôle et utilisation ?

Galaxy

Galaxy se place directement dans le JLFM2

```
simmons@earth:~/work/xterm/orig/xterm-XF86-4.3.0$ ls
256colres.h      error.h          misc.c           Tekparse.h      VTPrsTbl.c
256colres.pl    fontutils.c     mkdirs.sh       Tekproc.c       vtests
88colres.h      fontutils.h     os2main.c       TekPrsTbl.c     wwidth.c
88colres.pl     Imakefile       plink.sh        testcaps        xcharmouse.h
AAA_README_VMS.txt input.c         precompose.c    terminfo       xstrings.h
aclocal.m4      INSTALL        precompose.h    Tests           XTerm_ad
button.c        keysym2ucs.c   proto.h         testxmc.c       xterm_axp.opt
charclass.c     keysym2ucs.h   ptydata.c      trace.c         xtermcfg.hin
charclass.h     link_xp.com    README         util.c          XTerm-col.ad
charproc.c      charsets.c     main.c          README.os390   xterm_dat
charsets.c      config_guess   make.com        resize.c        xterm.h
config.sub      configure      Makefile        resize.man     xterm_io.h
configure.in    cursor.c       Makefile.in     screen.c       xterm_log.html
data.c          data.c         MANIFEST        scrollbar.c    xterm.man
data.h          data.h         menu.c          sininstall.sh  xutf8.c
doublechr.c     doublechr.c   menu.h          tabs.c          xutf8.h
[simmons@earth xterm-XF86-4.3.0]$
```

Communication



Communication

Galaxy

Galaxy se place directement dans le JLFM2

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', 'User', and a 'Using 0%' indicator. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: 'Get Data', 'Send Data', 'BASIC TOOLS', 'SEQUENCE ANALYSIS', 'NGS ANALYSIS', and 'SNP ANALYSIS'. The main content area features a banner for the 'South Green bioinformatics platform' with logos for CIRAD, IRD, Bioversity, INRA, and SupAgro. The banner text reads 'Welcome to GALAXY' and 'Our pre-configured and certified workflows'. Below this, a central graphic shows a Manhattan plot with vertical bars labeled 'NGS analyses', 'SNP calling', 'SNP analysis', and 'GWAS'. To the right of the plot, a box titled 'GWAS' describes the 'SNIPlay3 GWAS workflow' and includes an 'Access workflow' button. A dashed box at the bottom of the banner contains a note: 'In order to figure out which tools were made available by our team, please activate the "tool search" functionality from the Options drop-down and type "southgreen" in the lookup filter.' The right sidebar shows a 'History' section with a search bar and a list of recent datasets, including 'Copy of "MADS rice history" shared by baptiste.guitton@cirad.fr' and '76: Rappgreen statistics'.

Galaxy

Galaxy se place directement dans le JLFM2

The screenshot shows the Galaxy web interface. At the top, there's a navigation bar with 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. Below this is a header with logos for 'cirad', 'IRD', 'Bioversity', and 'INRA'. The main content area features the 'South Green bioinformatics platform' logo and a 'Welcome to GALAXY' message. A central banner highlights 'Our pre-configured and certified workflows' with a GWAS workflow card. The left sidebar lists various tool categories like 'Get Data', 'Text Manipulation', 'SEQUENCE ANALYSIS', and 'NGS ANALYSIS'. The right sidebar shows a list of shared items with details like 'Rapgreen statistics' and 'Reconciled Newick'. Three callout boxes are overlaid on the image: one on the left sidebar, one on the top right, and one on the central workflow banner.

Accès direct au cluster

Utilisable depuis n'importe quel poste connecté à internet

Centralisation et partage des démarches

Interface et compte utilisateur indépendants du poste client

Centralisation et partage des données

Galaxy - Vue générale

Galaxy

Analyze Data Workflow Shared Data Visualization Admin Help User Using 0%

Tools

Search tools

Gen Data
Send Data

BASIC TOOLS
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats

SEQUENCE ANALYSIS
Gene/Protein prediction
EMBOSS
Operate on Genomic Intervals
Fetch Sequences
Genomics
Fetch Alignments
Extract Features

NGS ANALYSIS
NGS: Quality Control
NGS: Mapping
NGS: GATK Tools
NGS: GATK2 Tools
NGS: SAM/BAM Manipulations
NGS: RNASeq
NGS: Assembly
NGS: Small RNAs

Bedtools
Picard Tools

SNP ANALYSIS

History

search datasets

Copy of 'MADS rice history' shared by baptiste.guitton@cirad.fr (active items only)
37 shown
9.45 MB

76: kaggreen statistics
75: Reconciled Newick
74: Output species
73: Output phyloxml
72: Newick
71: Pasted Entry
70: SouthGreen visualization on data 67, data 68, and data 58
69: Get alternative gene identifiers on data 66
68: Ideven : Identification of evolutive events based on syntenic studies on data 66
67: Differential expression on Genfam on data 66
66: Format Fasta Locus T on data 65
65: Format fasta header on data 64

South Green bioinformatics platform

Welcome to GALAXY

Our pre-configured and certified workflows

NGS analyses
SNP calling
SNP analysis
GWAS

GWAS

SNIPlay3 GWAS workflow: Tassel-based GWAS workflow (GLM model) including population structure and correction for structure (Dereeper et al, 2015)

Input: VCF + Phenotypic tabulated file

Access workflow

Structural variations
Chrom. reconstruction
Metagenomics

... at your disposal as part of the services provided by SouthGreen

In order to figure out which tools were made available by our team, please activate the "tool search" functionality from the Options drop-down and type "southgreen" in the lookup filter.

Boîte à outils

Données

Chaque programme peut être configuré précisément

Configuration d'un programme

The screenshot displays the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. A left sidebar lists various tool categories such as 'Tools', 'Get Data', 'Send Data', 'BASIC TOOLS', 'SEQUENCE ANALYSIS', 'Operate on Genomic Intervals', 'NGS ANALYSIS', and 'SNP ANALYSIS'. The main content area is titled 'PhyML, a ML tree builder (Galaxy Version 3.0)'. It features several configuration sections: 'Alignment in phylip format' (set to '76: Rappgreen statistics'), 'Data type' (set to 'Nucleic acids'), 'Evolution model' (set to 'HKY85'), 'Transition/transversion ratio' (set to 'e'), 'Discrete gamma model' (set to 'Use a gamma model'), 'Number of categories for the discrete gamma model' (set to '4'), 'Shape parameter of the gamma model' (set to 'e'), 'Branch support' (set to 'SH-like aLRT'), 'Proportion of invariant sites' (set to '0.0'), and 'Tree topology search operation' (set to 'NNI (Nearest Neighbor Interchange)'). A right sidebar shows a 'History' panel with a search bar and a list of recent jobs, including '76: Rappgreen statistics', '75: Reconciled Newick', '74: Output species', '73: Output phyloxml', '72: Newick', '71: Pasted Entry', '70: SouthGreen visualization on data 67, data 68, and data 58', '69: Get alternative gene identifiers on data 66', '68: IDeven - Identification of evolutive events based on syntenic studies on data 66', '67: Differential expression on Genfam on data 66', '66: Format Fasta Locus Tag on data 65', and '65: Format fasta header on data 64'.

Galaxy - Accès aux données

Les données peuvent être chargées depuis votre ordinateur local

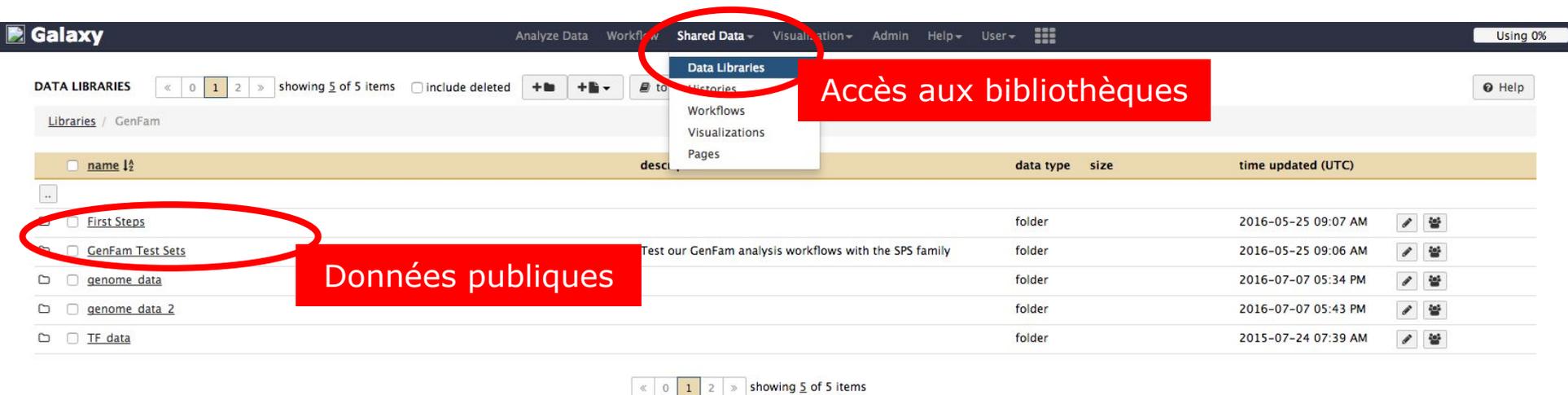
The screenshot shows the Galaxy web interface with a modal dialog box titled "Download from web or upload from disk". The dialog has two tabs: "Regular" (selected) and "Composite". Below the tabs is a large dashed box with the text "Drop files here". At the bottom of the dialog, there are two buttons: "Choose local file" and "Paste/Fetch data", both of which are circled in red. To the left of the dialog, the "Get Data" menu item in the Galaxy sidebar is also circled in red. Below the dialog, there are two red text boxes with white text: "Pour importer depuis votre ordinateur" and "Pour importer depuis une autre page web, ou copier-coller".

Pour importer depuis votre ordinateur

Pour importer depuis une autre page web, ou copier-coller

Galaxy - accès aux données

Les données peuvent être chargées depuis des bibliothèques partagées



The screenshot shows the Galaxy web interface. At the top, the 'Shared Data' menu is open, with 'Data Libraries' highlighted. A red box labeled 'Accès aux bibliothèques' points to this menu. Below the menu, a table lists data libraries. The 'First Steps' library is circled in red, with a red box labeled 'Données publiques' pointing to it. The table has columns for 'name', 'description', 'data type', 'size', and 'time updated (UTC)'. The 'name' column is sorted by name.

name	description	data type	size	time updated (UTC)
First Steps		folder		2016-05-25 09:07 AM
GenFam Test Sets	Test our GenFam analysis workflows with the SPS family	folder		2016-05-25 09:06 AM
genome_data		folder		2016-07-07 05:34 PM
genome_data_2		folder		2016-07-07 05:43 PM
TF_data		folder		2015-07-24 07:39 AM

Galaxy - Historiques des analyses

La notion d'historiques multiples est très importante pour gérer ses résultats

The screenshot displays the Galaxy interface with a 'History' sidebar on the left and a main content area. The 'History' sidebar includes a search bar, a list of datasets (e.g., 'Copy of 'MADS rice history' share by baptiste.guitton@cirad.fr'), and a 'HISTORY ACTIONS' menu. A red circle highlights the settings gear icon in the top right of the History sidebar. The 'HISTORY ACTIONS' menu includes options like 'Create New', 'Copy History', 'Share or Publish', 'Show Structure', 'Extract Workflow', 'Delete', 'Delete Permanently', 'DATASET ACTIONS', 'COPY', 'Dataset Security', 'Resume Paused Jobs', 'Collapse Expanded Datasets', 'Unhide Hidden Datasets', 'Delete Hidden Datasets', 'Purge Deleted Datasets', 'DOWNLOADS', and 'Export Tool Citations'. A red box at the bottom left of the History sidebar contains the text 'Historique courant'.

The main content area is divided into two sections: 'Saved Histories' and 'Published Histories'. Both sections have a search bar and an 'Advanced Search' link. The 'Saved Histories' section contains a table with columns: Name, Datasets, Tags, Sharing, Size on Disk, Created, and Last Updated. The table lists several histories, including 'Copy of 'MADS rice history' shared by baptiste.guitton@cirad.fr (active items only)', 'bordeaux_phylo_simple', 'proteique', 'formation_phylo_nucleique_supagro_2016', 'formation_phylo_proteique_supagro2016', and 'Demo galaxy'. A red box at the bottom right of the Saved Histories table contains the text 'Listes des historiques personnels, et publiés'. The 'Published Histories' section contains a table with columns: Name, Annotation, and Owner. The table lists several published histories, including 'Scaffremodler : Structural Variation', 'SNIPlay', 'Genome Improvement : 1. Refinement of scaffold miss-assemblies boundaries', 'Genome Improvement : 3. Performing scaffold fusions', 'Genome Improvement : 4. Performing scaffold junctions', 'Scaffhunter : Markers linkage visualization', and 'Genome Improvement : 2. Identification of scaffold fusions and junctions to perform on the newly split scaffolds'. The 'Owner' column lists 'droc', 'dereeper', and 'fallahmanel'.

Galaxy - Historiques des analyses

HISTORY LISTS

Saved Histories

Histories Shared with Me

HISTORY ACTIONS

Create New

Copy History

Share or Publish

Show Structure

Extract Workflow

Delete

Delete Permanently

DATASET ACTIONS

Copy Datasets

Dataset Security

Resume Paused Jobs

Collapse Expanded Datasets

Unhide Hidden Datasets

Delete Hidden Datasets

Purge Deleted Datasets

DOWNLOADS

Export Tool Citations

Export History to File

OTHER ACTIONS

Import from File

Saved Histories

search for names and tags

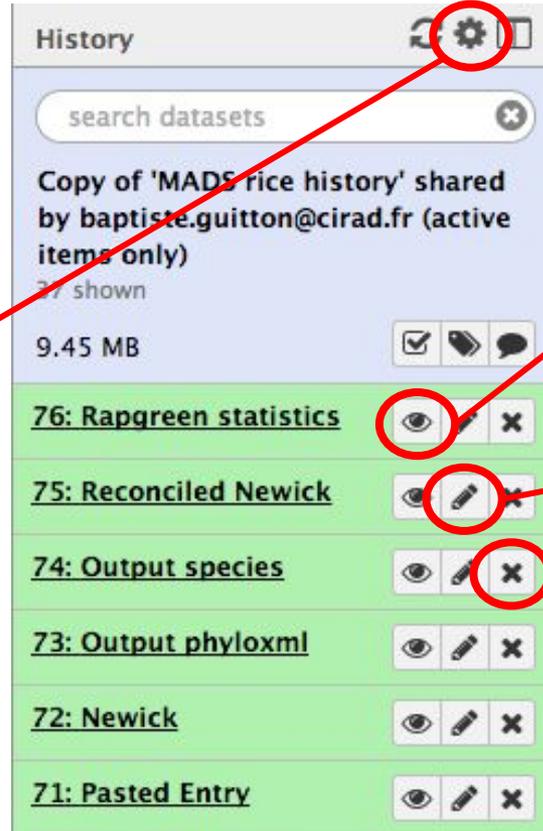
Advanced Search

Panneau de gestion

<input type="checkbox"/>	Name	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated
<input type="checkbox"/>	Unnamed history		0 Tags		0 bytes	Sep 23, 2016	Sep 23, 2016
<input type="checkbox"/>	Copy of 'MADS rice history' shared by baptiste.guitton@cirad.fr (active items only)	53	10	0 Tags	9.4 MB	Jun 20, 2016	Jun 20, 2016
<input type="checkbox"/>	Unnamed history		0 Tags		0 bytes	Jun 20, 2016	Jun 20, 2016
<input type="checkbox"/>	bordeaux_phylo_simple	15	0 Tags		2.2 MB	May 24, 2016	May 25, 2016
<input type="checkbox"/>	proteique	23	2	0 Tags	260.9 KB	Feb 18, 2016	Feb 19, 2016
<input type="checkbox"/>	formation_phylo_nucleique_supagro_2016	10	0 Tags		1.1 MB	Feb 17, 2016	Feb 18, 2016
<input type="checkbox"/>	formation_phylo_proteique_supagro2016	20	0 Tags		807.0 KB	Feb 18, 2016	Feb 18, 2016
<input type="checkbox"/>	Demo galaxy	8	0 Tags		9.3 KB	Jul 23, 2015	Feb 15, 2016

For 0 selected histories:

Galaxy - Historique des analyses



Visualiser

Éditer les
méta-données

Suppression
temporaire

La notion d'historiques multiples est très importante pour gérer ses données et résultats

Galaxy - Workflows

Un workflow est un enchaînement d'outils paramétrés, ils sont partageables et publiables

Galaxy Analyze Data **Workflow** Shared Data Visualization Admin Help User

Workflow Canvas | imported: GenFam : Phylogeny

Canvas d'édition

Paramétrage

Tools

search tools

Inputs

Get Data
Send Data

BASIC TOOLS

Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats

SEQUENCE ANALYSIS

Gene/Protein prediction
EMBOSS
Operate on Genomic Intervals
Fetch Sequences
Genomics
Fetch Alignments
Extract Features

NGS ANALYSIS

NGS: Quality Control
NGS: Mapping
NGS: GATK Tools
NGS: GATK2 Tools
NGS: SAM/BAM Manipulations
NGS: RNASeq
NGS: Assembly
NGS: Small RNAs
Bedtools
Picard Tools

SNP ANALYSIS

NGS: SNP Calling

Format fasta header
Convert these sequences
output (fasta)

MAFFT
Source file
output (fasta)
output_tree (txt)

Fasta2Phylip
Source file
output (txt)

PhyML
Alignment in phylip format
output_tree (nhx)
output_stats (txt)

Gblocks
Source file
output_alignment (fasta)
output_stats (txt)

RAP-Green
Gene tree newick source file
Species tree phyloxml source file
output_gene (txt)
output_gene_phyloxml (txt)
output_species (txt)
output_reconciled (txt)
output_stats (txt)

Format Fasta Locus Tag
Fasta file
output (fasta)

Input dataset
output

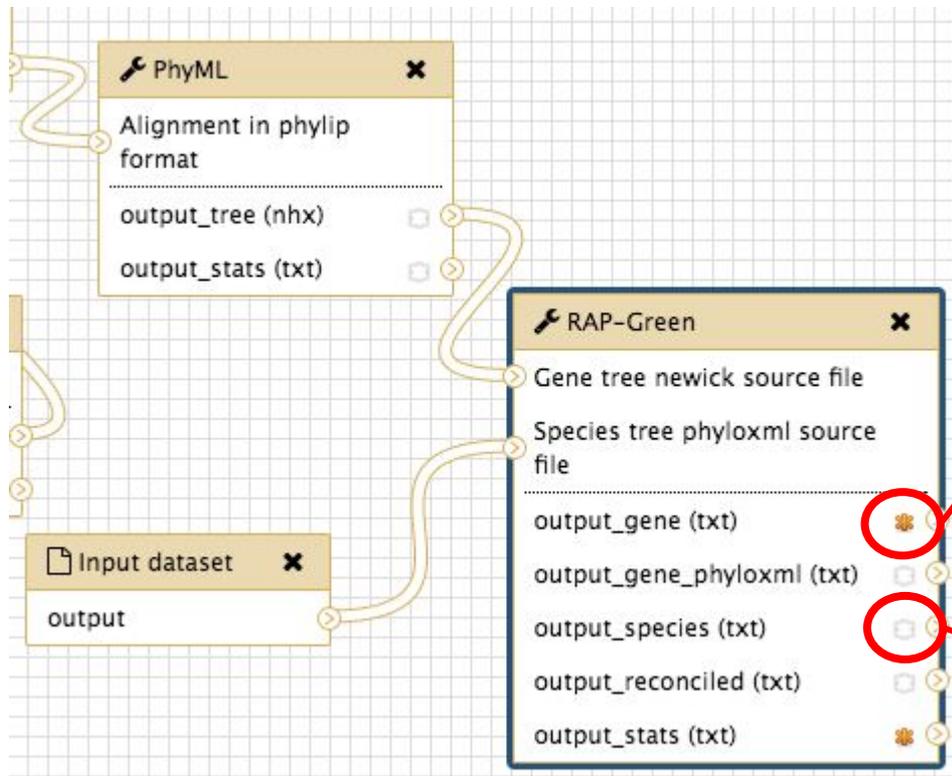
Input dataset
output

Configuration Panel (RAP-Green):

- Source file: Data input 'input' (txt), Fasta format
- Data type: Protein
- Minimum number of sequences for a conserved position: 51 (Percentage, must be superior to 50)
- Minimum number of Sequences for a flank position: 52 (Percentage, must be superior to the minimum number of sequences for a conserved position)
- Maximum number Of contiguous nonconserved positions: 3 (Any integer)
- Minimum length of a block: 3 (Any integer equal or bigger than 2)
- Allowed gap positions: With half
- Annotation / Notes

Galaxy - Workflows

Lors de la construction d'un workflow vous pouvez décider des fichiers qui seront visibles dans l'historique après l'analyse



Le fichier apparaîtra dans l'historique après analyse

Le fichier sera masqué dans l'historique après analyse



Si rien n'est coché, tout est coché !

Galaxy au sein de Southgreen

Galaxy, sa place dans la plateforme

Reproductibilité des analyses

Données à analyser

The screenshot shows the Galaxy web interface. At the top, there are navigation tabs: 'Analyze Data', 'Workflow', 'Shared Data', 'Admin', 'Help', and 'User'. Below the navigation is a 'Tools' sidebar with categories like 'search tools', 'Convert Formats', 'NGS: Mapping', etc. The main content area displays a 'Welcome to GALAXY' message with instructions on how to use the 'tool' search functionality. To the right, a 'History' panel shows a list of recent jobs, including 'PhyML on data_18', 'Fasta2Phylo on data_16', and 'MAFFT on data_14'.

Données analysées et explorables

The screenshot shows the 'Home' page of the South Green bioinformatics platform. It features a search bar, a navigation menu with options like 'Computer center', 'Databases', and 'Tools', and a grid of featured services including OryGenesDB, Oryza Tag Line, EUROGEN, GNPannot, SAT, EST-TEA, TropiGENE, SNIPlay, Haplophyle, G-DIVERSITY, and Galaxy. The page also includes a 'Login/Register' section and a list of 'Announcements', 'Search', 'Team', 'Publications', 'Seminar', 'Trainings', 'Contact', and 'Documentation'.

Utilisateur averti

Utilisateur expert

```
simmons@earth:~/work/xterm/orig/xterm-XF86-4.3.0
[simmons@earth xterm-XF86-4.3.0]$ ls
256colres.h          misc.c               Tekparse.h          VTPrsTbl.c
error.h              mkdirs.sh            Tekproc.c           wtfasta
256colres.pl         fontutils.c          os2main.c           wwidth.c
88colres.h           fontutils.h          link.sh              wwidth.h
88colres.pl         Imakefile             precompose.c        xcharmouse.h
AAA_README_VMS.txt  input.c              precompose.h        xstrings.c
aclocal.m4           INSTALL              print.c             xstrings.h
button.c            install.sh            proto.h              XTerm.ad
charclass.c         keysym2ucs.c         ptydata.c          testxmc.c
charclass.h         keysym2ucs.h         pttyx.h             trace.c
charproc.c          link_axp.com         README              util.c
charsets.c          main.c               README.os390        uxterm
config.guess        main.h               resize.c            UXTerm.ad
config.sub          make.com             resize.man          version.h
configure           Makefile             screen.c           vms.c
configure.in        Makefile.in          scrollbar.c        vms.h
cursor.c            data.c               sininstall.sh       tabs.c
data.h              data.h               mininstall.sh       VTparse.def
doublechr.c         doublechr.c          misc.c              VTparse.h
```



Galaxy, démonstration