

A - Training on Galaxy: Metabarcoding

March 2020 - Nancy

GALAXY Practice

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*THESE AUTHORS HAVE CONTRIBUTED EQUALLY TO THE PRESENT WORK.

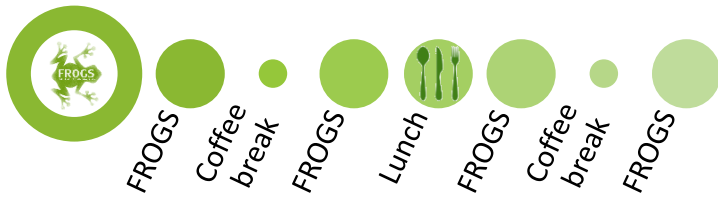
Chitchat time!

- What is your computer skills level?
- Have you ever heard of or used Galaxy?

Feedback on metagenomics:

- What are your needs in “metagenomics”?
- 454 / MiSeq/ HiSeq?
- 16S/ITS/ other ?
- Your background ?

Tuesday



9.15 am to 5.15 pm

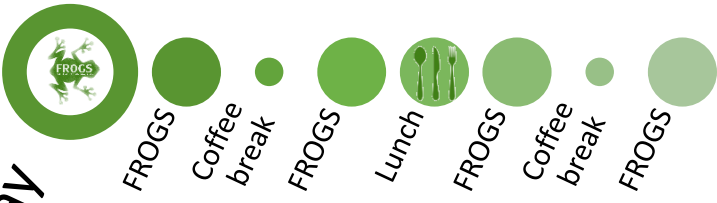


2 short coffee breaks morning and afternoon

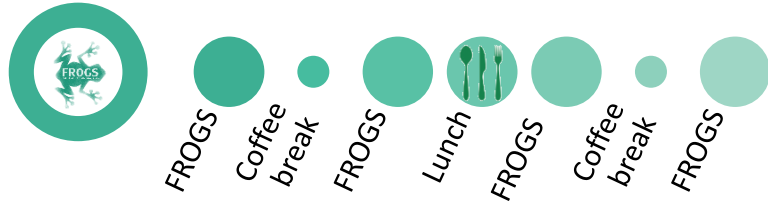


Lunch
12.30 to 2.00 pm

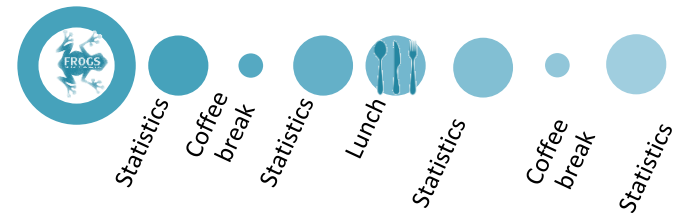
Wednesday



Thursday



Friday



Objectives of the 1st part

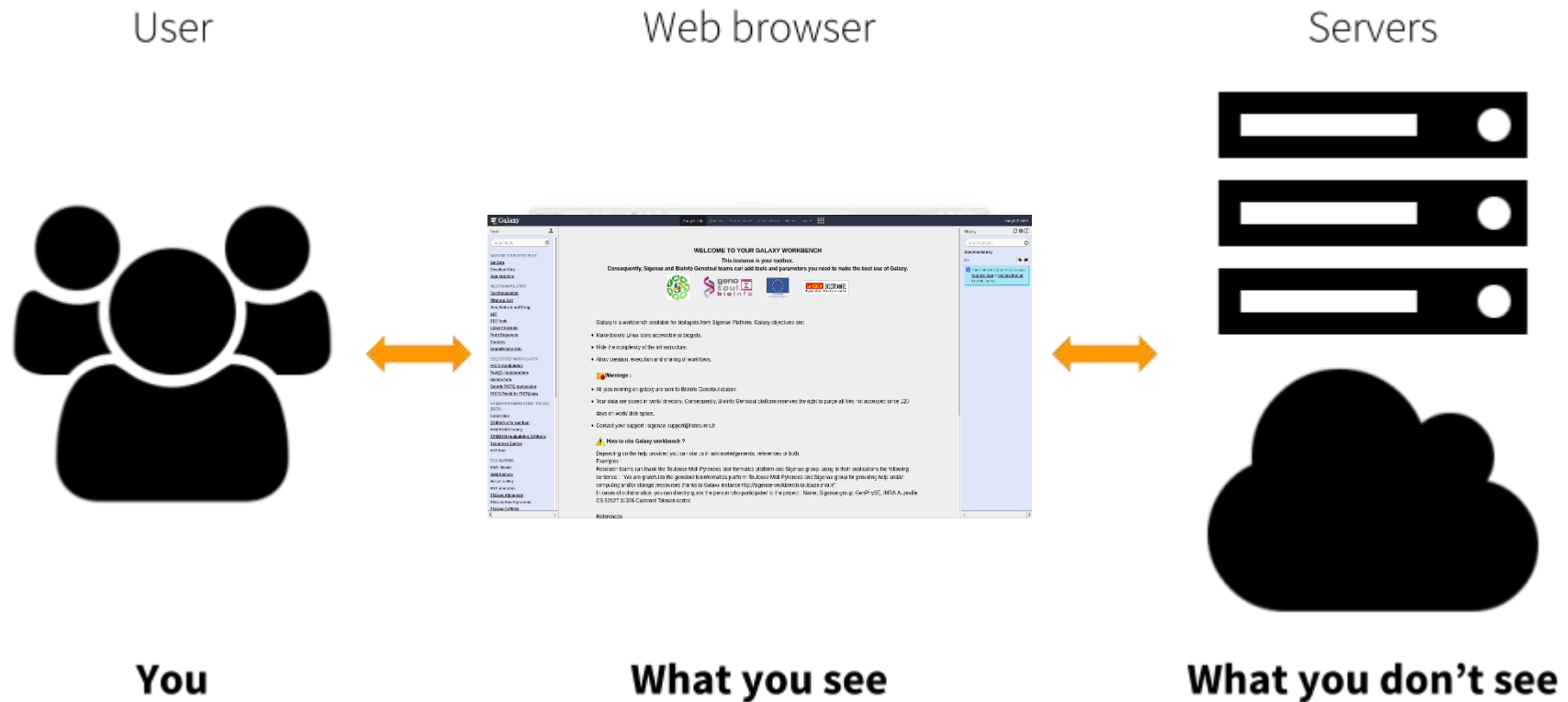
- Learn the basics of Galaxy
- Being independent when using it
- Prepare the datasets for FROGS formation

What is Galaxy?

Galaxy software framework

- Galaxy is an overlay that allows researchers without computer expertise to perform computational analyses online, automate them and share the results easily.
- Developed by the Galaxy Team Project.
- Relies on a computational infrastructure (Server).
- Open source

Galaxy software framework



<https://galaxyproject.org/tutorials/g101/>

Where to use Galaxy?

- Galaxy software can be installed and run on powerful server farms (Cluster) or on your individual PC.

- Genotoul Bioinfo



- Cluster: Many computers tightly connected that work together
- High performance computer:
 - More than 5000 cores
 - 34 TB of RAM
 - More than 1 Peta Byte (1024 TB) of hard drive



Where to use Galaxy?

- The Toulouse Galaxy platform is <http://sigenae-workbench.toulouse.inra.fr/galaxy/>

⚠ The different platforms of Galaxy are not connected together

- Galaxy is installed on many clusters across the world.
- Some tools are in our Galaxy platform but not in other platforms.
- Your data is not shared with other Galaxy platforms than ours.

Exemple of 2 INRAE Galaxy platforms

Galaxy / Migale Analyze Data Workflow Shared Data Visualization Help User

Tools

Migale Tools
[Get Data](#)
[Send Data](#)
[Lift-Over](#)
[Gene Annotation](#)
[Gene Prediction](#)
[Text Manipulation](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[GFFtools](#)
[Convert Formats](#)
[Extract Features](#)
[Fetch Sequences](#)
[Fetch Alignments](#)
[Get Genomic Scores](#)
[Statistics](#)
[Graph/Display Data](#)
[Phenotype Association](#)
[Sequence Alignment/Pairwise Alignment](#)
[Metagenomic analyses](#)
[Metagenomics FROGS](#)
[Metagenomics Qiime](#)
[Metagenomics Mothur](#)
[FASTA manipulation](#)
[NGS: QC and manipulation](#)
[NGS: Assembly](#)
[NGS: Mapping](#)
[NGS: RNA Analysis](#)
[NGS: SAM Tools](#)
[NGS: Peak Calling](#)
[SNP/WGA: Data: Filters](#)
[Variant Analysis](#)
[NGS: Picard](#)
[NGS: Variant analysis](#)

Workflows
▪ [All workflows](#)

✓ Bienvenue sur le portail Galaxy de la plateforme Migale. Pour tous renseignements, demandes ou remarques, veuillez contacter galaxy-help@jouy.inra.fr

migale
Plateforme de BioInformatique - INRA Jouy en Josas

Galaxy est une plateforme qui propose une « constellation » d'outils pour analyser, manipuler et visualiser des données génomiques, sans avoir besoin de connaissance en programmation. Elle est développée par The Center for Comparative Genomics and Bioinformatics. L'utilisateur peut réaliser quatre grands types d'opérations :

- **manipulation de fichiers** : ajout ou suppression de colonnes, trier les fichiers, concaténer plusieurs fichiers, comparaison de listes, ...
- **opérations sur les données** : sommer, moyenner, soustraire, calculer la couverture d'une région déterminée, ...
- **analyse de séquences** : calculer des corrélations, utiliser des outils d'EMBOSS, aligner les données de séquençage, ...
- **visualisation des données** : afficher des alignements multiples, générer des graphiques, ...

Contact : galaxy-help@jouy.inra.fr

Pour toutes demandes d'intégration de nouvel outil au sein du portail, veuillez remplir le [formulaire](#) mis à votre disposition sur le [site web de la plateforme Migale](#).

Une [Foire Aux Questions](#) autour de Galaxy a été mise en place sur le [site web de la plateforme Migale](#).

Si vous utilisez le portail Galaxy de la plateforme Migale pour effectuer vos analyses, merci de [citer Galaxy](#) ET de [remercier la plateforme dans les acknowledgements](#).

INRA
SCIENCE & IMPACT

This project is supported in part by NSF, NHGRI, and the Huck Institutes of the Life Sciences.

Exemple of 2 INRAE Galaxy platforms

Galaxy | Analyze Data | Workflow | Shared Data | Visualization | Help | User | Using 0%

Tools | search tools

MANAGE YOUR DATA FILES
[Get Data](#)
[Download Data](#)
[Jobs statistics](#)

FILES MANIPULATION
[Text Manipulation](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[GFF](#)
[BED Tools](#)
[Convert Formats](#)
[Fetch Sequences](#)
[Statistics](#)
[Graph/Display Data](#)

SEQUENCES MANIPULATION
[FASTA manipulation](#)
[FastQC: fastq/sam/bam](#)
[Illumina fastq](#)
[Generic FASTQ manipulation](#)
[FASTX-Toolkit for FASTQ data](#)

SAMBAM MANIPULATION : PICARD (BETA)
[Conversion](#)
[QC/Metrics for sam/bam](#)
[BAM/SAM Cleaning](#)
[SAMBAM manipulation: SAMtools](#)
[Sequences Queries](#)
[VCF Tools](#)

SGS MAPPING
[BWA - Bowtie](#)
[Indel Analysis](#)
[Variant calling](#)
[SNP annotation](#)
[RNAseq Alignment](#)
[RNAseq Raw Expression](#)
[RNAseq Cufflinks](#)

Genotoul Bioinfo | European Union | LA REGION OCCITANIE Pyrénées-Méditerranée

Welcome on Galaxy Sigene / BioInfo Genotoul.
Contact your support : support.sigene@inra.fr

Ready to use Workflows

- 1/ [FROGS - Find, Rapidly, Otus with Galaxy Solution](#)
- 2/ [Tax4Fun workflow](#)
- 3/ [Function Table for Tax4Fun matrix workflow](#)

Galaxy News

- 1/ How to use [datasets collections](#) ?
- 2/ How to [upload several files in Galaxy](#) ?
- 3/ New tools : [Tax4Fun \(manual\)](#), [VIP \(manual\)](#), [Salmon](#), [multiQC](#).
- 4/ Tools availables for [virologie analyses](#)
- 5/ [Virology tools](#)
- 6/ How to use [Function Table tool](#) ?
- 7/ How to [export](#) and [import](#) your histories ?

E-learning

<https://inra.classilio.com/Login>

2 e-learning availables : Galaxy initiation and Quality sequences analysis

Training resources : [BioInfo Genotoul / Sigene](#)

History | search datasets

Data Collection
3 shown
33 b

- 3: [seq1.fasta](#)
- 2: [seq2.fasta](#)
- 1: [seq3.fasta](#)

Your Turn!

CONNECT TO OUR GALAXY WORKBENCH

Exercise

During this formation, we will use a remote computer.

Connect to a distant computer by clicking on the remote desktop connection icon in the task bar.



Ask trainers for the address and password.

**All your data will be
erased at the end of the
week of the remote
computer**


Exercise

During this formation if you have a personal account, use it.

This account will save all the work done during this week and your future work.

If you don't have a personal account ask us for a temporary account.


You can request a personal account later on : <http://bioinfo.genotoul.fr/index.php/ask-for/create-an-account/>



All your data will be
erased at the end of the
week on a temporary
account

Exercise

Our Galaxy platform is: <http://sigenae-workbench.toulouse.inra.fr/galaxy/>



Before starting, check if your browser is not already connected to a Galaxy account. If this is the case, log out or use a private browser window!
Risk of data duplication

Exercise

Our Galaxy platform is: <http://sigenae-workbench.toulouse.inra.fr/galaxy/>

Be careful, to fully login you must enter your credentials twice:

- The first time in this pop-up window:



Authentication requise

 Le site <http://galaxy-workbench.toulouse.inra.fr> demande un nom d'utilisateur et un mot de passe. Le site indique : « Please enter your Genotoul LDAP password »

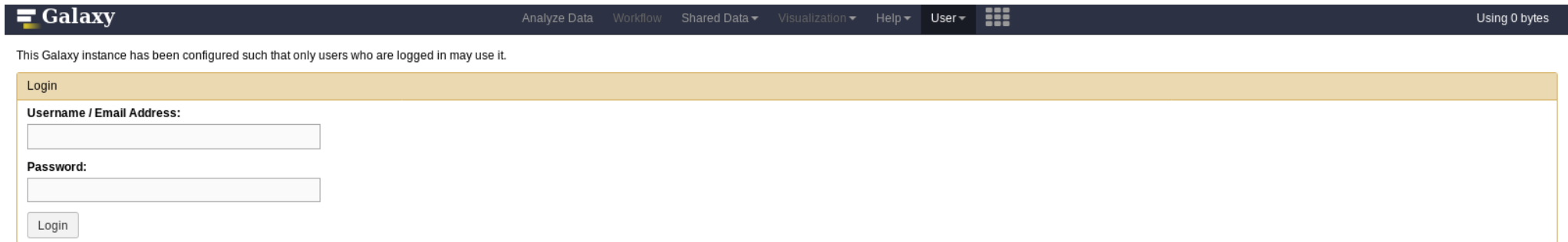
Utilisateur :

Mot de passe :

Annuler OK

Exercise

- And a second time, in the browser:



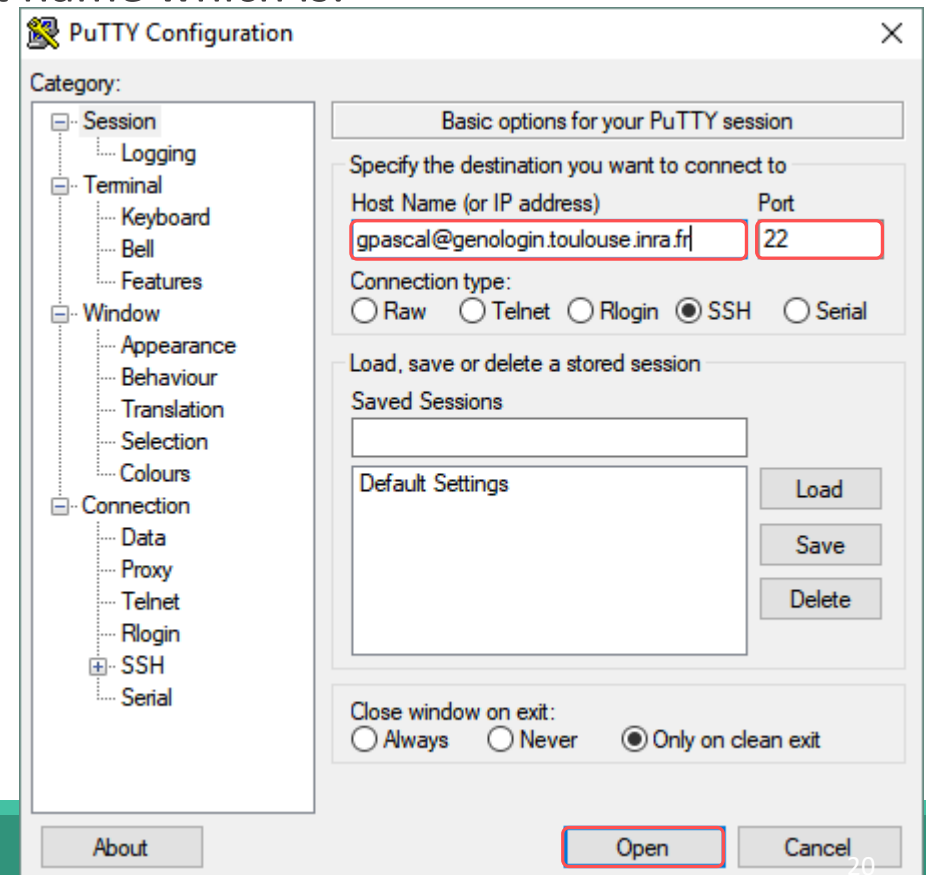
The screenshot shows the Galaxy web interface. At the top, there is a dark navigation bar with the Galaxy logo on the left and several menu items: "Analyze Data", "Workflow", "Shared Data", "Visualization", "Help", and "User". On the far right of the navigation bar, it says "Using 0 bytes". Below the navigation bar, a message states: "This Galaxy instance has been configured such that only users who are logged in may use it." Below this message is a light-colored box containing a login form. The form has a title "Login" and two input fields: "Username / Email Address:" and "Password:". A "Login" button is located at the bottom left of the form.

Change your password

- In order to change your password, you need to download PuTTY: <http://www.putty.org/>
- PuTTY is a terminal emulator, it allows to connect directly to the server in command line.
- You can not change your password via the Galaxy's interface for the moment.

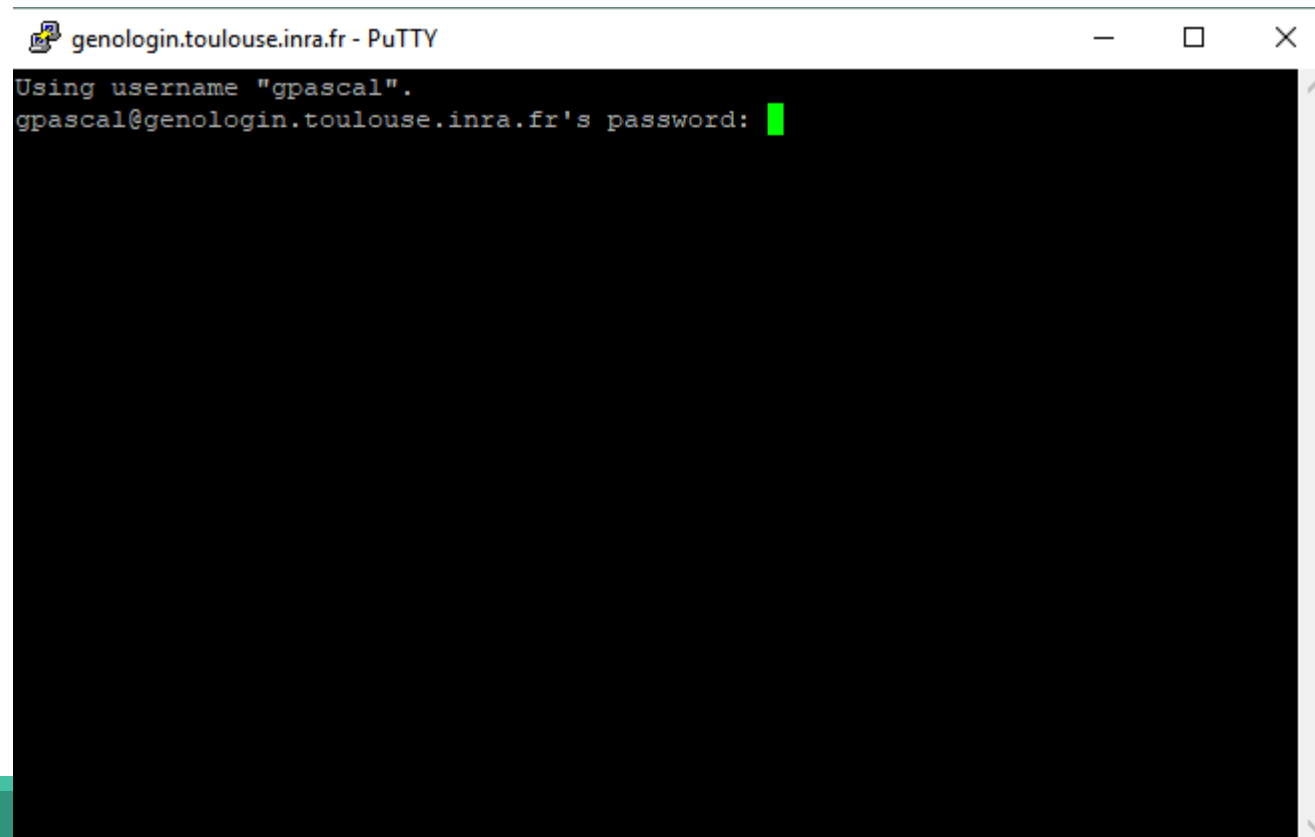
Change your password

- Launch PuTTY.
- In the following window, you must enter your host name which is:
YourGenotoulName@genologin.toulouse.inra.fr
- The connection type must be SSH.
- Click on « Open » .



Change your password

- A new window appear, click on « Yes ».
- In the following window, enter your password and hit « Enter ».



The image shows a PuTTY terminal window titled "genologin.toulouse.inra.fr - PuTTY". The terminal output is as follows:

```
Using username "gpascal".
gpascal@genologin.toulouse.inra.fr's password: █
```

The terminal has a black background with white text. A green cursor is positioned at the end of the password prompt line. The window title bar includes standard minimize, maximize, and close buttons.

Change your password

- Type « passwd » and hit « Enter ».



```
genologin.toulouse.inra.fr - PuTTY
e cluster).
Pour obtenir plus de memoire, veuillez consulter la FAQ de notre site web (cf +
bas)

=====
Informations concernant le quota de temps de calcul
=====

Il existe un quota de temps de calcul annuel de 100.000H pour les academiques (5
00H pour les entreprises privees).
Au dela il faut renseigner le formulaire de demande de ressources exceptionnelle
s sur notre site web.

Vous pouvez verifier votre quota de calcul avec la commande: squota_cpu

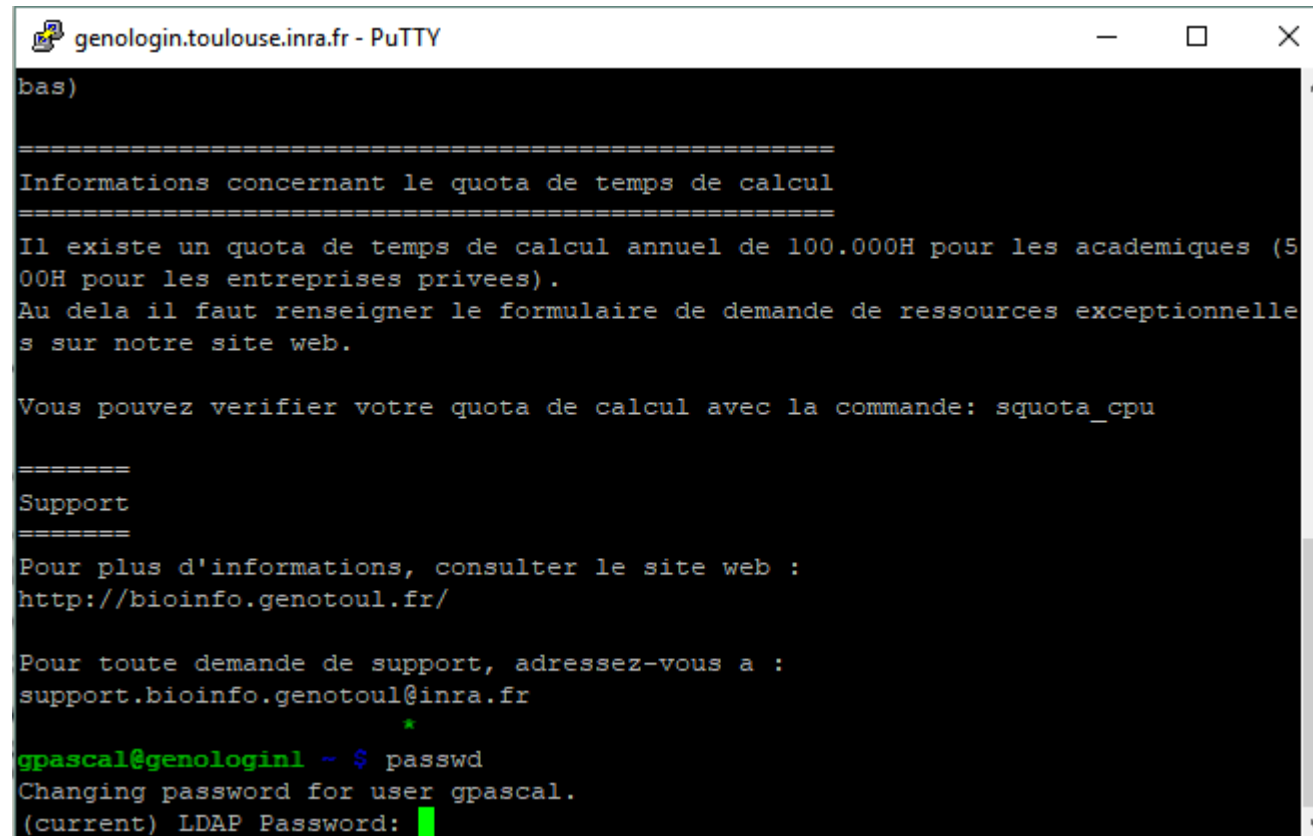
=====
Support
=====

Pour plus d'informations, consulter le site web :
http://bioinfo.genotoul.fr/

Pour toute demande de support, adressez-vous a :
support.bioinfo.genotoul@inra.fr
*
gpascal@genologin1 ~ $ passwd
```

Change your password

- Enter your current password and hit « Enter ».



```
genologin.toulouse.inra.fr - PuTTY
bas)

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Informations concernant le quota de temps de calcul
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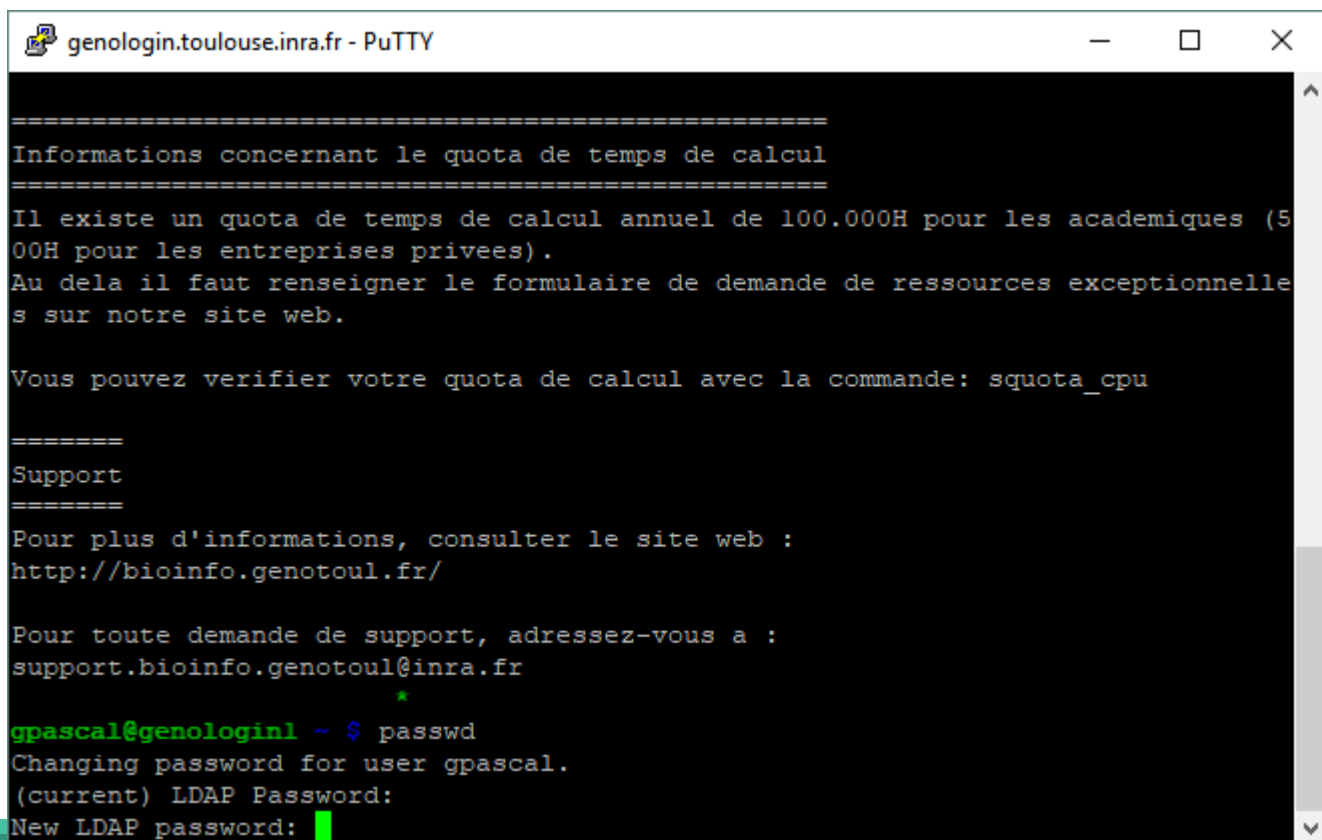
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http://bioinfo.genotoul.fr/

Pour toute demande de support, adressez-vous a :
support.bioinfo.genotoul@inra.fr
*
gpascal@genologin1 ~ $ passwd
Changing password for user gpascal.
(current) LDAP Password: █
```

Change your password

- Enter your new password (with an upper case, a number and a special character in it) and hit « Enter ».



```
genologin.toulouse.inra.fr - PuTTY
=====
Informations concernant le quota de temps de calcul
=====
Il existe un quota de temps de calcul annuel de 100.000H pour les academiques (5
00H pour les entreprises privees).
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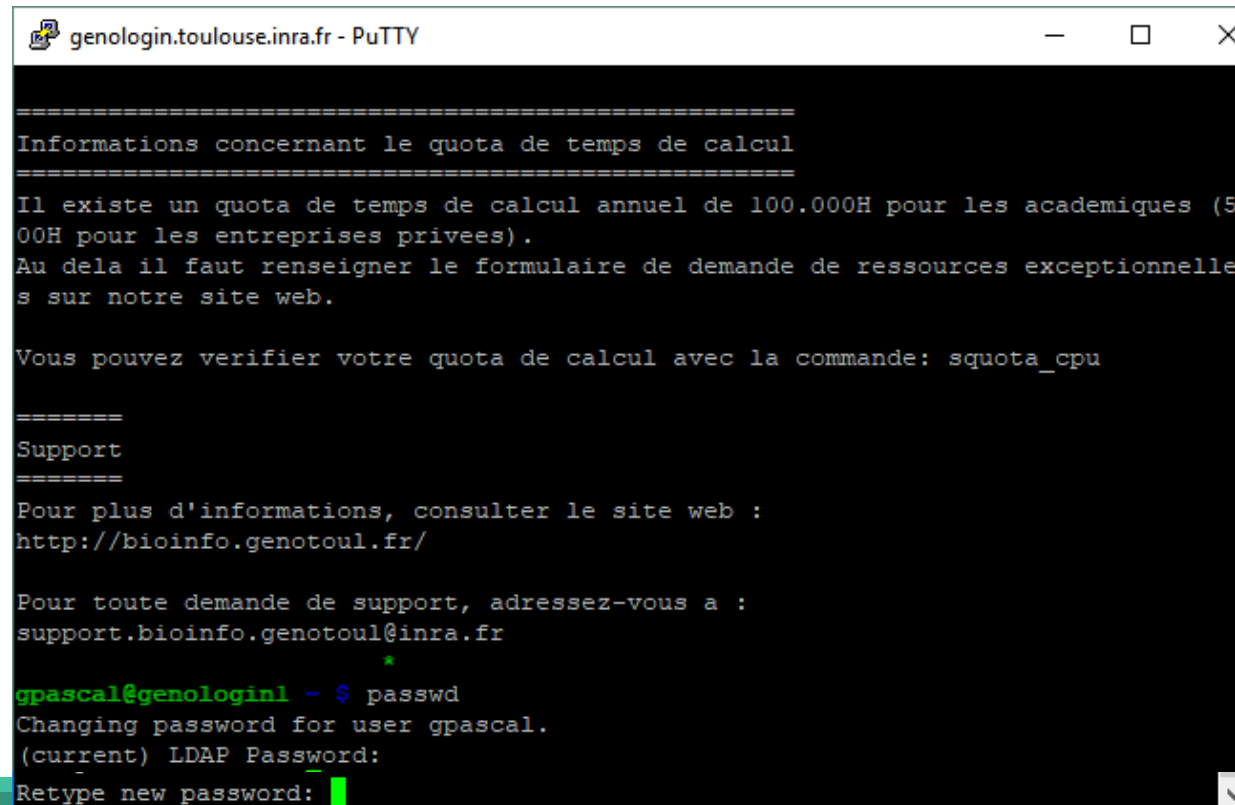
Vous pouvez verifier votre quota de calcul avec la commande: squota_cpu

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Support
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Pour plus d'informations, consulter le site web :
http://bioinfo.genotoul.fr/

Pour toute demande de support, adressez-vous a :
support.bioinfo.genotoul@inra.fr
*
gpascal@genologin1 ~ $ passwd
Changing password for user gpascal.
(current) LDAP Password:
New LDAP password: █
```


Change your password

- Enter a second time your new password and hit « Enter ». You have changed your Genotoul password, you can close PuTTY.



```
genologin.toulouse.inra.fr - PuTTY
=====
Informations concernant le quota de temps de calcul
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Il existe un quota de temps de calcul annuel de 100.000H pour les academiques (5
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Pour toute demande de support, adressez-vous a :
support.bioinfo.genotoul@inra.fr

gpascal@genologin1 ~ $ passwd
Changing password for user gpascal.
(current) LDAP Password:
Retype new password: █
```

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

Tools

search tools

MANAGE YOUR DATA FILES

[Get Data](#)

[Download Data](#)

[Jobs statistics](#)

FILES MANIPULATION

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[GFF](#)

[BED Tools](#)

[Convert Formats](#)

[Fetch Sequences](#)

Statistics

[Graphical Analysis](#)

SEQUENCES MANIPULATION

[FASTA manipulation](#)

[FastQC: fastq/sam/bam](#)

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[Sequences Queries](#)

[VCF Tools](#)

SGS MAPPING

[BWA - Bowtie](#)

[Indel Analysis](#)


[Variant calling](#)

[SNP annotation](#)

[RNAseq Alignment](#)

[RNAseq Raw Expression](#)

[RNAseq Cufflinks](#)



RESULTS VISUALISATION —AND— TOOL PARAMETER WINDOW

How to cite Galaxy workbench ?


Depending on the help provided you can cite us in acknowledgements, references or both.

Examples :

Research teams can thank the Toulouse Midi-Pyrenees bioinformatics platform and Sigeneae group, using in their publications the following sentence : "We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigeneae group for providing help and/or computing and/or storage resources thanks to Galaxy Instance <http://sigeneae-workbench.toulouse.inra.fr>".


In cases of collaboration, you can directly quote the person who participated to the project : Name, Sigeneae group, GenPhySE, INRA Auzeville CS 52627 31326 Castanet Tolosan cedex.

References
X. SIGENAE [<http://www.sigeneae.org/>]




Ready to use Workflows

- 1/ FROGS - Find, Rapidly, Otus with Galaxy Solution
- 2/ Tax4Fun workflow
- 3/ Function Table for Tax4Fun matrix workflow



Galaxy News

- 1/ How to use [datasets collections](#) ?
- 2/ How to [upload several files in Galaxy](#) ?
- 3/ New tools : Tax4Fun ([manual](#)), VIP ([manual](#)), Salmon, multiQC.
- 4/ Tools availables for [virologie analyses](#)
- 5/ Virology tools
- 6/ How to use [Function Table tool](#) ?



E-learning

<https://inra.classilio.com/Login>

2 e-learning availables : Galaxy initiation and Quality sequences analysis

History

search datasets

Data Collection

3 shown

33 b

3: seq1.fasta

2: seq2.fasta

1: seq3.fasta

DATASETS HISTORY

AVAILABLE TOOLS

Vocabulary of Galaxy

- **Tools:**

- A tool has a function which is explained when you click on it.
- Each Galaxy platform has its own tools.

- **Dataset:**

- A dataset is a file, uploaded to Galaxy by you or produced by a tool.
- Be careful: a dataset has a datatype.

- **History:**

- A tool generates datasets and these datasets are stored in the current history.
- Everything is permanently saved.
- If you log off your computer or browser, it's ok, everything will keep running and be saved!

Your Turn!

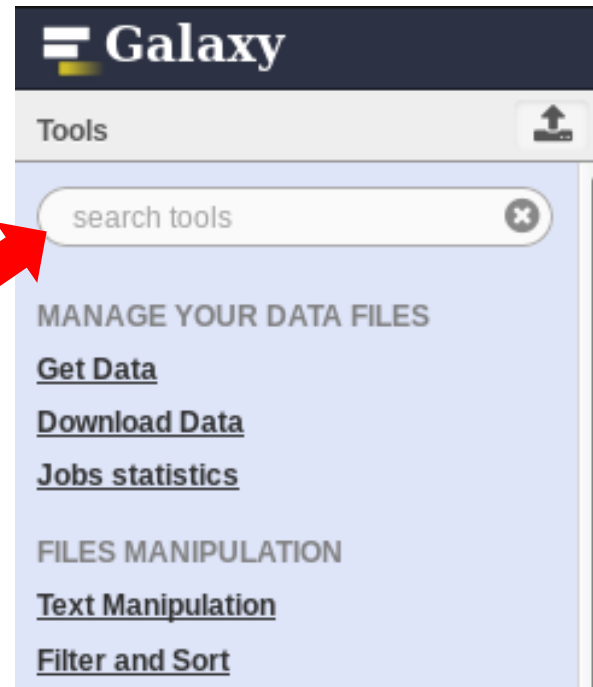
DISCOVER GALAXY

Exercise

1. Visit the Galaxy Platform.
2. Look at the tool list.
3. Display only FROGS tools.
4. Display all tools concerning fastq files.

Exercise

Search a tool by name.



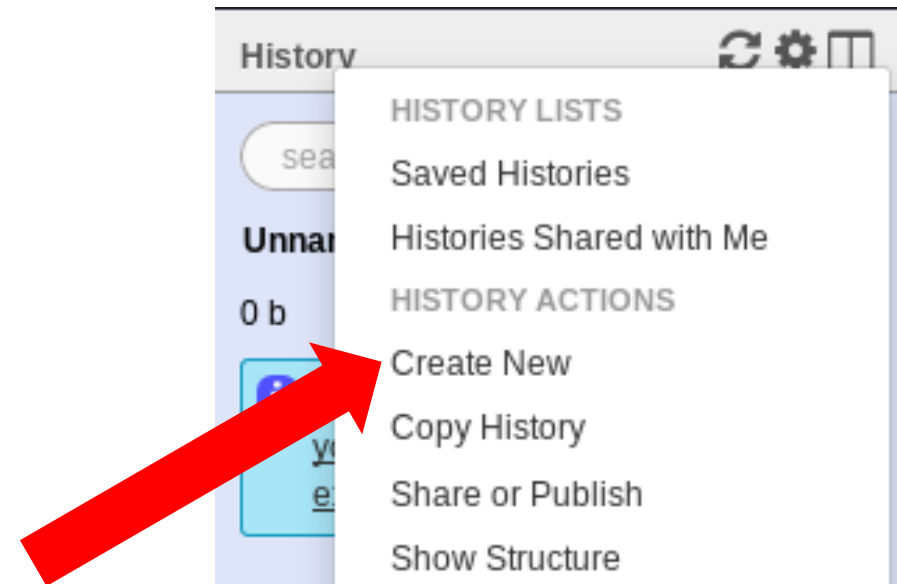
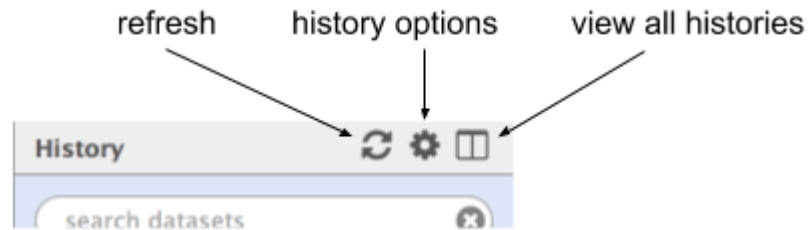
Manipulate Histories

Your Turn!

CREATE THE 4 HISTORIES NEEDED FOR THE FROGS FORMATION

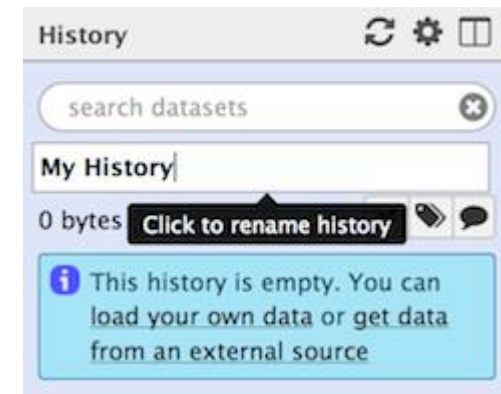
To create a new history:

- Click on the wheel.
- Click on « create new ».



To rename a history:

- Click on the history name (at the top).
- Enter « **multiplex** ».
- Hit « **Enter** » to validate.



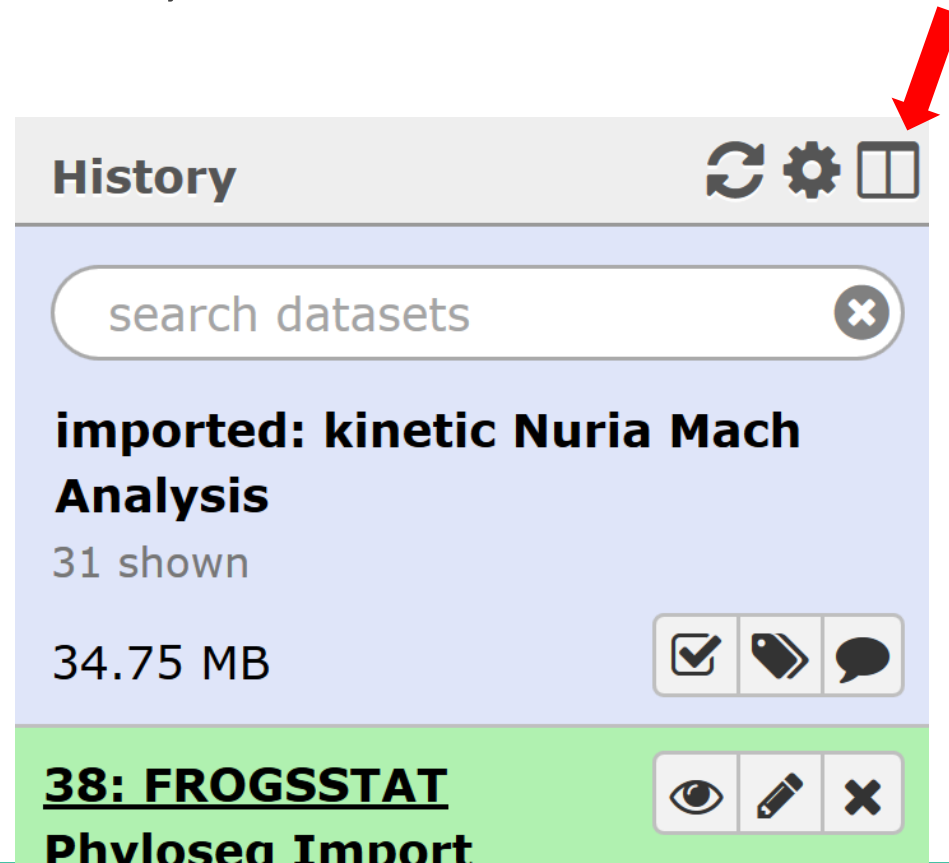
Don't use special characters or accents!

Exercise

- Create histories named:
 - ITS
 - merged
 - temp
- Switch to the history named « multiplex » as current history.
- Go back to the main interface.

How to list all histories?

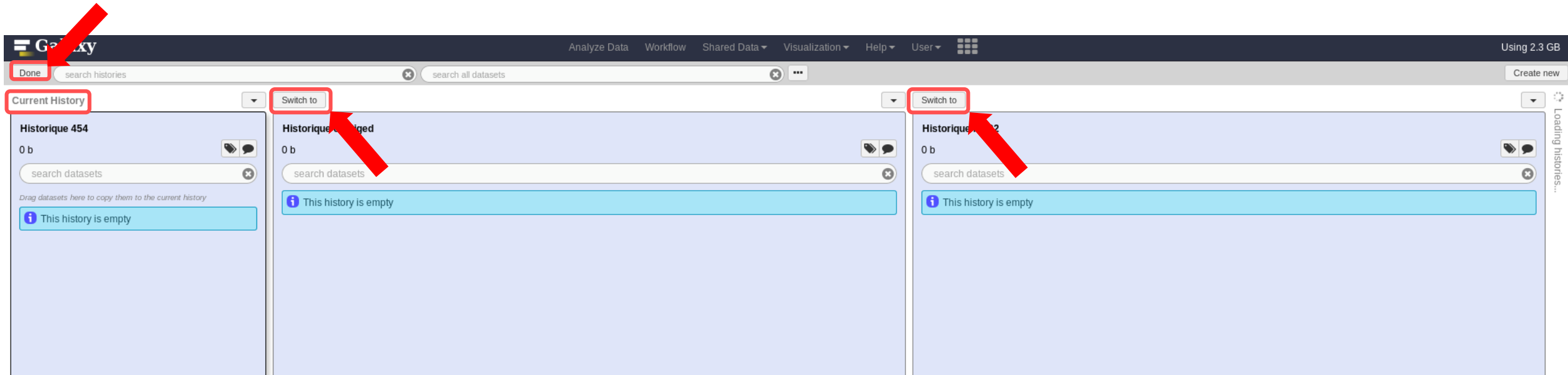
- To view all histories, click on this icon.



Explore the « View all histories » section

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Help, and User. Below the navigation bar, there are search bars for 'search histories' and 'search all datasets', along with a 'Create new' button. The main content area shows three history panels. The first panel is titled 'imported: kinetic Nuria Mach Analysis' and contains 31 datasets with a size of 34.75 MB. The second panel is titled 'Test Ta Thi's tools' and contains 73 datasets with a size of 233.76 MB. The third panel is titled 'Copy of 'full ph maria.bernard'' and contains 14 datasets with a size of 11.32 MB. A red box highlights a dropdown arrow in the first panel, which is connected by a red line to a context menu. The context menu has three options: 'Copy', 'Delete', and 'Purge'. Below the history panels, there are tool outputs, including '76: FROGS Pre-process: report.html' and '14: FROGS Phv'.

Switch current history



- Switch to the history named « multiplex » as current history.
- Click on “Done” to go back to the main interface.

Data import

How to import your data to Galaxy

- Several ways to upload your data to Galaxy:

- From your computer



- By URL



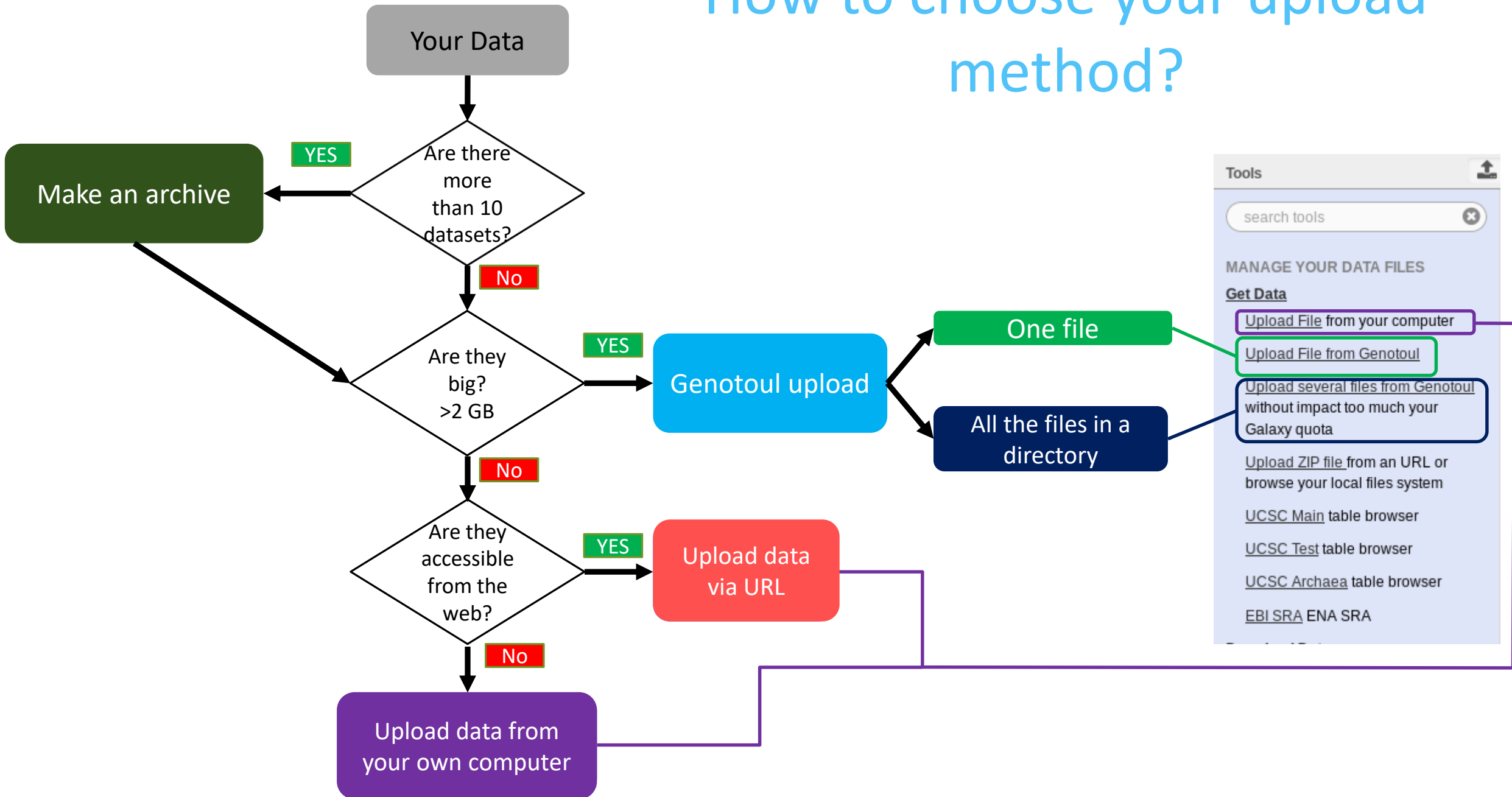
- From Genotoul Bioinfo clusters



- Shared by other users of Galaxy

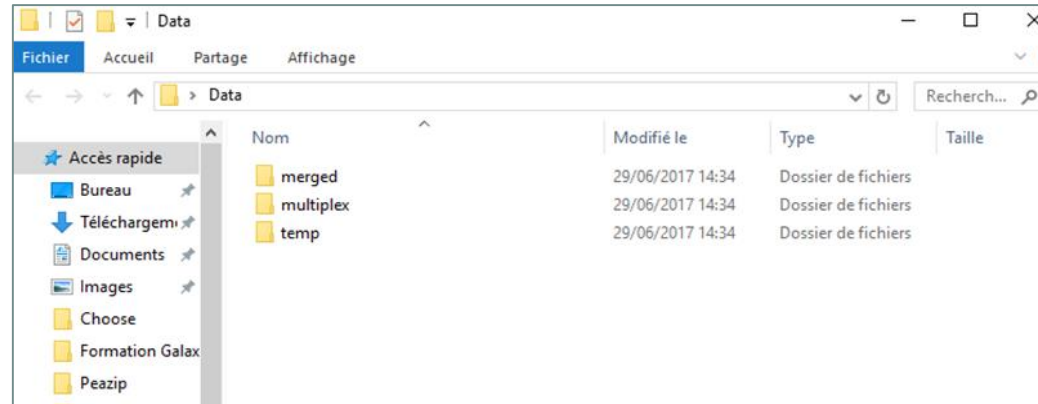


How to choose your upload method?



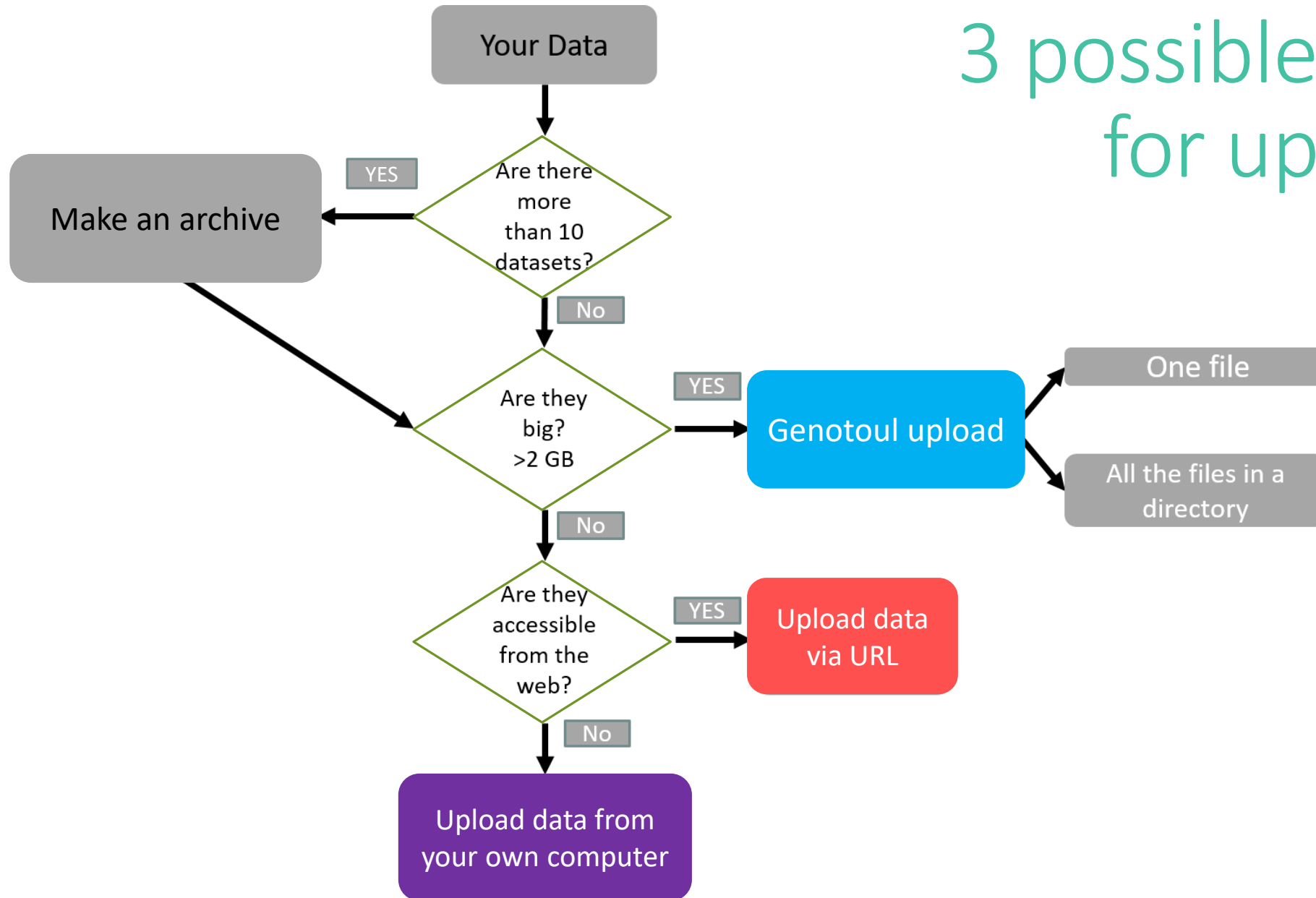
Formation data

- All the formation data are in the Data folder on your desktop.

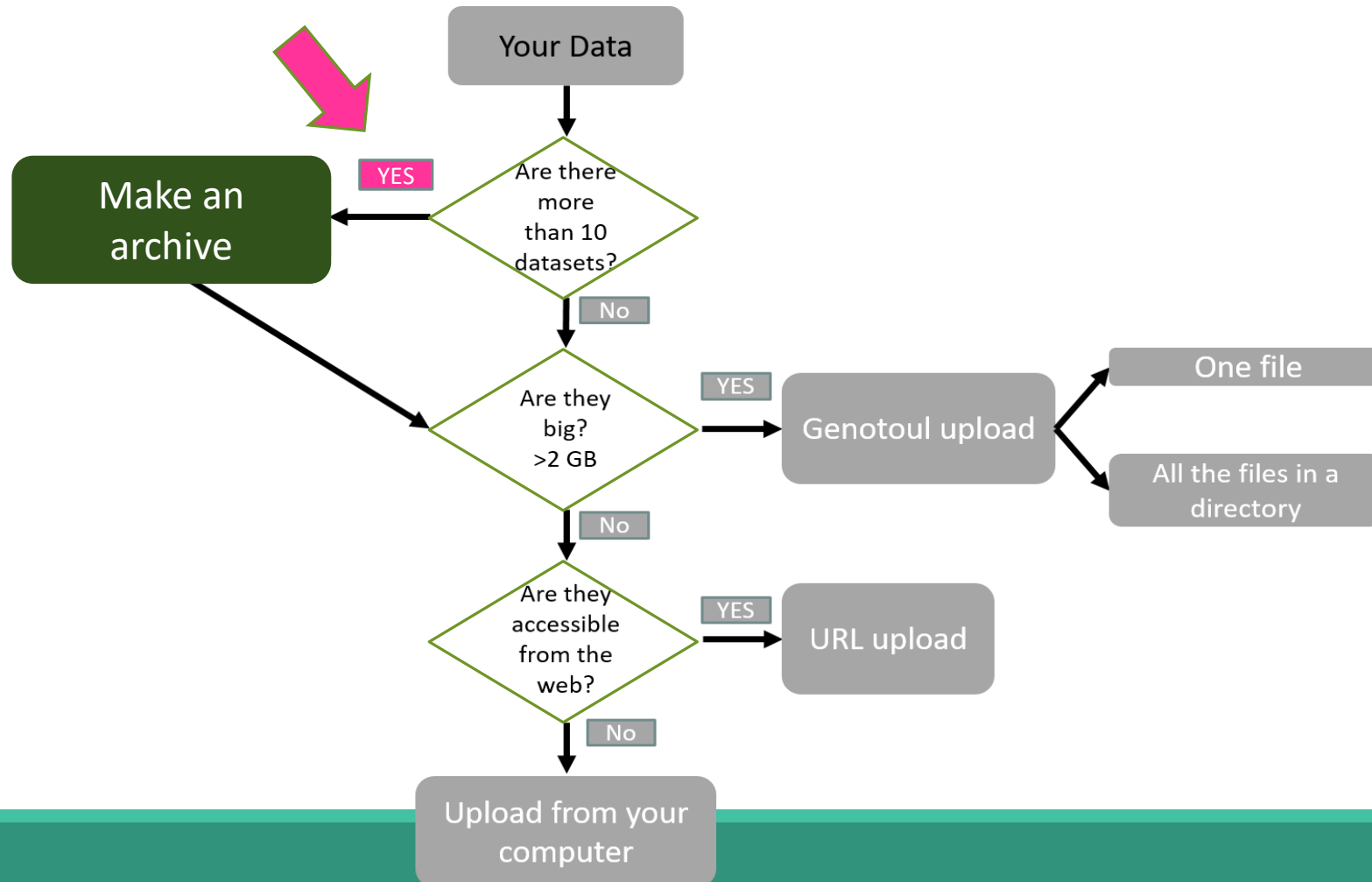


- If you don't have this directory on your desktop, ask us.
- You can find all the formation data online on:
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/Dataset/

3 possible modes for uploading

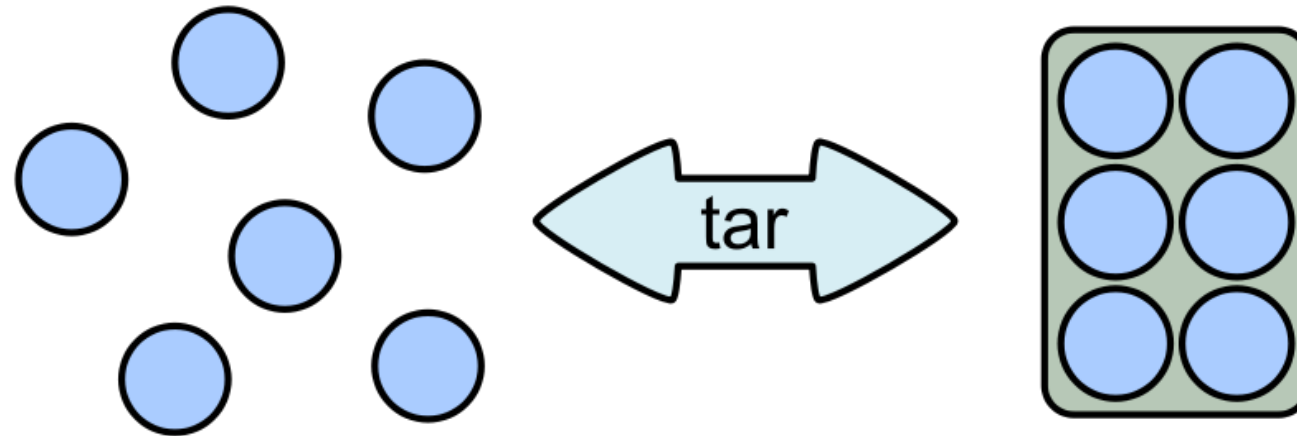


Above all: create an archive



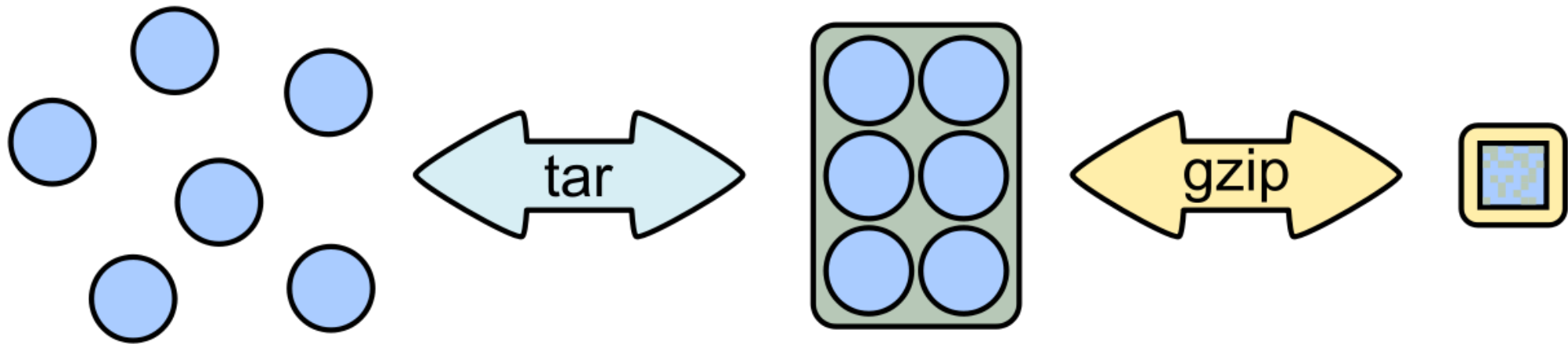
Create a Tar file

- Uploading multiple local files is time consuming.
- Solution: put all your files in an archive!
- What is a tar file?



Create a Tar.gz

- Moreover, we can compress the archive to free up space.



Your Turn!

CREATE AN ARCHIVE WITH THE FILES IN MERGED

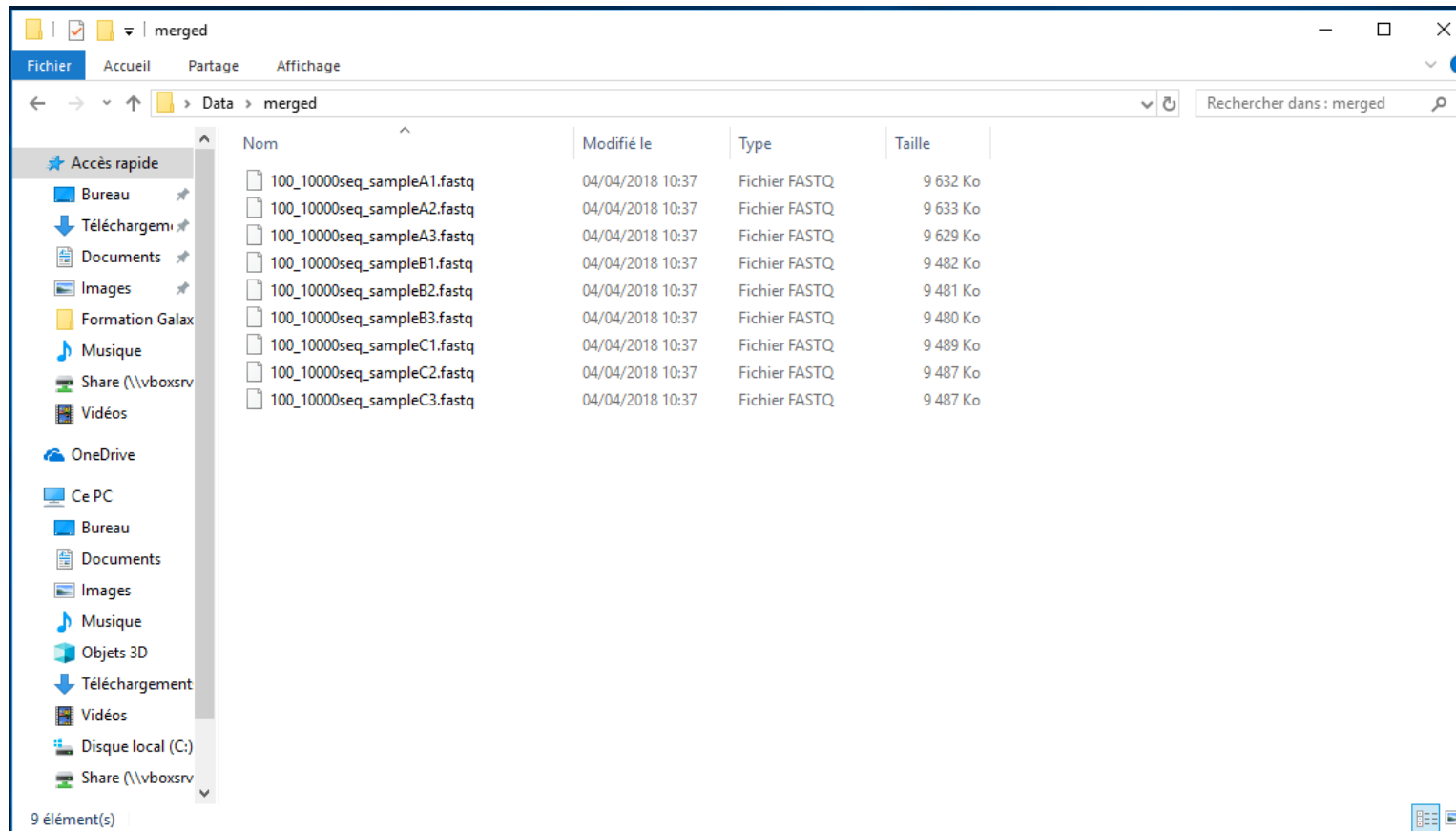
7-Zip

- 7-Zip is a software called a file archiver.
- Can archive and compress files.
- Open source
- At the lab, you could download it at: <http://www.7-zip.org/>



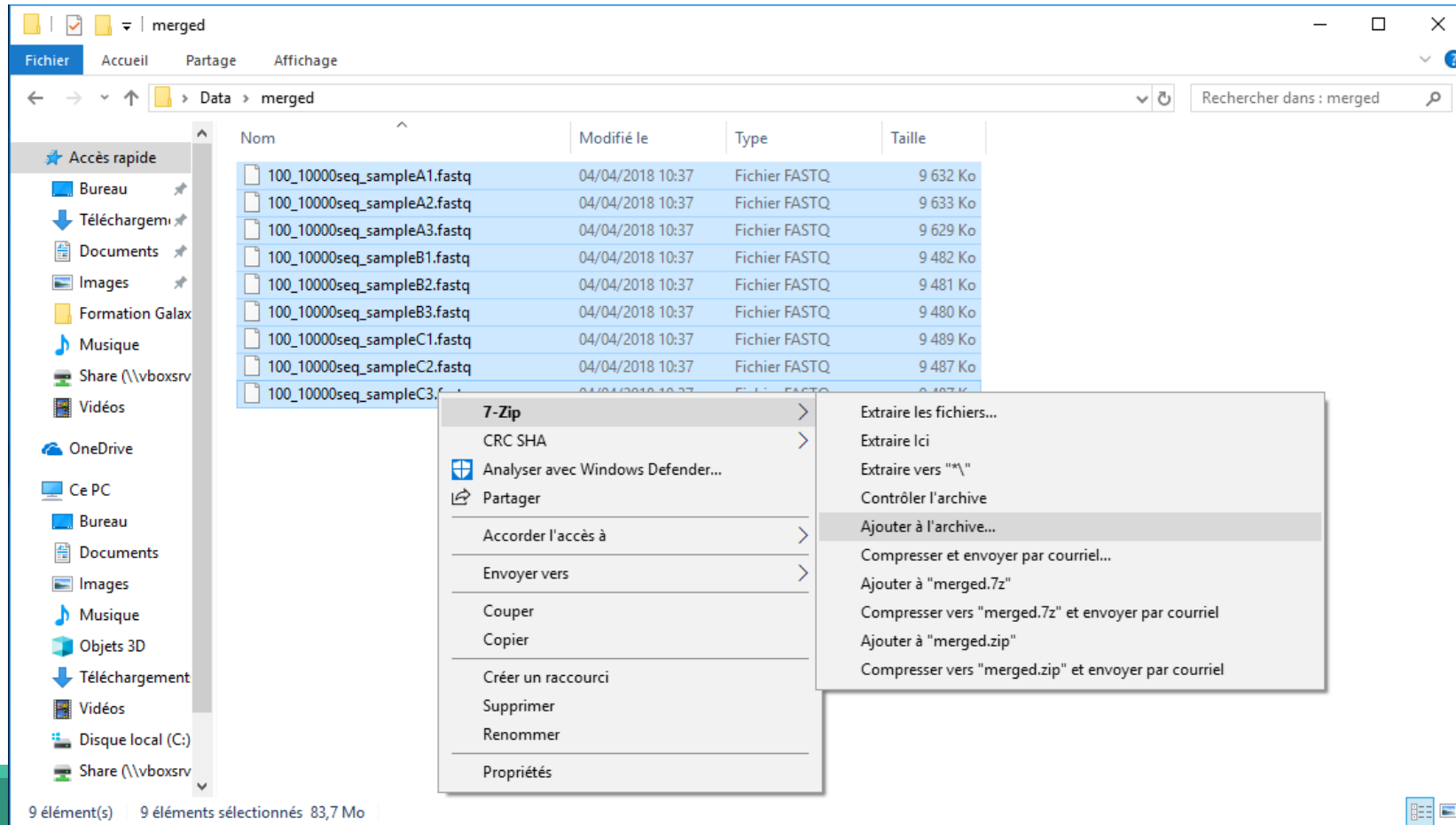
Create a Tar file with 7-Zip

- Browse into the Data directory and next into the merged directory.



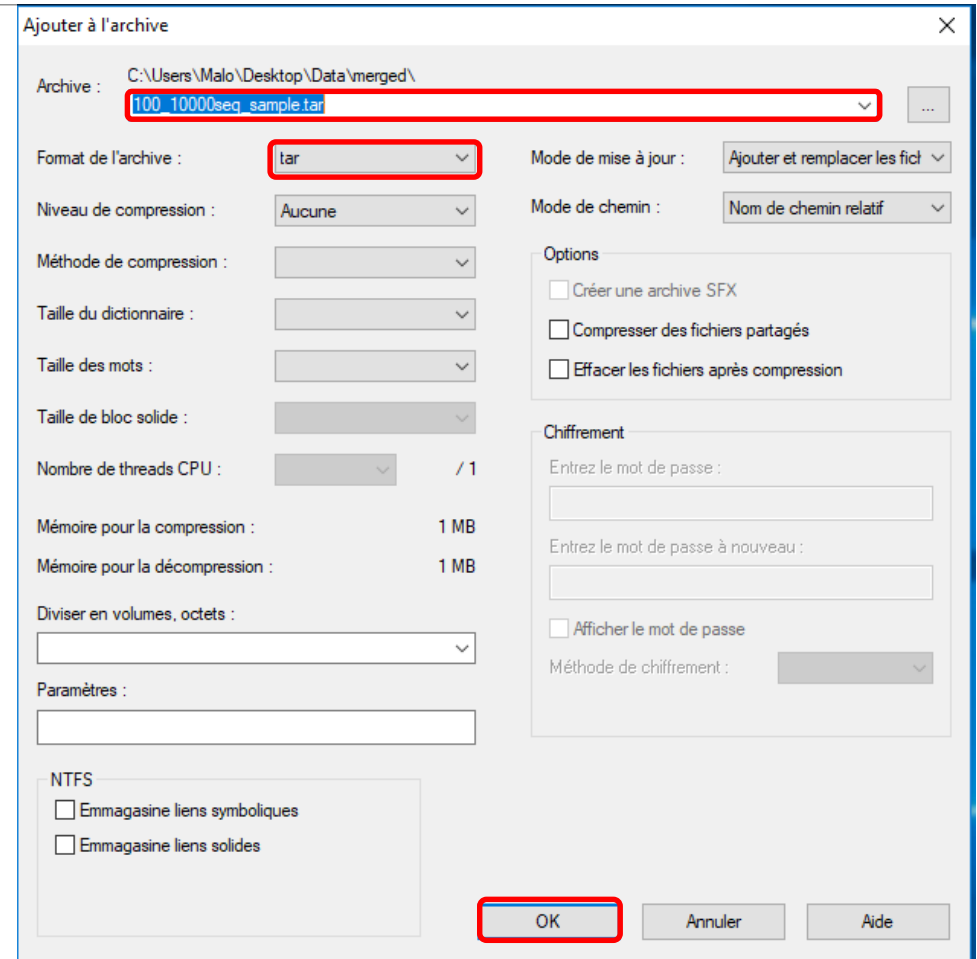
Create a Tar file with 7-Zip

- Select all files and right click on it > 7-Zip > Add to archive . . .



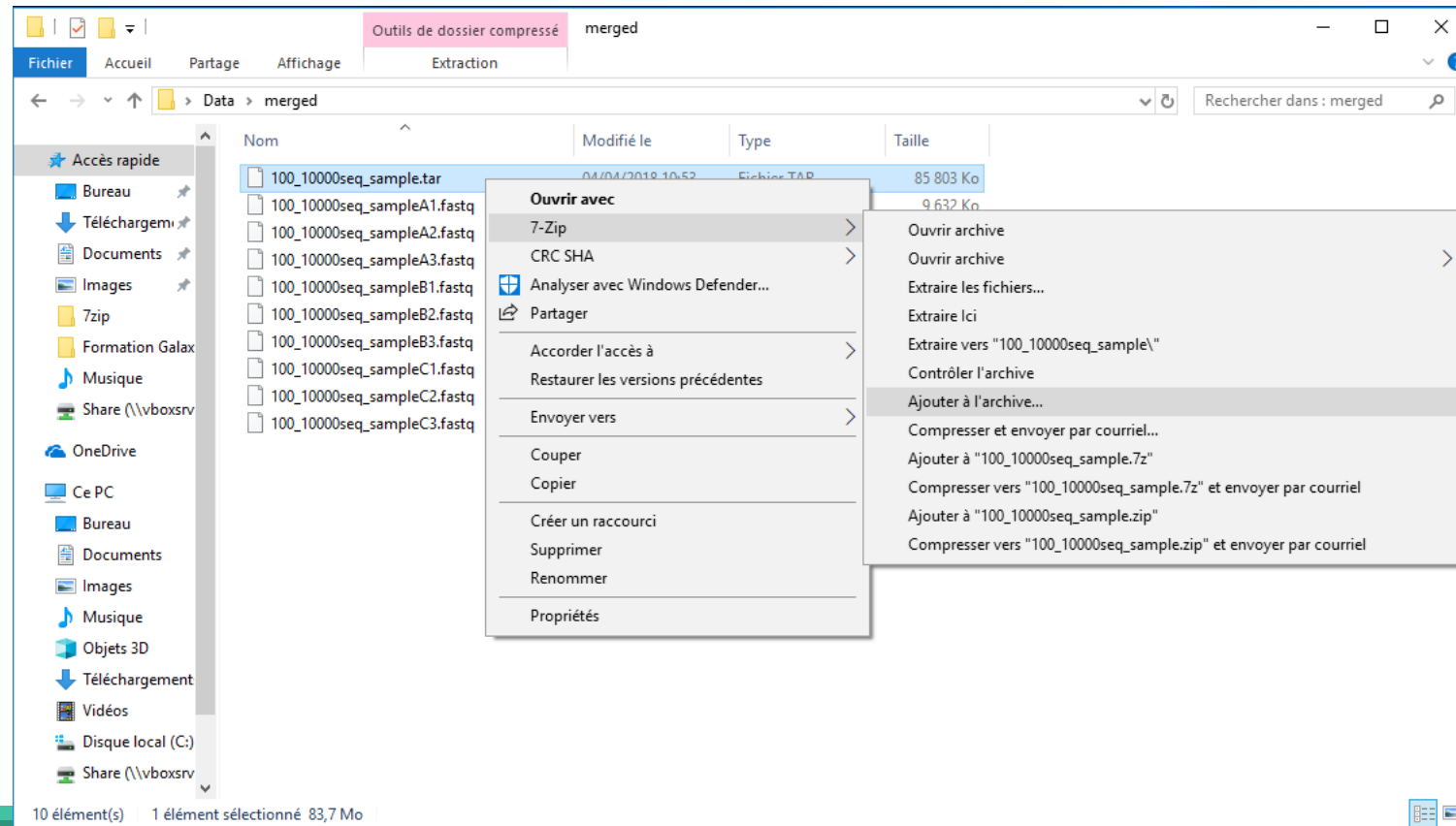
Create a Tar file with 7-Zip

- Change the name of the archive to:
« 100_10000seq_sample.tar »
- Choose « tar » as archive format .
- Click on OK .



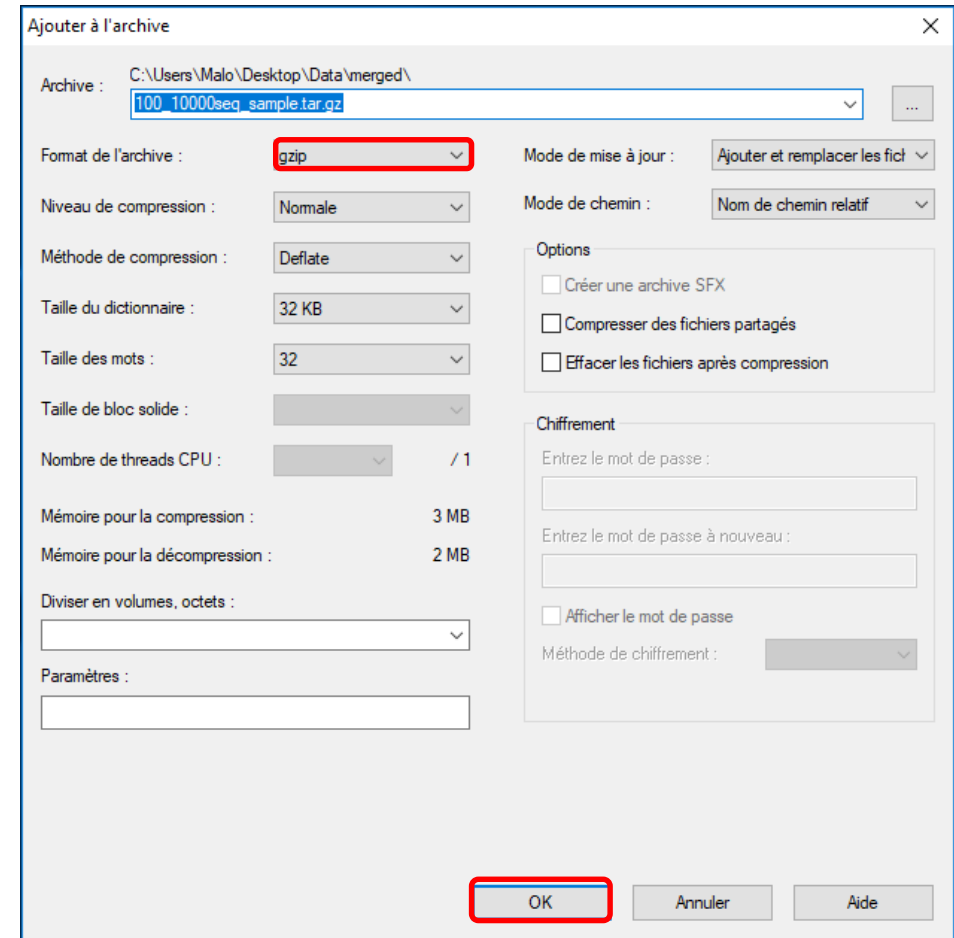
Create a Tar file with 7-Zip

- Select the newly created archive and right click on it > 7-Zip > Add to archive . . .

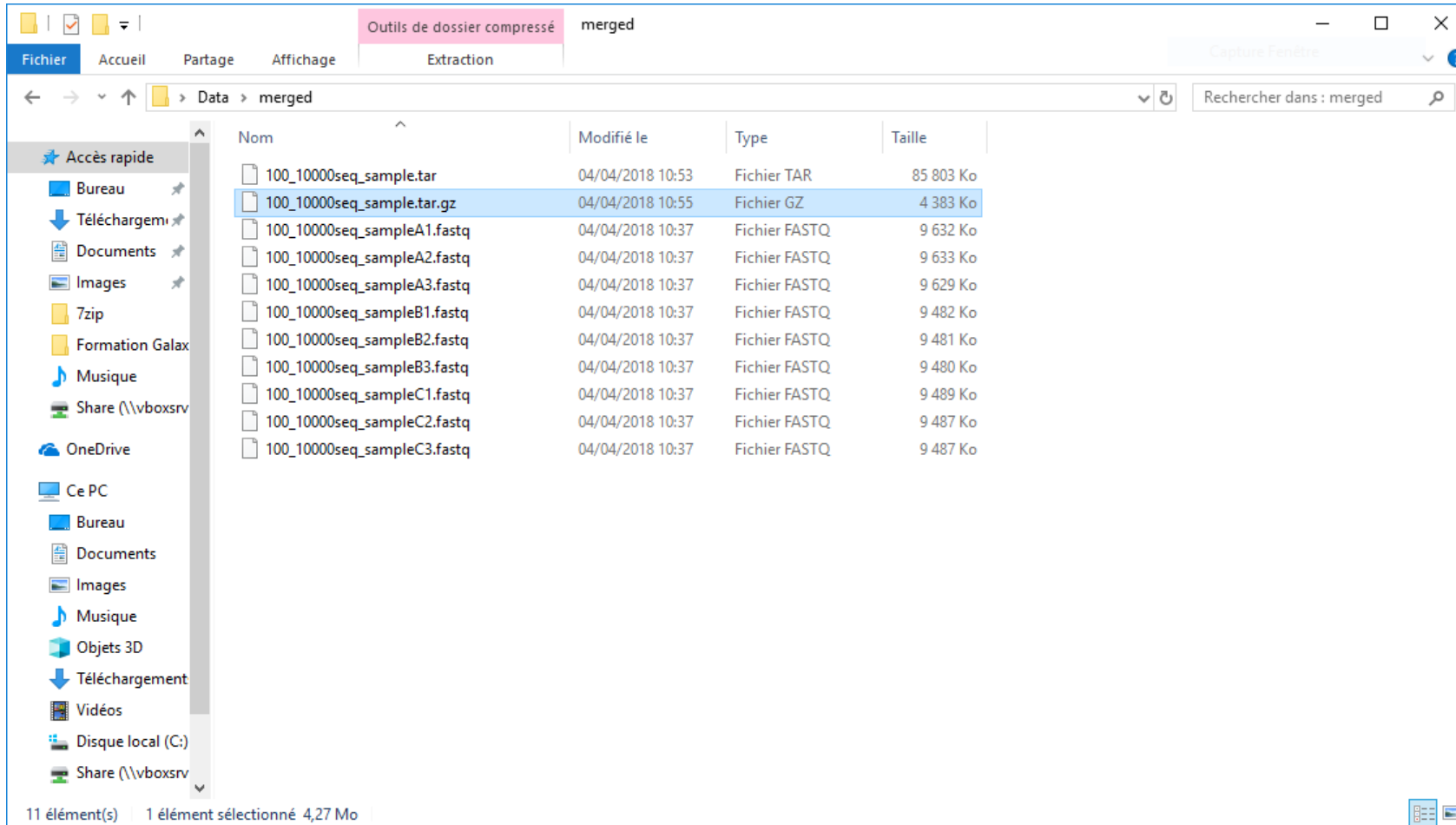


Create a Tar file with 7-Zip

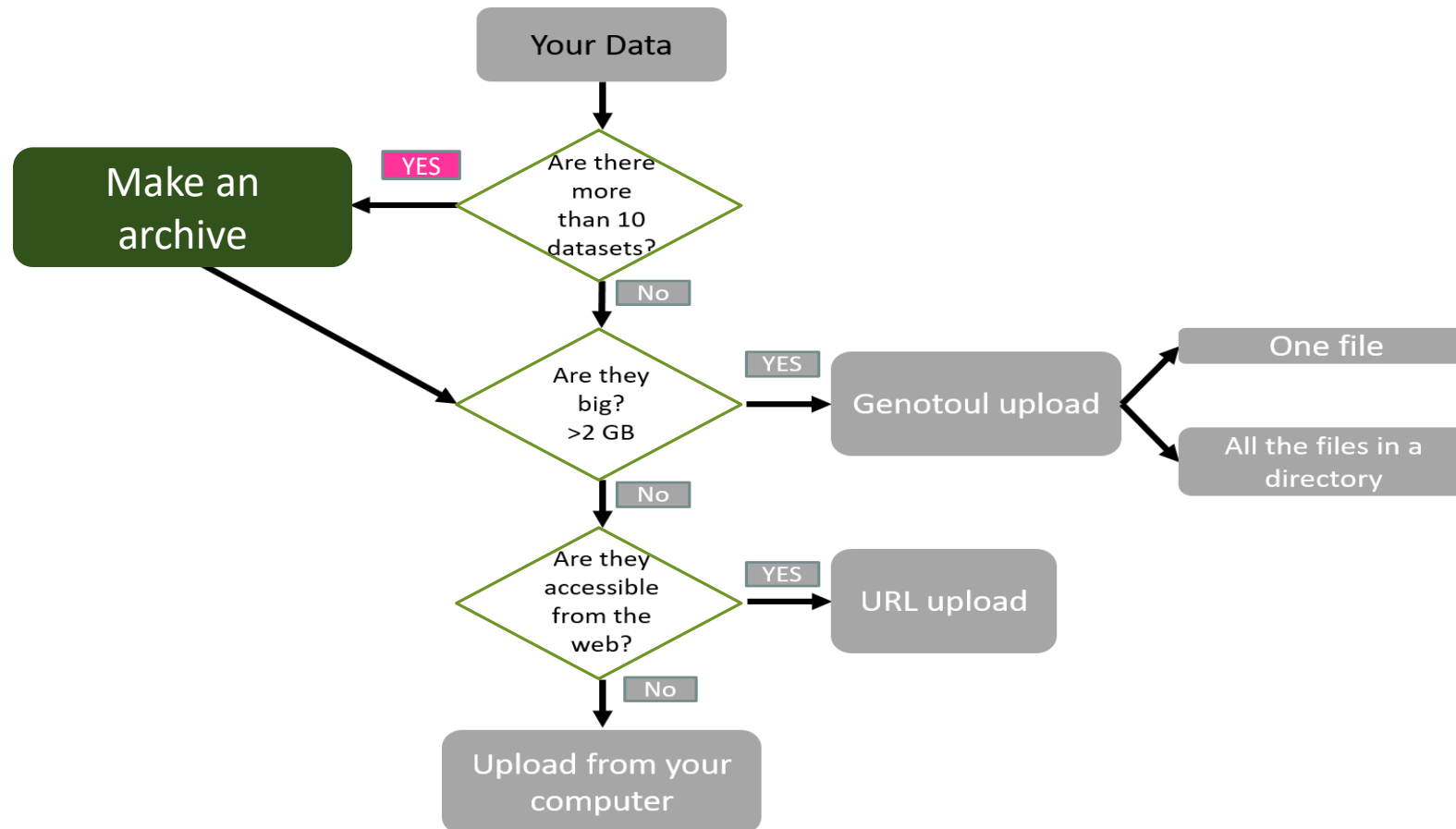
- Choose « gzip » as archive format .
- Click on OK .



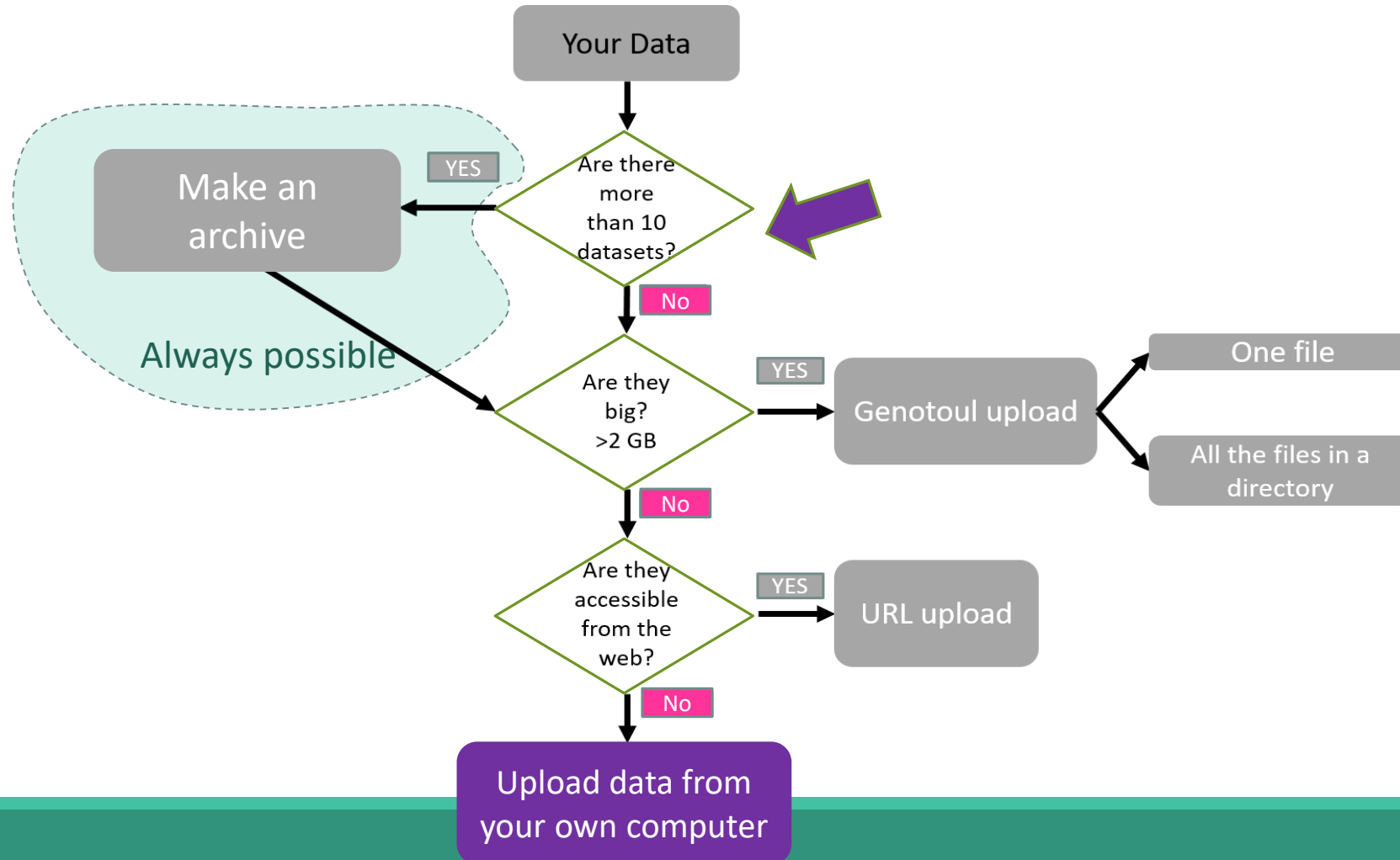
Create a Tar file with 7-Zip



Create an archive= OK



1st case for uploading your data



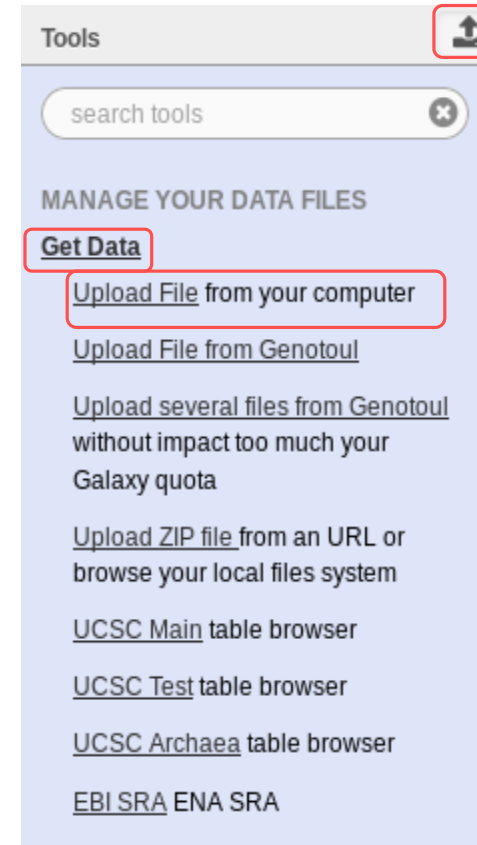
Your Turn!

UPLOAD FILES FROM YOUR COMPUTER

Upload local files

- In Galaxy, your current history must be multiplex.
- Click on the « Get Data » tool.
- Upload file from your computer.

⚠ For files smaller than 2 GB



Upload local files

Download from web or upload from disk

Regular

Composite

Drop files here

Click here to choose a file on your hard drive.

Upload one of the two files in the multiplex directory.

Type (set all):

Auto-detect



Genome (set all):

unspecified (?)

Choose local file

Paste/Fetch data

Pause

Reset

Start

Close

Upload local files

The datatype of a file indicates the content of it.

.fasta = fasta

.fastq = fastq

.tar = tar







Select the type corresponding to your file.

Do not trust blindly the auto-detect!




Download from web or upload from disk






Regular Composite

You added 2 file(s) to the queue. Add more files or click 'Start' to proceed.

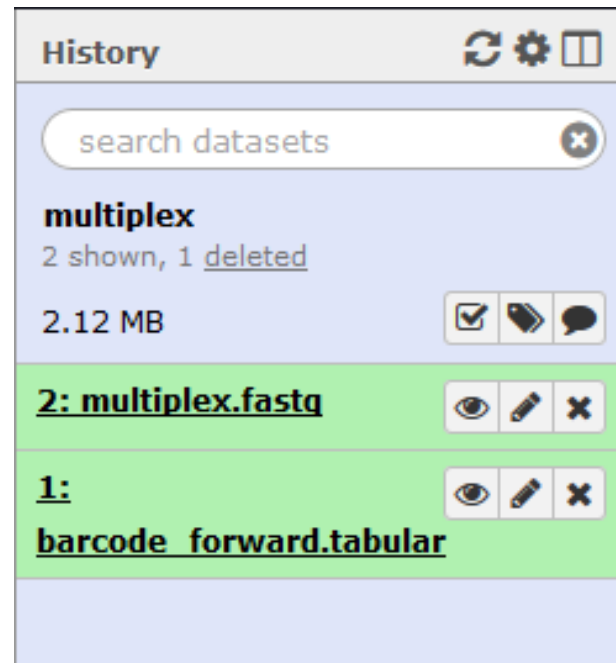
Name	Size	Type	Genome	Settings	Status
 barcode_forward.tabular	260 b	Auto-det...	unspecified (?)		0% 
 multiplex.fastq	2.1 MB	Auto-det...	unspecified (?)		0% 

1. Select the type of file (Do not leave on Auto-Detect!).
2. Select your other files the same way.
3. Begin upload.

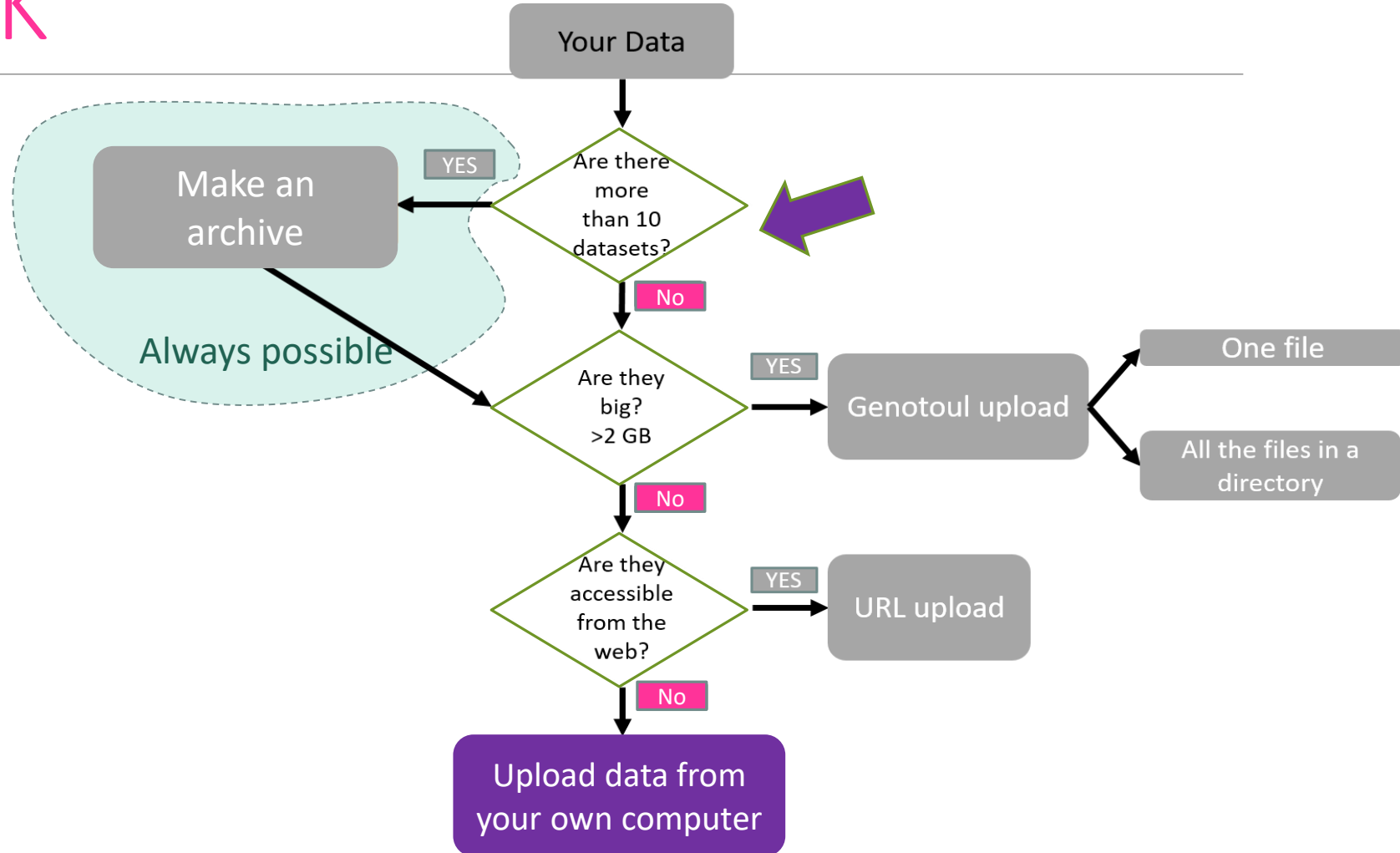
Type (set all): Auto-detect   Genome (set all): unspecified (?) 

 Choose local file  Paste/Fetch data   **Start** 

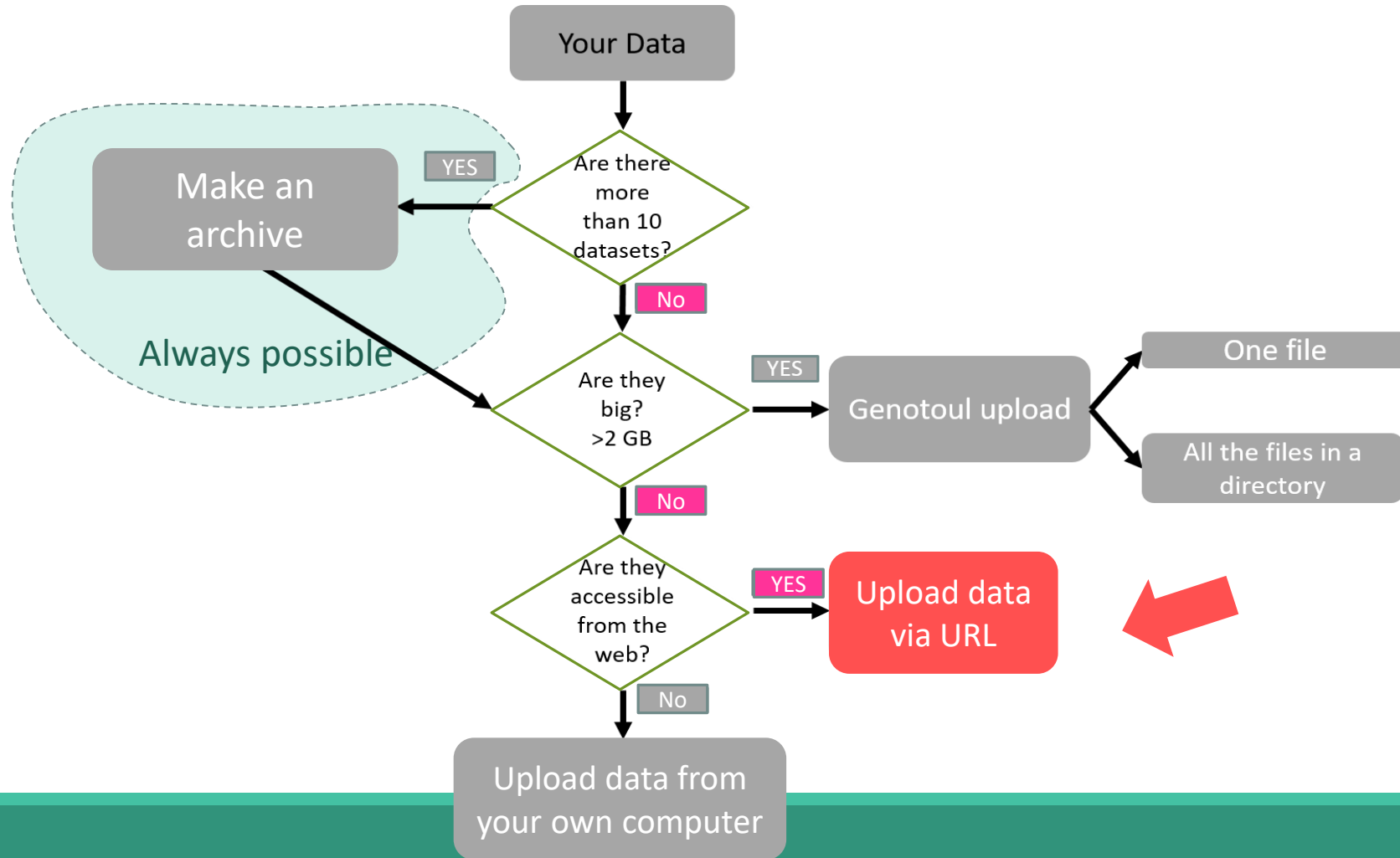
Upload local files



1st case = OK



2nd case for uploading your data



Your Turn!

UPLOAD FILE FROM AN URL




Upload file from URL

1. Switch to ITS history as current history.
2. Go to **Get Data > Upload File from your computer**
3. Click on **Paste/Fetch Data**
4. Copy the address of the file:
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/ITS.tar.gz
5. Change the type!
6. Click on Start.
7. You can put one address per line for multiple uploads.

Download from web or upload from disk

Regular Composite

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.




Name	Size	Type	Genome	Settings	Status
 New File	76 b	Auto-detect	unspecified (?)		


You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file




```
http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/ITS.tar.gz
```




Type (set all): Auto-detect Genome (set all): unspecified (?)

Upload file from URL

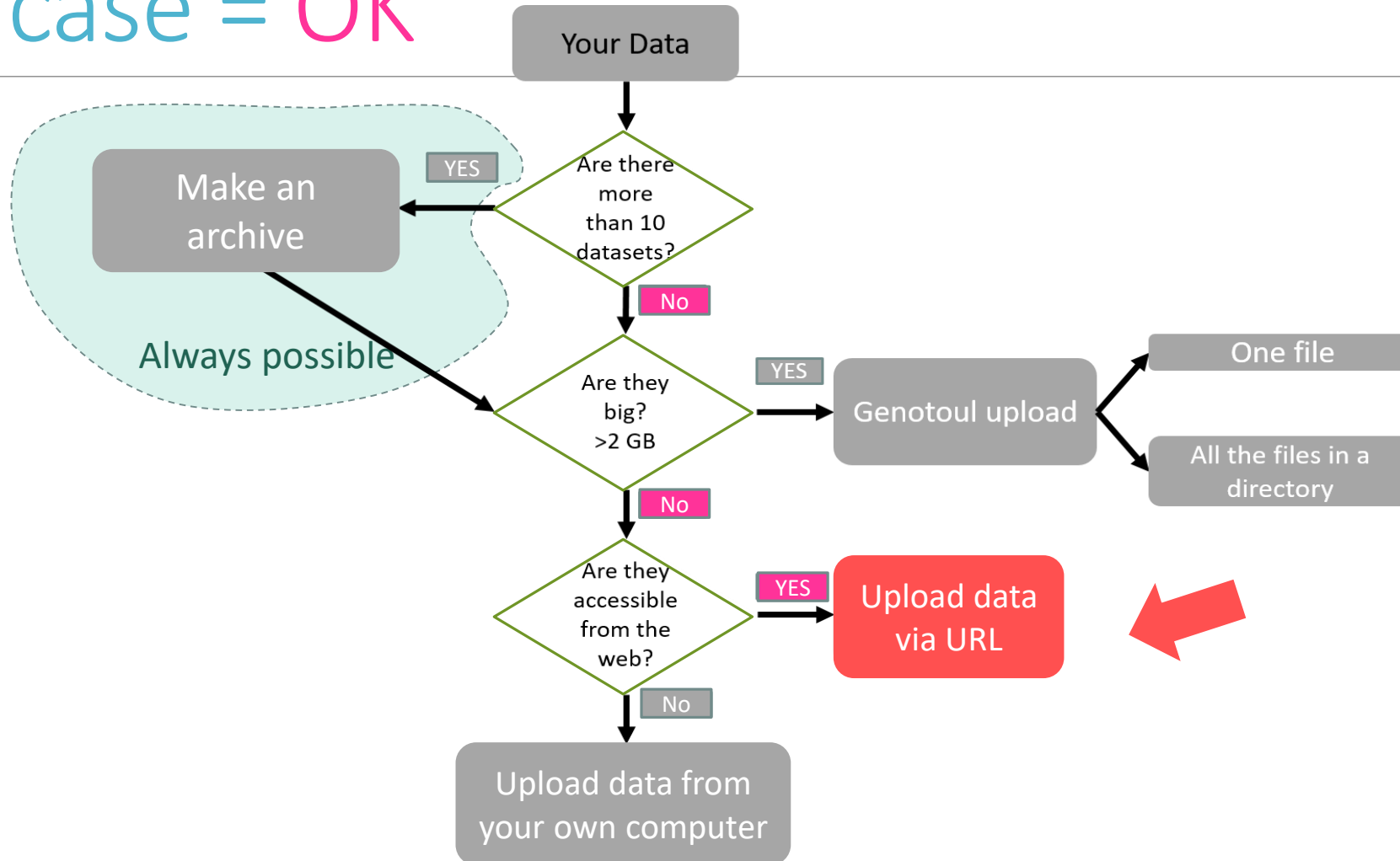
History   

search datasets 

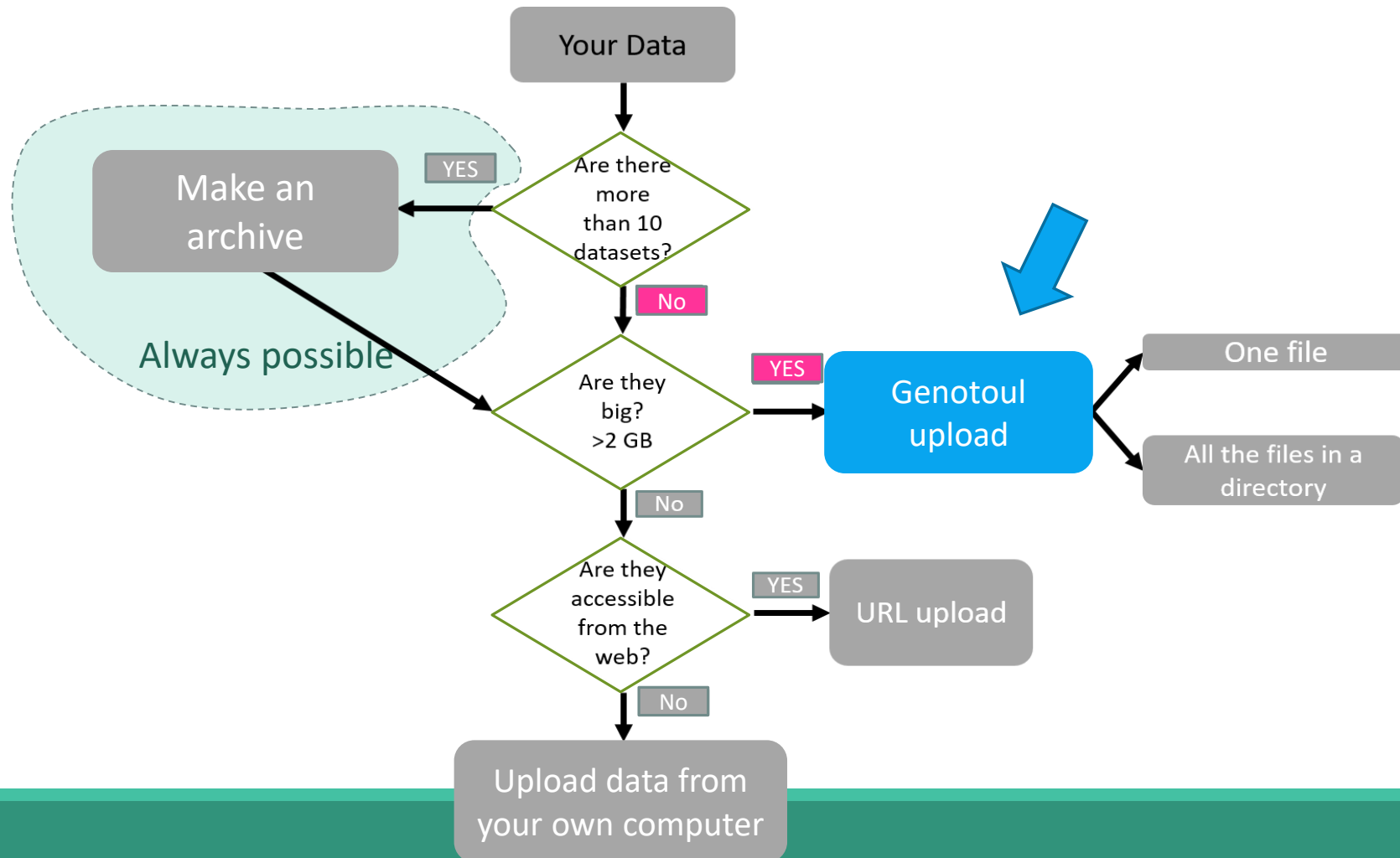
ITS
1 shown
156.91 MB   

1:   
http://qenoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/ITS.tar.gz

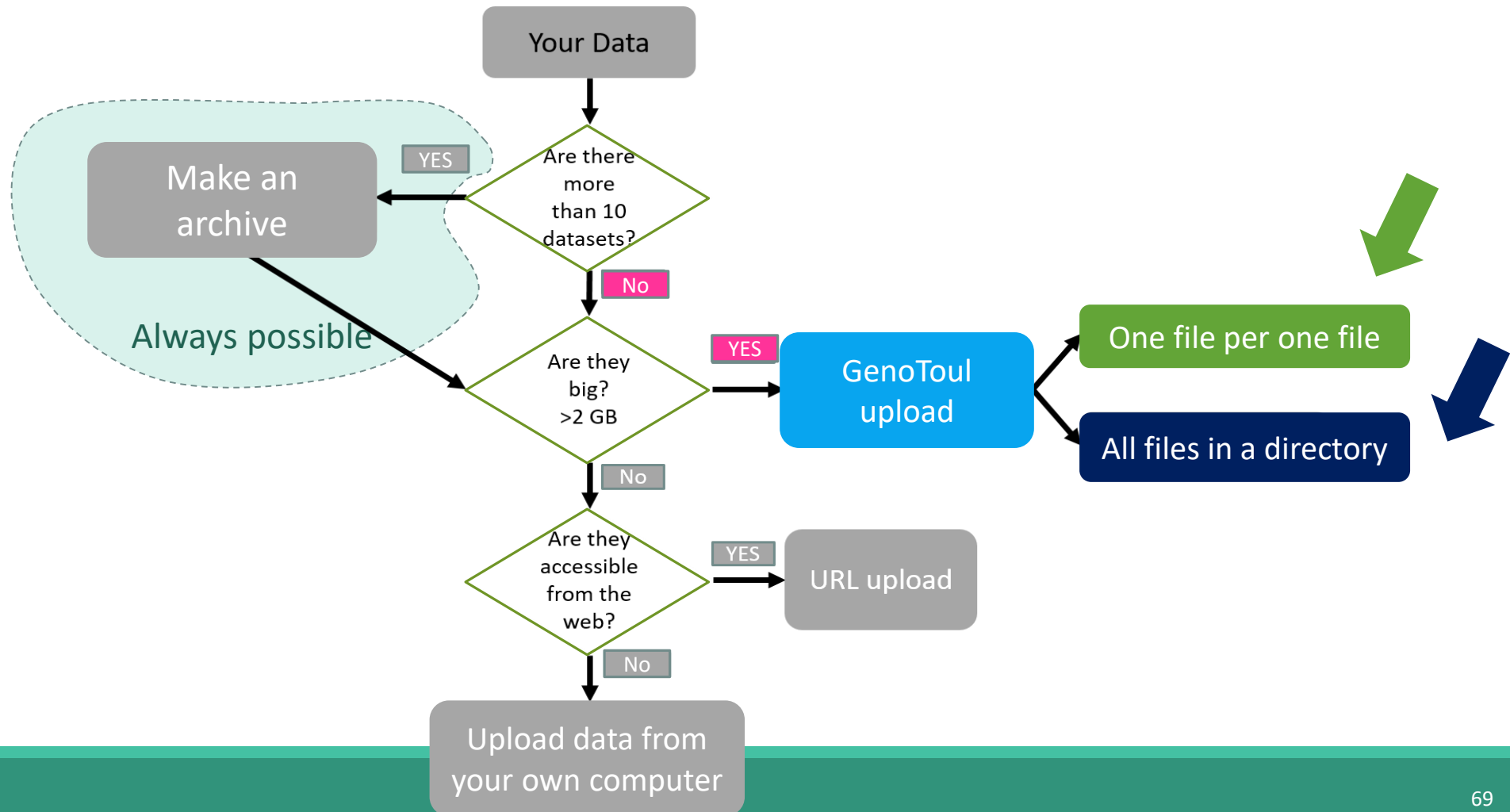
2nd case = OK



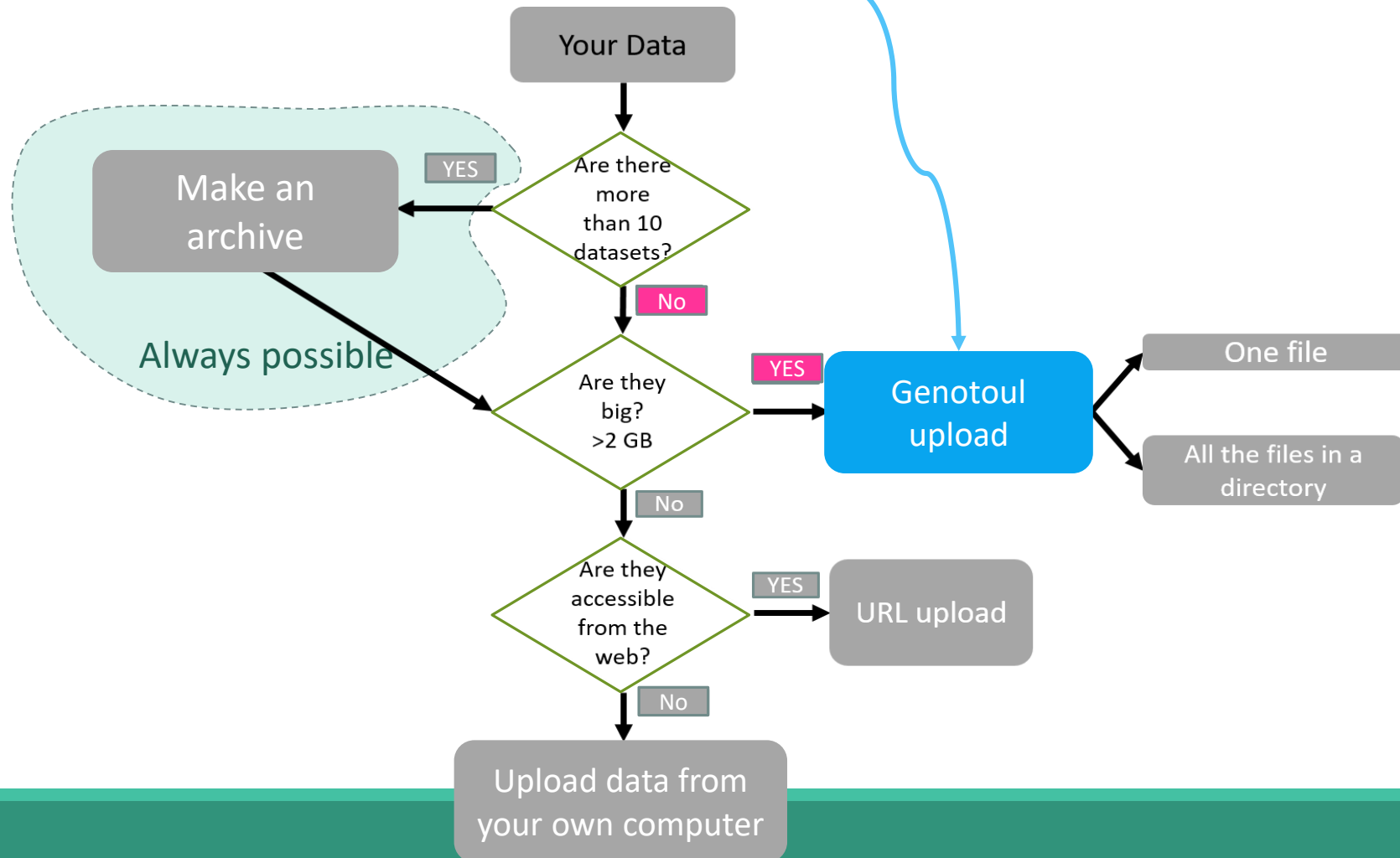
3rd case for uploading your data



3rd case for uploading your data



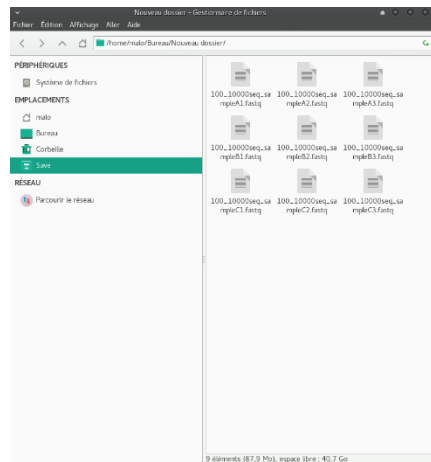
Above all: put data on Genotoul server



Your Turn!

PUT DATA ON GENOTOUL SERVER

Objectives: Transfer your files to your Genotoul account and link the file to Galaxy



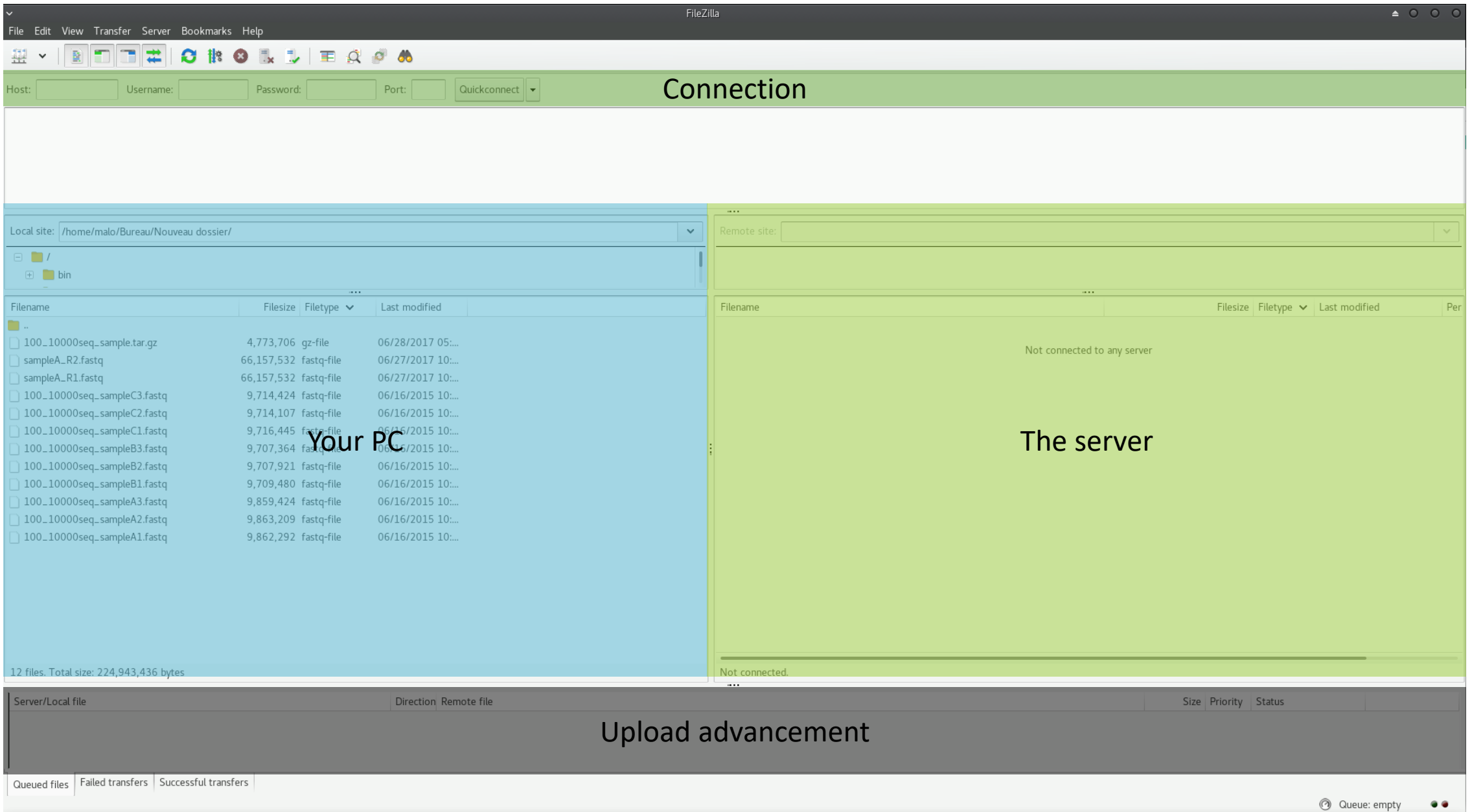
genotoul



Objectives: Transfer your files to your Genotoul **with Filezilla**

- Open the data directory on your desktop.
- Launch Filezilla.
 - Filezilla is a FTP client *i.e.* can transfer files to a distant server.
 - You can download it on : <https://filezilla-project.org/>





Connection

Your PC

The server

Upload advancement

Host: Username: Password: Port: Quickconnect

Status: retrieving directory listing of /home/mlebo...
Status: Listing directory /work/mlebo...
Status: Directory listing of "/work/mlebo..." successful
Status: Retrieving directory listing of "/work/mlebo.../Formation"...
Status: Listing directory /work/mlebo.../Formation
Status: Directory listing of "/work/mlebo.../Formation" successful
Status: Deleting 2 files from "/work/mlebo.../Formation"
Status: Disconnected from server

Local site: /home/malo/Bureau/Data/

- Data
 - merged

Filename	Filesize	Filetype	Last modified
..			
temp		Directory	06/29/2017 05:...
multiplex		Directory	06/29/2017 05:...
merged		Directory	06/29/2017 05:...

3 directories

Remote site: /work/mlebo.../Formation

- mlebo...
 - Formation

Filename	Filesize	Filetype	Last modified	Per
..				

Empty directory listing

Empty directory.

Server/Local file	Direction	Remote file	Size	Priority	Status
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Queued files | Failed transfers | Successful transfers (2)

Queue: empty

Browse to the data directory on your desktop.

Local site: /home/mal...reau/Data/

Filename	Filesize	Filetype	Last modified
..			
temp		Directory	06/29/2017 05:...
multiplex		Directory	06/29/2017 05:...
merged		Directory	06/29/2017 05:...

3 directories

Remote site: /work/mleboulch/Formation

Empty directory listing

Empty directory.

Server/Local file | Direction | Remote file | Size | Priority | Status

Queued files | Failed transfers | Successful transfers (2)

Queue: empty

To connect to Genotoul click on this icon.

- Host: genologin.toulouse.inra.fr
- Port: 22
- Protocol: SFTP
- User: your Genotoul login
- Logon Type: Ask for password
- Click on connect.

- Password: your password

The screenshot shows the 'Site Manager' dialog box with the 'General' tab selected. The 'Select Entry' pane on the left shows a tree view with 'My Sites' expanded, containing 'Formation' and 'Genotoul'. The 'Genotoul' entry is selected. The main configuration area contains the following fields:

- Protocol: SFTP - SSH File Transfer Protocol
- Host: genologin.toulouse.inra.fr
- Port: 22
- Logon Type: Ask for password
- User: mlebulch
- Password: (empty field)
- Background color: None
- Comments: (empty text area)

At the bottom of the dialog, there are three buttons: 'Connect', 'OK', and 'Cancel'. Below the 'Select Entry' pane, there are six buttons: 'New Site', 'New Folder', 'New Bookmark', 'Rename', 'Delete', and 'Duplicate'.


 Host: Username: Password: Port: Quickconnect

 Status: Connecting to genotoul.toulouse.inra.fr...
 Status: Connected to genotoul.toulouse.inra.fr
 Status: Retrieving directory listing...
 Status: Listing directory /home/mleboulch
 Status: Directory listing of "/home/mleboulch" successful

Local site: /home/malo/Bureau/Data/

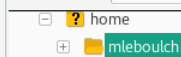


Filename	Filesize	Filetype	Last modified
..			
temp		Directory	06/29/2017 05:...
multiplex		Directory	06/29/2017 05:...
merged		Directory	06/29/2017 05:...

Double click on work directory to access it.



Remote site: /home/mleboulch



Filename	Filesize	Filetype	Last modified
..			
.recently-used.xbel	4,162	xbel-file	03/30/2017 02:26:33 PM
.viminfo	615	File	02/14/2017 09:59:45 AM
.python_history	542	File	06/01/2017 11:08:10 AM
.bashrc	52	File	02/14/2017 09:59:45 AM
.bash_profile	226	File	05/15/2017 03:39:59 PM
.bash_history	17,308	File	06/23/2017 11:15:47 AM
.Xauthority	4,608	File	06/23/2017 11:15:15 AM
work		Directory	10/21/2016 04:37:06 PM
save		Directory	10/21/2016 04:37:06 PM
AIC-prefs		Directory	02/14/2017 10:04:44 AM
.ssh		Directory	01/10/2017 02:28:16 PM
.pki		Directory	03/30/2017 02:56:02 PM
.pathway-tools		Directory	06/01/2017 10:45:23 PM
.gnome2		Directory	02/01/2017 06:14:17 PM
.gconfd		Directory	03/30/2017 02:26:51 PM
.gconf		Directory	03/30/2017 09:08:21 AM
.dbus		Directory	02/01/2017 06:12:40 PM
.config		Directory	04/25/2017 04:13:46 PM

Selected 1 directory.

Server/Local file

Direction Remote file

Size Priority Status

Queued files Failed transfers Successful transfers

Queue: empty

sftp://mleboulch@genotoul.toulouse.inra.fr - FileZilla

File Edit View Transfer Server Bookmarks Help

Host: Username: Password: Port: Quickconnect

Status: Deleting 2 files from /work/mleboulch/Formation
Status: Disconnected from server
Status: Retrieving directory listing of "/work/mleboulch" ...
Status: Listing directory /work/mleboulch
Status: Directory listing of "/work/mleboulch" successful
Status: Retrieving directory listing of "/work/mleboulch/Formation" ...
Status: Listing directory /work/mleboulch/Formation
Status: Directory listing of "/work/mleboulch/Formation" successful

Local site: /home/malo/Bureau/Data/ Remote site: /work/mleboulch/

Local site: Data merged

Remote site: mleboulch Formation

Filename	Filesize	Filetype	Last modified
..		Directory	06/29/2017 05:...
temp		Directory	
multiplex		Directory	
merged		Directory	

3 directories

Empty directory listing

- Download
- Add files to queue
- View/Edit
- Create directory**
- Create directory and enter it
- Create new file
- Refresh
- Delete
- Rename
- Copy URL(s) to clipboard
- File permissions...

Empty directory.

Server/Local file Direction Remote file Size Priority Status

Queued files Failed transfers Successful transfers (2)

Queue: empty

- Create new directory with right click > Create directory.
 - Name it « Formation ».
 - Go inside this directory next.



sftp://mleboulch@genotoul.toulouse.inra.fr - FileZilla

File Edit View Transfer Server Bookmarks Help

Host: Username: Password: Port: Quickconnect

Status: Listing directory /home/mleboulch
Status: Directory listing of "/home/mleboulch" successful
Status: Retrieving directory listing of "/home/mleboulch/work"...
Status: Listing directory /work/mleboulch
Status: Directory listing of "/work/mleboulch" successful
Status: Retrieving directory listing of "/work/mleboulch/Formation"...
Status: Listing directory /work/mleboulch/Formation
Status: Directory listing of "/work/mleboulch/Formation" successful

Local site: /home/malo/Bureau/Data/ Remote site: /work/mleboulch/Formation

Local site: /
bin

Remote site: mleboulch
Formation

Filename	Filesize	Filetype	Last modified
..			
temp		Directory	06/29/2017 05:...
multiplex		Directory	06/29/2017 05:...
merged		Directory	06/29/2017 05:...

Selected 1 directory.

Server/Local file	Direction	Remote file	Size	Priority	Status
-------------------	-----------	-------------	------	----------	--------

Queued files Failed transfers Successful transfers

Queue: empty

- Select the temp directory and drag and drop it following the arrow.
- Double click on the merge directory.

Host: Username: Password: Port: Quickconnect

```
Status: Listing directory /work/mleboulch/Formation/temp
Command: put "/home/malo/Bureau/Data/temp/temp2.fastq" "temp2.fastq"
Command: local:/home/malo/Bureau/Data/temp/temp2.fastq => remote:/work/mleboulch/Formation/temp/temp2.fastq
Status: File transfer successful, transferred 2,226,378 bytes in 1 second
Status: File transfer successful, transferred 2,226,378 bytes in 1 second
Status: Retrieving directory listing of "/work/mleboulch/Formation"...
Status: Listing directory /work/mleboulch/Formation
Status: Directory listing of "/work/mleboulch/Formation" successful
```

Local site: /home/malo/Bureau/Data/merged/

▾ Data
 ▾ merged

Filename	Filesize	Filetype	Last modified
..			
100_1000seq_sample.tar.gz	4,773,706	gz-file	06/28/2017 05:...
100_1000seq_sampleC3.fastq	9,714,424	fastq-file	06/16/2015 10:...
100_1000seq_sampleC2.fastq	9,714,107	fastq-file	06/16/2015 10:...
100_1000seq_sampleC1.fastq	9,716,445	fastq-file	06/16/2015 10:...
100_1000seq_sampleB3.fastq	9,707,364	fastq-file	06/16/2015 10:...
100_1000seq_sampleB2.fastq	9,707,921	fastq-file	06/16/2015 10:...
100_1000seq_sampleB1.fastq	9,709,480	fastq-file	06/16/2015 10:...
100_1000seq_sampleA3.fastq	9,859,424	fastq-file	06/16/2015 10:...
100_1000seq_sampleA2.fastq	9,863,209	fastq-file	06/16/2015 10:...
100_1000seq_sampleA1.fastq	9,862,292	fastq-file	06/16/2015 10:...

Selected 1 file. Total size: 4,773,706 bytes

Server/Local file

Dire

Queued files | Failed transfers | Successful transfers (2)

Remote site: /work/mleboulch/Formation

▾ mleboulch
 + ▾ Formation

Filename	Filesize	Filetype	Last modified	Per
..				
temp		Directory	06/29/2017 06:01:32 PM	drw

- Select the 100_1000seq_sample.tar.gz file and drag and drop it following the arrow.
- Double click on the merge directory.

Host: Username: Password: Port: Quickconnect

Status: Directory listing of "/work/.vle" successful
Status: Retrieving directory listing of "/work/BPMP" ...
Status: Listing directory /work/BPMP
Status: Directory listing of "/work/BPMP" successful
Status: Retrieving directory listing of "/work/mlebeurier2" ...
Command: cd "/work/mlebeurier2"
Error: Directory /work/mlebeurier2: permission denied
Error: Failed to retrieve directory listing

Local site: /home/malo/Bureau/Data/merged/

Remote site: /work/mleboulch

Data
merged
multipler

Filename	Filesize	Filetype	Last modified
100_10000seq_sampleB1.fastq	9,709,480	fastq-file	04/04/2018 10:...
100_10000seq_sampleC2.fastq	9,714,107	fastq-file	04/04/2018 10:...
100_10000seq_sampleC3.fastq	9,714,424	fastq-file	04/04/2018 10:...
100_10000seq_sampleC1.fastq	9,716,445	fastq-file	04/04/2018 10:...
100_10000seq_sampleA3.fastq	9,859,424	fastq-file	04/04/2018 10:...
100_10000seq_sampleA1.fastq	9,862,292	fastq-file	04/04/2018 10:...

Select your work directory.

Right click on it and click on File Attributes.

mleboulch
Database

- Download
- Add to queue
- Create directory
- Create directory and enter it
- Delete
- Rename
- Copy URL(s) to clipboard
- File Attributes...

Filename	Filesize	Filetype	Last modified	Permis
Directory		Directory	06/08/2018 11:19:08 AM	drwxr->
Directory		Directory	03/14/2018 02:21:50 PM	drwxr->
Directory		Directory	03/13/2018 11:50:00 AM	drwxr->
Directory		Directory	03/09/2018 04:09:45 PM	drwxr->
Directory		Directory	03/06/2018 04:25:02 PM	drwxr->
Directory		Directory	03/06/2018 01:24:27 PM	drwxr->
Directory		Directory	02/28/2018 03:48:40 PM	drwxr->
Directory		Directory	02/28/2018 03:47:01 PM	drwxr->
Directory		Directory	02/28/2018 09:29:46 AM	drwxr->
Directory		Directory	10/30/2017 05:07:06 PM	drwxr->
Directory		Directory	06/30/2017 04:26:59 PM	drwxr->

11 directories

Server/Location | Direction | Remote file | Size | Priority

Queued files | Failed transfers | Successful transfers

Queue: empty

Change file attributes

Please select the new attributes for the directory "Formation".

Owner permissions

<input checked="" type="checkbox"/> Read	<input checked="" type="checkbox"/> Write	<input checked="" type="checkbox"/> Execute
--	---	---

Group permissions

<input checked="" type="checkbox"/> Read	<input type="checkbox"/> Write	<input checked="" type="checkbox"/> Execute
--	--------------------------------	---

Public permissions

<input checked="" type="checkbox"/> Read	<input type="checkbox"/> Write	<input checked="" type="checkbox"/> Execute
--	--------------------------------	---

Numeric value:

You can use an x at any position to keep the permission the original files have.

Recurse into subdirectories

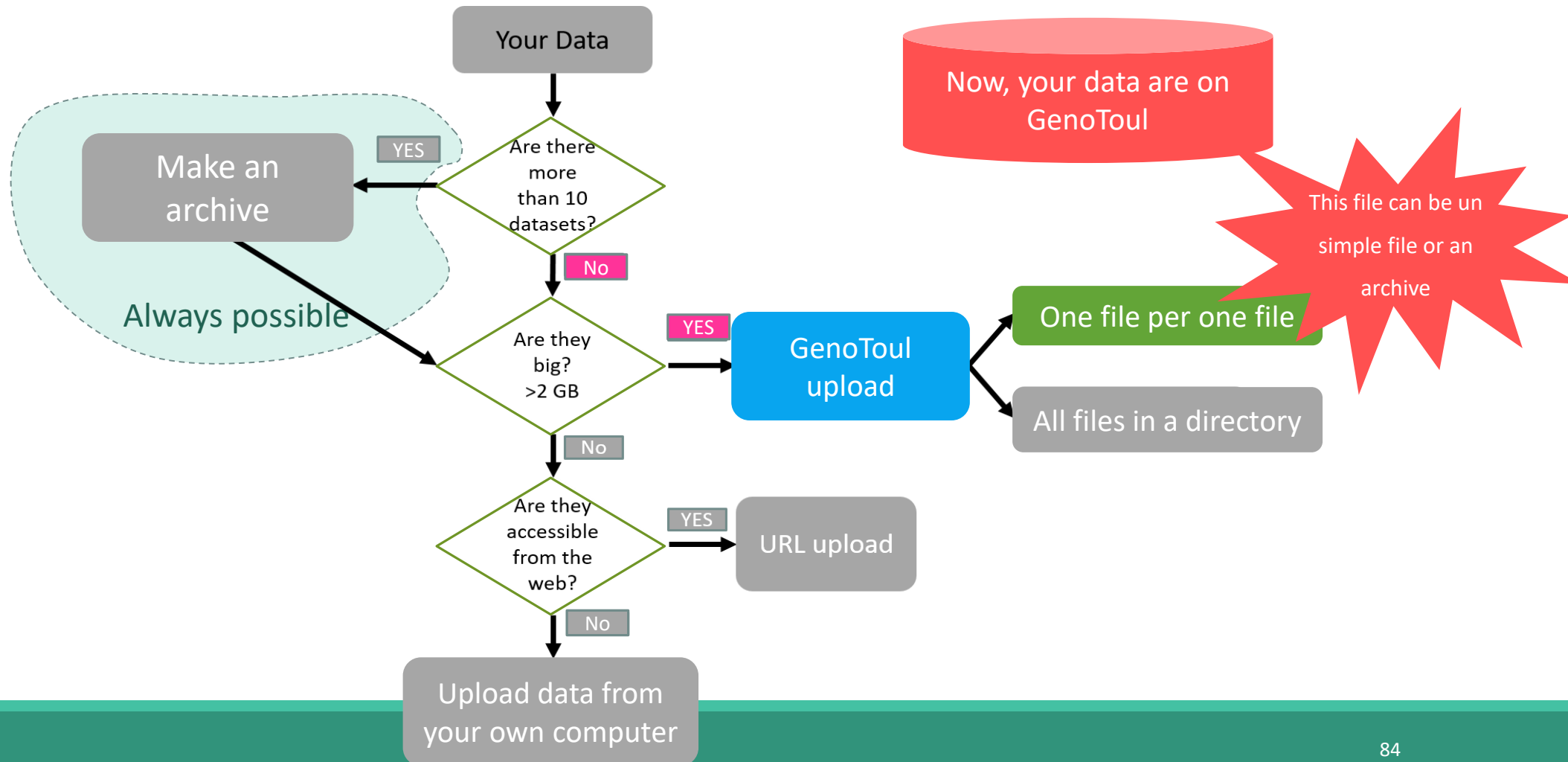
Apply to all files and directories

Apply to files only

Apply to directories only

- Check that all boxes for execute and read are checked.
- Recurse this action to all files and subdirectories.
- That allows Galaxy to access your files on Genotoul.
 - Click on Ok.

3rd case for uploading your data « one file per one file »



File Edit View Transfer Server Bookmarks Help

Host: Username: Password: Port: Quickconnect

Status: Setting permissions of /work/mleboulch/Formation/temp/temp2.fastq to 755
Status: /work/mleboulch/Formation/temp/temp2.fastq: 0644 -> 0755
Status: Retrieving directory listing of "/work/mleboulch/Formation"
Status: Listing directory /work/mleboulch/Formation
Status: Directory listing of "/work/mleboulch/Formation" successful
Status: Retrieving directory listing of "/work/mleboulch/Formation/temp"
Status: Listing directory /work/mleboulch/Formation/temp
Status: Directory listing of "/work/mleboulch/Formation/temp" successful

Local site: /home/malo/Bureau/Data/merged/

Remote: /work/mleboulch/Formation

Data
merged

Filename	Filesize	Filetype	Last modified	Per
..				
100_10000seq_sampleB2.fastq	9,707,921	fastq-file	06/16/2015 10:...	
100_10000seq_sampleB1.fastq	9,709,480	fastq-file	06/16/2015 10:...	
100_10000seq_sampleA3.fastq	9,859,424	fastq-file	06/16/2015 10:...	
100_10000seq_sampleA2.fastq	9,863,209	fastq-file	06/16/2015 10:...	
100_10000seq_sampleA1.fastq	9,862,292	fastq-file	06/16/2015 10:...	

10 files. Total size: 92,628,372 bytes

Formation
temp

Filename	Filesize	Filetype	Last modified	Per
..				
100_10000seq_sample.tar.gz	4,773,706	gz-file	06/29/2017 06:04:35 PM	-rwx
temp		Directory	06/29/2017 06:01:32 PM	drwx

1 file and 1 directory. Total size: 4,773,706 bytes

Server/Local file | Direction | Remote file | Size | Priority | Status

Queued files | Failed transfers | Successful transfers (3)

Queue: empty

Select this text and copy it by pressing the keyboard keys Ctrl+C.

Tools

search tools

MANAGE YOUR DATA FILES

Get Data

- Upload File from your computer
- Upload File from Genotoul**
- Upload several files from Genotoul without impact too much your Galaxy quota
- Upload ZIP file from an URL or browse your local files system
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- EBI SRA ENA SRA

Download Data

Jobs statistics

FILES MANIPULATION

- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- GFF
- BED Tools
- Convert Formats
- Fetch Sequences
- Statistics
- Graph/Display Data

SEQUENCES MANIPULATION

- FASTA manipulation
- FastQC: fastq/sam/bam
- Illumina fastq
- Generic FASTQ manipulation
- FASTX-Toolkit for FASTQ data

SAM/BAM MANIPULATION : PICARD (BETA)

- Conversion
- QC/Metrics for sam/bam

Upload File from Genotoul (Galaxy Version 1.0.0)

Options

Path to file

Path must be like : /work/USERNAME/somewhere/afile

File type

tar.gz

Execute

What it does

This procedure allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.

Path to file

This must be an absolute path

valid path : /work/LinuxUserName/...
invalid path : /home/LinuxUserName/...

⚠ To use this tool and to maintain the confidentiality of yours directories:

1. Create a "galaxy" directory in your work : `mkdir galaxy`
2. `chmod a+x /work/LinuxUserName`

Example : `drwxr-x--x 4 smaman sigenae 16384 mar 9 14:15 /work/smaman`- 3. `chmod a+r /work/LinuxUserName/dataGalaxy.fasta`

ℹ Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.

For example, if your data to download in Galaxy are: `/work/LinuxUserName/galaxy/data.fasta`:

1. Add "x" rights to "others" on `/work/LinuxUserName/` and on `galaxy/`

It is not useful that "others" have "r" rights of these directories.

2. Add "r" rights (only) to "others" on `data.fasta` file.

Thus, Galaxy can access and read `data.fasta` but all other files in those directories will not be accessible or readable.

⚠ fastq files have to be uploaded in a correct format (for instance, `fatsqsanger`) in order to be used by Galaxy tools. If this is not the case, your fastq files uploaded will not be listed among available datasets in Galaxy tools.

Version Galaxy Tool : V1.0

Versions of bioinformatics tools used : No bioinformatique tool used.

▪ Switch to merged history.

▪ Next go to Get Data > Upload File from Genotoul.

History

search datasets

merged

0 b

ℹ This history is empty. You can [load your own data](#) or [get data from an external source](#)

Tools

search tools

MANAGE YOUR DATA FILES

Get Data

- Upload File from your computer
- Upload File from Genotoul
- Upload several files from Genotoul without impact too much your Galaxy quota
- Upload ZIP file from an URL or browse your local files system
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- EBI SRA ENA SRA

Download Data

Jobs statistics

FILES MANIPULATION

- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- GFF
- BED Tools
- Convert Formats
- Fetch Sequences
- Statistics
- Graph/Display Data

SEQUENCES MANIPULATION

- FASTA manipulation
- FastQC: fastq/sam/bam
- Illumina fastq
- Generic FASTQ manipulation
- FASTX-Toolkit for FASTQ data

SAM/BAM MANIPULATION : PICARD (BETA)

- Conversion
- QC/Metrics for sam/bam

Upload File from Genotoul (Galaxy Version 1.0.0)

Options

Path to file

Path must be like : /work/USERNAME/somewhere/afile

File type

Execute

What it does

This program allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.

Path to file

This must be an absolute path to a file located in your genotoul work directory. The path must start with `/work/YOUR_USER_NAME/blablabla.extension`

valid path : `/work/LinuxUserName/galaxy/file.extension`
invalid path : `/home/LinuxUserName/work/galaxy/file.extension`

⚠ To use this tool and to maintain the confidentiality of yours directories:

1. Create a "galaxy" directory in your work : `mkdir galaxy`
2. `chmod a+x /work/LinuxUserName`

Example : `drwxr-x--x 4 smaman sigenae 16384 mar 9 14:15 /work/smaman`- 3. `chmod a+r /work/LinuxUserName/dataGalaxy.fasta`

ℹ Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.

For example, if your data to download in Galaxy are: `/work/LinuxUserName/galaxy/data.fasta`:

1. Add "x" rights to "others" on `/work/LinuxUserName/` and on `galaxy/`

It is not useful that "others" have "r" rights of these directories.

2. Add "r" rights (only) to "others" on `data.fasta` file.

Thus, Galaxy can access and read `data.fasta` but all other files in those directories will not be accessible or readable.

⚠ fastq files have to be uploaded in a correct format (for instance, fastqsanger) in order to be used by Galaxy tools. If this is not the case, your fastq files uploaded will not be listed among available datasets in Galaxy tools.

Version Galaxy Tool : V1.0

Versions of bioinformatics tools used : No bioinformatique tool used.

History

search datasets

merged

0 b

ℹ This history is empty. You can [load your own data](#) or [get data from an external source](#)

Copy the text here by pressing Ctrl+V.

Don't forget to change the Datatype!

Path to file

`/work/mleboulch/Formation`

Path must be like : `/work/USERNAME/somewhere/afile`



Path to file

`/work/mleboulch/Formation/100_10000seq_sample.tar.gz`

Path must be like : `/work/USERNAME/somewhere/afile`

You must add « / » and the name of the file at the end of the text.

Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 813.2 MB

Tools ↑

search tools

MANAGE YOUR DATA FILES

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- [Illumina fastq](#)
- [Generic FASTQ manipulation](#)
- [FASTX-Toolkit for FASTQ data](#)

SAM/BAM MANIPULATION : PICARD (BETA)

- [Conversion](#)
- [QC/Metrics for sam/bam](#)

History ↻ ⚙️ 📄

search datasets

merged

1 shown

4.55 MB ✔️ 🗑️ 💬

1: /work/mleboulch /Formation /100_10000seq_sample.tar.gz 👁️ ✎ ✕

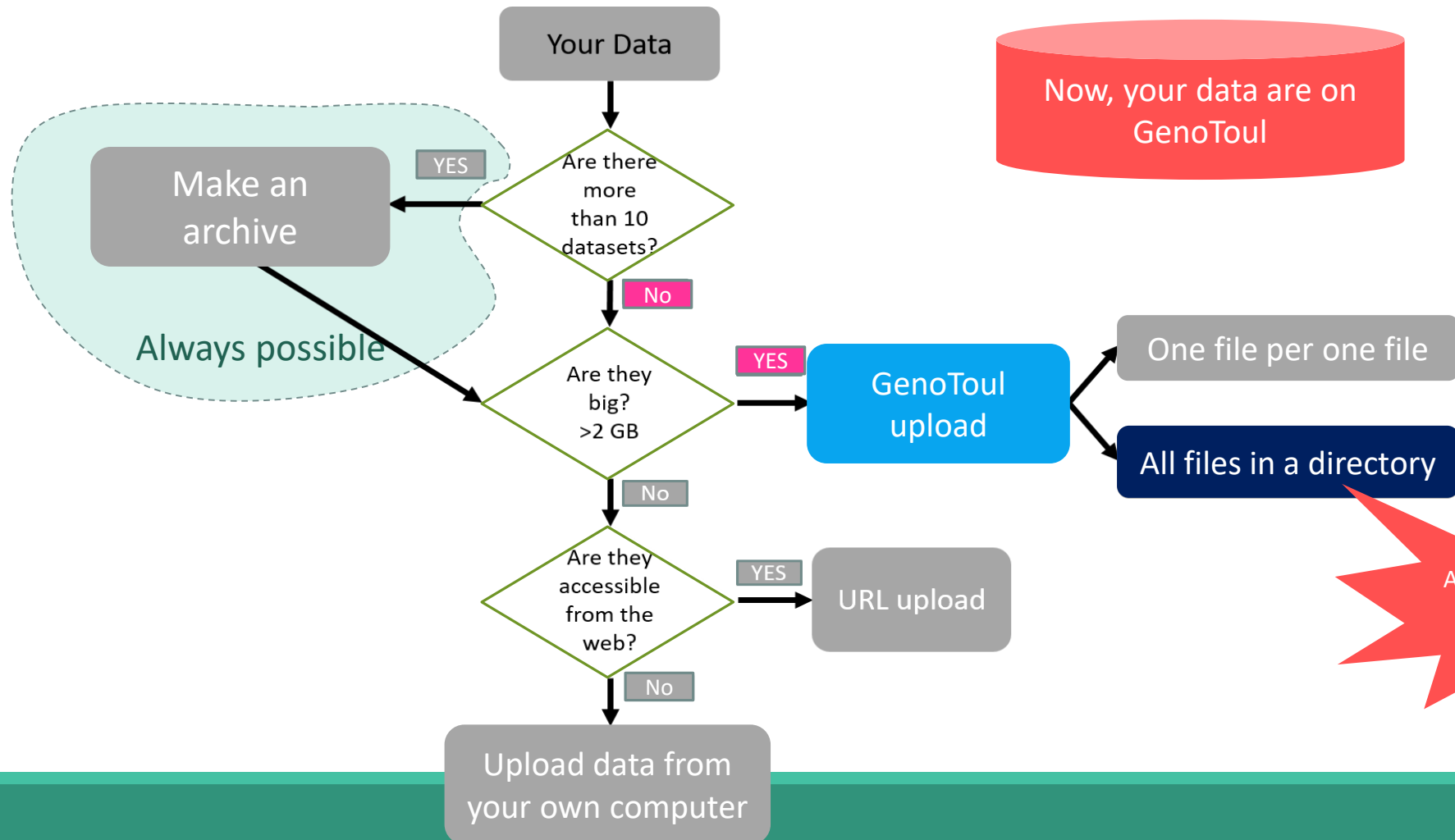
1 job has been successfully added to the queue - resulting in the following datasets:

1: /work/mleboulch/Formation/100_10000seq_sample.tar.gz

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

After executing, the file is imported into Galaxy.

3rd case for uploading your data « All files in a directory »



Host: Username: Password: Port: Quickconnect

Status: Setting permissions of /work/mleboulch/Formation/temp/temp2.fastq to 755
Status: /work/mleboulch/Formation/temp/temp2.fastq: 0644 -> 0755
Status: Retrieving directory listing of "/work/mleboulch/Formation"
Status: Listing directory /work/mleboulch/Formation
Status: Directory listing of "/work/mleboulch/Formation" successful
Status: Retrieving directory listing of "/work/mleboulch/Formation/temp"
Status: Listing directory /work/mleboulch/Formation/temp
Status: Directory listing of "/work/mleboulch/Formation/temp" successful

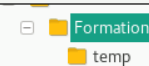
Local site: /home/malo/Bureau/Data/merged/



Filename	Filesize	Filetype	Last modified
..			
100_10000seq_sample.tar.gz	4,773,706	gz-file	06/28/2017 05:...
100_10000seq_sampleC3.fastq	9,714,424	fastq-file	06/16/2015 10:...
100_10000seq_sampleC2.fastq	9,714,107	fastq-file	06/16/2015 10:...
100_10000seq_sampleC1.fastq	9,716,445	fastq-file	06/16/2015 10:...
100_10000seq_sampleB3.fastq	9,707,364	fastq-file	06/16/2015 10:...
100_10000seq_sampleB2.fastq	9,707,921	fastq-file	06/16/2015 10:...

10 files. Total size: 92,628,372 bytes

Remote site: /work/mleboulch/Formation



Filename	Filesize	Filetype	Last modified	Per
..				
100_10000seq_sample.tar.gz	4,773,706	gz-file	06/29/2017 06:04:35 PM	-rw
temp		Directory	06/29/2017 06:01:32 PM	drw

1 file and 1 directory. Total size: 4,773,706 bytes

Double click on the temp directory.

Server/Local file	Direction	Remote file	Size	Priority	Status
-------------------	-----------	-------------	------	----------	--------

Queued files | Failed transfers | Successful transfers (3)

Queue: empty


 Host: Username: Password: Port: Quickconnect

Listing directory /work/mleboulch/Formation
 Status: Directory listing of "/work/mleboulch/Formation" successful
 Status: Retrieving directory listing of "/work/mleboulch/Formation/temp"...
 Status: Listing directory /work/mleboulch/Formation/temp
 Status: Directory listing of "/work/mleboulch/Formation/temp" successful
 Status: Retrieving directory listing of "/work/mleboulch/Formation/temp"...
 Status: Listing directory /work/mleboulch/Formation/temp
 Status: Directory listing of "/work/mleboulch/Formation/temp" successful

Local site: /home/malo/Bureau/Data/merged/

 Data
 merged

Filename	Filesize	Filetype	Last modified
..			
100_10000seq_sample.tar.gz	4,773,706	gz-file	
100_10000seq_sampleC3.fastq	9,714,424	fastq-file	
100_10000seq_sampleC2.fastq	9,714,107	fastq-file	
100_10000seq_sampleC1.fastq	9,716,445	fastq-file	06/16/2015 10:...
100_10000seq_sampleB3.fastq	9,707,364	fastq-file	06/16/2015 10:...
100_10000seq_sampleB2.fastq	9,707,921	fastq-file	06/16/2015 10:...
100_10000seq_sampleB1.fastq	9,709,480	fastq-file	06/16/2015 10:...
100_10000seq_sampleA3.fastq	9,859,424	fastq-file	06/16/2015 10:...
100_10000seq_sampleA2.fastq	9,863,209	fastq-file	06/16/2015 10:...
100_10000seq_sampleA1.fastq	9,862,292	fastq-file	06/16/2015 10:...

10 files. Total size: 92,628,372 bytes

Remote site: sftp://mleboulch@genotoul.toulouse.inra.fr/work/mleboulch/Formation/temp

 Formation
 temp

Filename	Filesize	Filetype	Last modified	Per
..				
temp2.fastq	2,226,378	fastq-file	06/29/2017 06:01:33 PM	-rw
temp.fastq	2,226,378	fastq-file	06/29/2017 06:01:33 PM	-rw

2 files. Total size: 4,452,756 bytes


 Copy this address.

Server/Local file	Direction	Remote file	Size	Priority	Status

Queued files | Failed transfers | Successful transfers (3)

Queue: empty

Tools



search tools

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SAM/BAM MANIPULATION : PICARD (BETA)

[Conversion](#)[QC/Metrics for sam/bam](#)

Upload several files from Genotoul without impact too much your Galaxy quota (Galaxy Version 1.0.1)

Options

Path to your directory which contains several files

Path must be like : /work/USERNAME/somewhere/

Execute

What it does

This program allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.

Path to file

This must be an absolute path to a file located in your genotoul work directory. The path must start with **/work/YOUR_USER_NAME/directory**

valid path : /work/LinuxUserName/directory

invalid path : /home/LinuxUserName/work/directory

To use this tool and to maintain the confidentiality of yours directories:

1. Create a "galaxy" directory in your work : mkdir galaxy
2. chmod a+x /work/LinuxUserNam

Example : drwxr-x--x 4

Thanks to the fact that this tool

For example, if your data to downl

Add "x" rights to "others" on /work

It is not useful that "others" ha

Thus, Galaxy can access and rea

Version Galaxy Tool : V1.0

Versions of bioinformatics tools us

Contacts (noms et emails) : [sigena](#)

E-learning available : Yes.

Please cite :

Depending on the help provided you can cite us in acknowledgements, references or both.

Examples : Acknowledgements We wish to thank the SIGENAE group for

References : SIGENAE [http://www.sigena](#)

- Go back to Galaxy and switch to temp history.
- Go to Get Data > Upload Several files from Genotoul
 - Paste the address into field.
- Be careful all the files from the directory will be uploaded!

History



search datasets

temp

0 b

This history is empty. You can [load your own data](#) or [get data from an external source](#)

Tools



search tools



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SAM/BAM MANIPULATION : PICARD (BETA)

[Conversion](#)[QC/Metrics for sam/bam](#)

1 job has been successfully added to the queue - resulting in the following datasets:

1: Upload several files from Genotoul

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

- Click on execute.

- All the files from the directory are uploaded.

History



search datasets

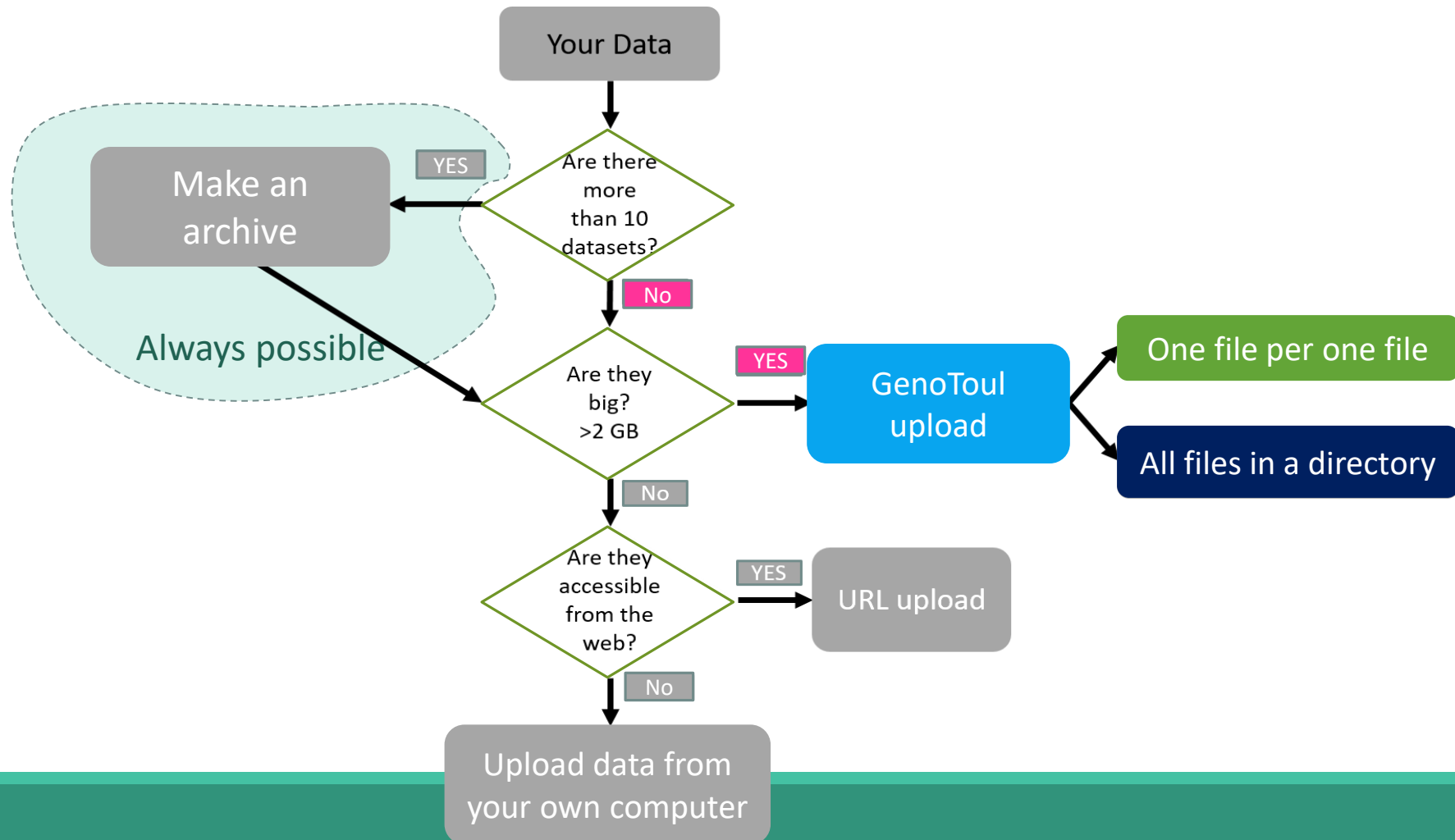
**temp**

3 shown

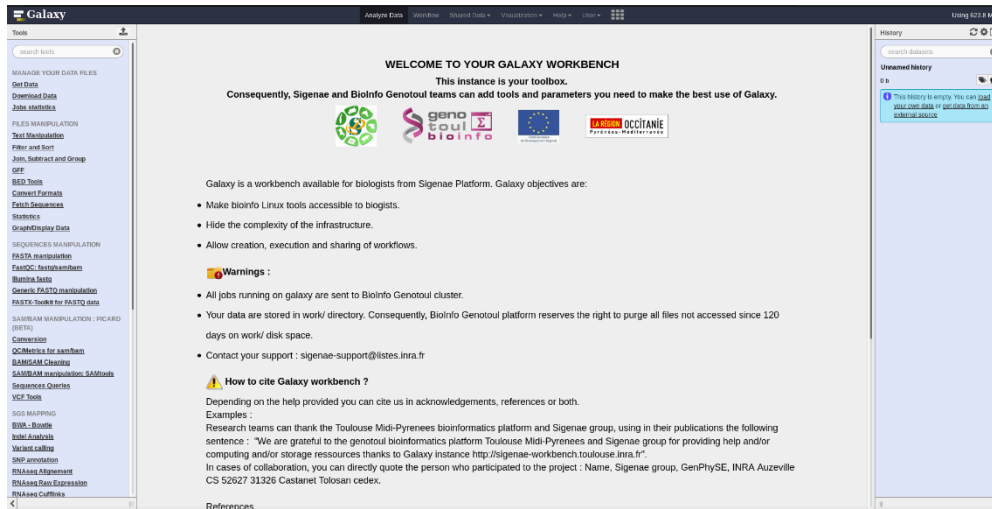
4.25 MB

**3: Upload several files from Genotoul (temp2)****2: Upload several files from Genotoul (temp)****1: Upload several files from Genotoul**

3rd case for uploading your data = OK



Advantage to put your data on Genotoul:



1TB of space



/work: 1TB (1024GB) of space
/save: 250GB of space

- This method allows you to have more space disk and to upload bigger files.
- Files not used in the last 180 days can be purged at any time.

Share a History

Share a history

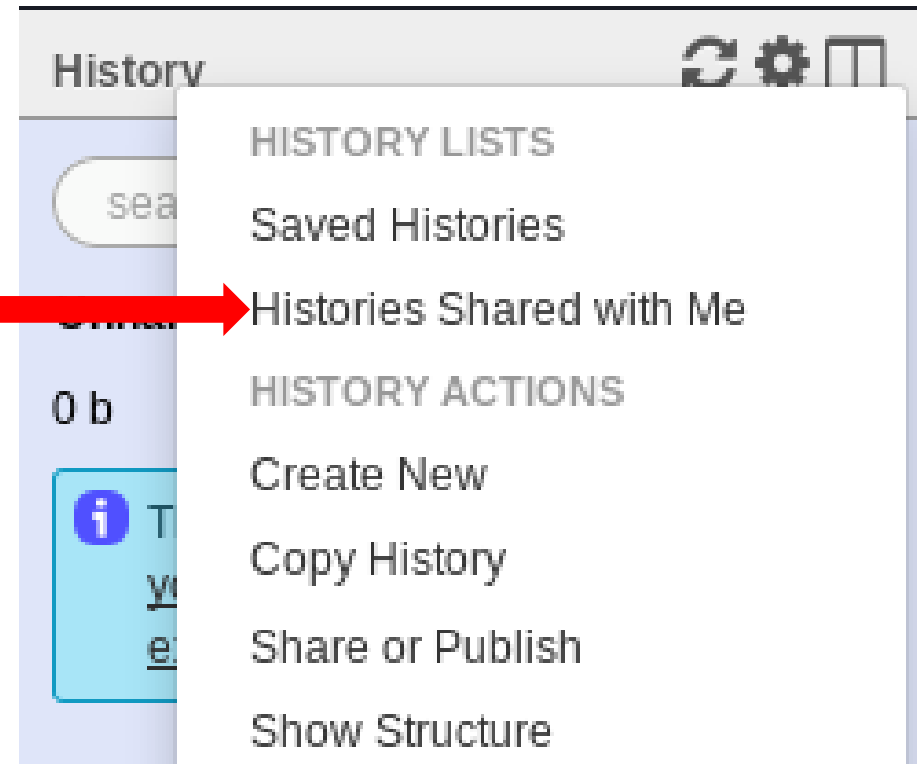
- You can share a history with another Galaxy user:
 - For working with your colleague.
 - For support, so we can help you better and faster.
- You can import shared history to your account too.

Your Turn!

IMPORT A SHARED HISTORY TO YOUR ACCOUNT

Import a shared history

Click on the wheel and click here.



Tools



Histories shared with you by others

<input type="checkbox"/>	Name	Datasets	Created	Last Updated	Shared by
<input type="checkbox"/>	ASMA2016	27	Nov 18, 2016	Mar 09, 2017	geraldine.pascal@inra.fr
<input type="checkbox"/>	Copy of 'ASMA_2016_FE0802' shared by laurent.cauquil@toulouse.inra.fr (active items only)	24	Dec 09, 2016	Jan 03, 2017	geraldine.pascal@inra.fr

0 selected histories:

- Check the box and click on copy to import R1R2 history into your Galaxy account.
- You must import the « R1R2 » history.

Name of the history.

The person who shared the history.

History



search datasets

Historique R1R2

3 shown

126.19 MB

**3: Upload several files from Genotoul (sampleA_R2)****2: Upload several files from Genotoul (sampleA_R1)****1: Upload several files from Genotoul**

empty

format: **txt**, database: ?

Epilog : job finished at Tue Jun 27 22:53:52 CEST 2017

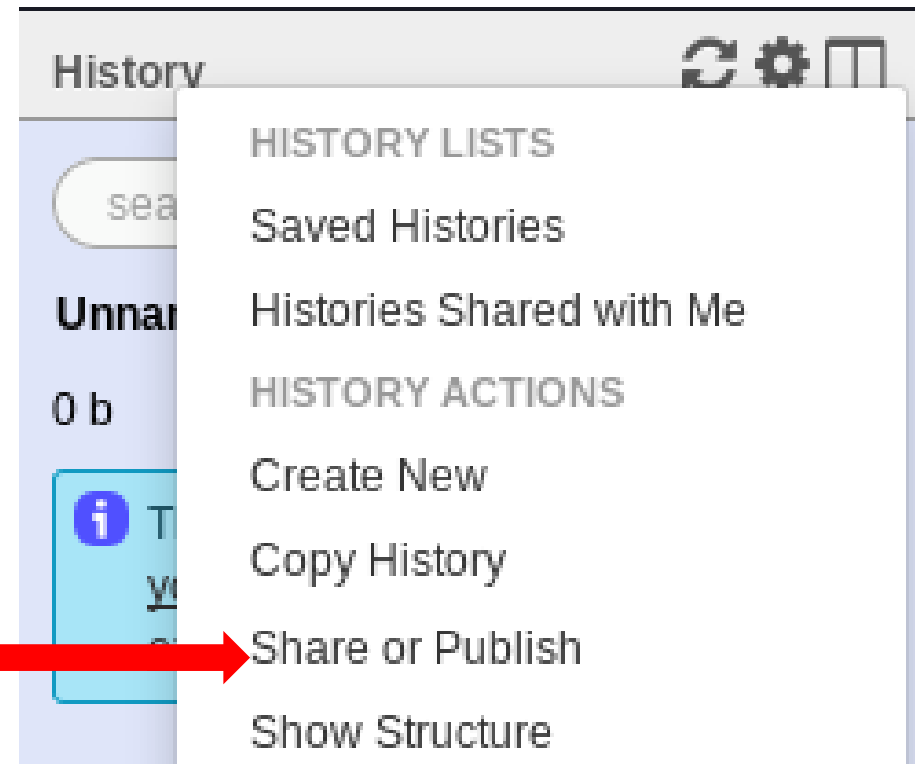


Your Turn!

SHARE A HISTORY WITH YOUR NEIGHBOUR

Share a history

- Switch to the history you want to share.
- Click on the wheel and click here.



Tools



search tools



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SEQUENCES MANIPULATION

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(BETA)[Conversion](#)[QC/Metrics for sam/bam](#)[BAM/SAM Cleaning](#)[SAM/BAM manipulation: SAMtools](#)[Sequences Queries](#)[VCF Tools](#)

Share or Publish History 'Historique R1R2'

Make History Accessible via Link and Publish It

This history is currently restricted so that only you and the users listed below can access it. You can:

[Make History Accessible via Link](#)

Generates a web link that you can share with other people so that they can view and import the history.

[Make History Accessible and Publish](#)

Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Share History with Individual Users

You have not shared this history with any users.

[Share with a user](#)[Back to Histories List](#)

Click on « share with a user ».

History



search datasets



Historique R1R2

3 shown

126.19 MB



3: Upload several files from Genotoul (sampleA_R2)



2: Upload several files from Genotoul (sampleA_R1)



1: Upload several files from Genotoul



empty

format: **txt**, database: ?

Epilog : job finished at Tue Jun 27
22:53:52 CEST 2017



Tools

search tools

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SAM/BAM MANIPULATION : PICARD (BETA)

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Share 1 histories

Histories to be shared:

History Name	Number of Datasets
Historique R1R2	3

Galaxy user emails with which to share histories

Enter a Galaxy user email address or a comma-separated list of addresses if sharing with multiple users

- Enter an email address from a Galaxy user.
- Auto-completion helps you to find your co-worker

History

search datasets

Historique R1R2

3 shown

126.19 MB

3: Upload several files from Genotoul (sampleA_R2)**2: Upload several files from Genotoul (sampleA_R1)****1: Upload several files from Genotoul**

empty

format: **txt**, database: ?

Epilog : job finished at Tue Jun 27 22:53:52 CEST 2017

Galaxy user emails with which to share histories

malo.leboulch@inra.fr

malo.leboulch@inra.fr a-separat

Submit



- You must click on the address in the dropdown menu.
- Click on submit.
- The history will appear in your co-worker's history.

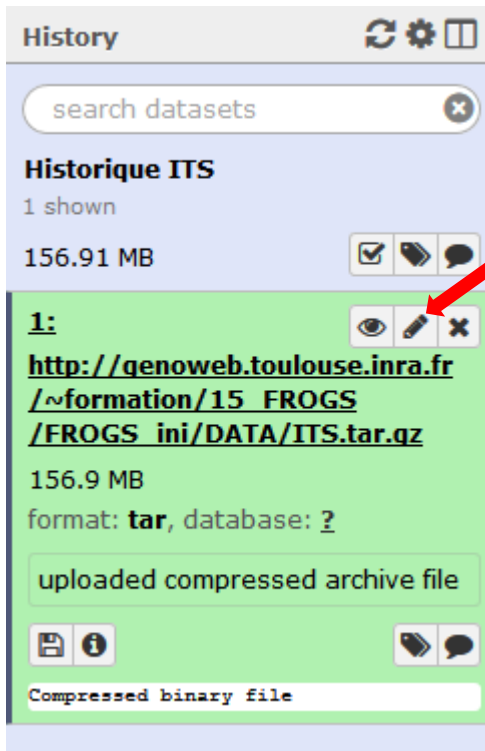
Manipulate datasets

Your Turn!

RENAME A DATASET

Rename a dataset

- Switch to ITS history



The screenshot shows a web interface titled "History". At the top, there is a search bar labeled "search datasets" and a refresh icon. Below the search bar, the section is titled "Historique ITS" and indicates "1 shown" and "156.91 MB". A list of items is shown, with the first item highlighted in green. The item is labeled "1:" and contains the following text: http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/ITS.tar.qz, "156.9 MB", and "format: tar, database: ?". Below this text is a button labeled "uploaded compressed archive file". At the bottom of the item, there are icons for a document, an information icon, and a speech bubble, followed by the text "Compressed binary file". A red arrow points from a blue callout box to the pencil icon in the top right corner of the green highlighted item.

Click here to display attributes and change the name.

Rename a dataset

Change the name here
and call it « ITS1.tar.gz »

[Attributes](#) [Convert Format](#) [Datatype](#) [Permissions](#)

Edit Attributes

Name:

Info:

Annotation / Notes:

Add an annotation or notes to a dataset; annotations are available when editing a dataset.

Database/Build:

This will inspect the dataset and attempt to correct the above column values.

Rename a dataset

Attributes Convert Format Datatype Permissions

Edit Attributes

Name:

Info:

Annotation / Notes:

Add an annotation or notes to a dataset; annotations are available when a history is viewed.

Database/Build:

Save

Auto-detect

This will inspect the dataset and attempt to correct the above column values if they are not accurate.

If you put the wrong datatype in during the upload, you can change it here.

Rename a dataset

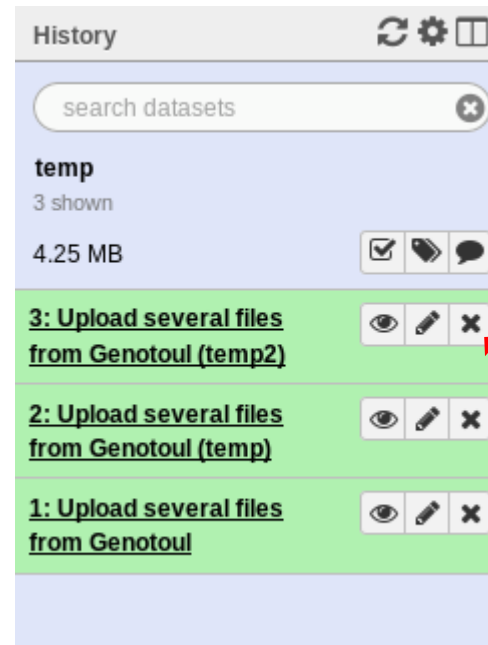
- Do the same with the merged history:
 - Switch to the merged history.
 - Change the name of the file to «100_10000seq_sample.tar.gz ».

Your Turn!

DELETE A DATASET

Delete a dataset

- Switch to temp history.



Click here to delete a dataset.

Delete a dataset

The image shows two screenshots of the Galaxy History interface, connected by a large green arrow pointing from left to right. The left screenshot shows a dataset named 'temp' with a size of 4.25 MB. A red box highlights the text '1 deleted' next to the dataset name. A blue callout box with the text 'Click here.' has a red arrow pointing to this text. Below the dataset name, there are two entries: '2: Upload several files from Genotoul (temp)' and '1: Upload several files from Genotoul'. The right screenshot shows the same dataset 'temp' with a size of 4.25 MB. A red box highlights a warning message: 'This dataset has been deleted. Undelete it. Permanently remove it from disk'. A blue callout box with the text 'Delete this dataset permanently.' has a red arrow pointing to the 'Permanently remove it from disk' link. Below the warning, there are three entries: '3: Upload several files from Genotoul (temp2)', '2: Upload several files from Genotoul (temp)', and '1: Upload several files from Genotoul'.

Click here.

temp
2 shown, 1 deleted
4.25 MB

2: Upload several files from Genotoul (temp)

1: Upload several files from Genotoul

History

search datasets

temp
3 shown, [hide deleted](#)
4.25 MB

This dataset has been deleted
Undelete it
[Permanently remove it from disk](#)

3: Upload several files from Genotoul (temp2)

2: Upload several files from Genotoul (temp)

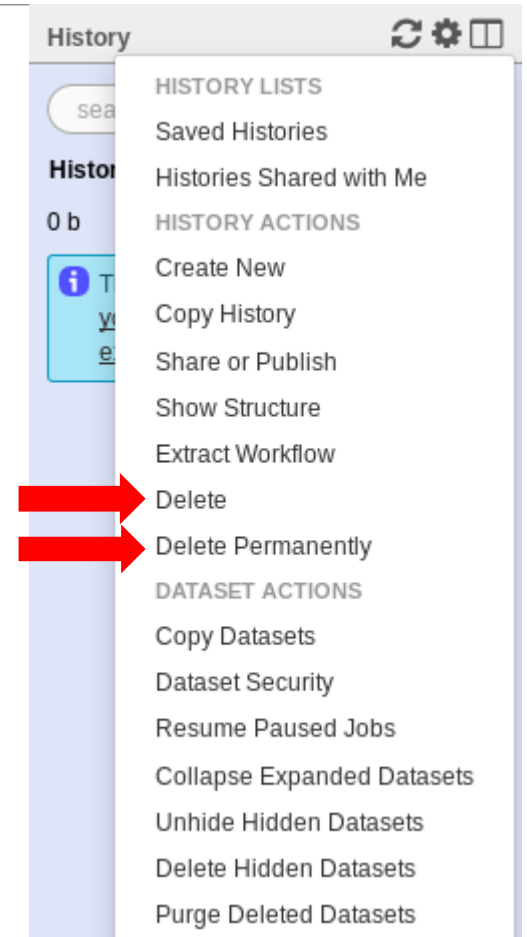
1: Upload several files from Genotoul

Delete this dataset permanently.

Nothing is deleted in Galaxy until you delete it permanently (=purge).

How to delete a history?

- Stay in the temp history.
- Click on the wheel.
- Click on delete.
- A deleted item on Galaxy is recoverable.
- To definitively delete it:
click on « Delete Permanently ».



Current History

Switch to

multiplex
2 shown, 1 [deleted](#)
2.12 MB

search datasets

Drag datasets here to copy them to the current history

2: multiplex.fastq

1: barcode_forward.tabular

Switch to

merged
1 shown
4.55 MB

search datasets

1: 100_10000seq_sample.tar.gz

Switch to

454
1 shown
26.13 MB

search datasets

1: 454.fastq

Switch to

Historique R1R2
2 shown, 1 [deleted](#)
126.19 MB

search datasets

3: sampleA_R2

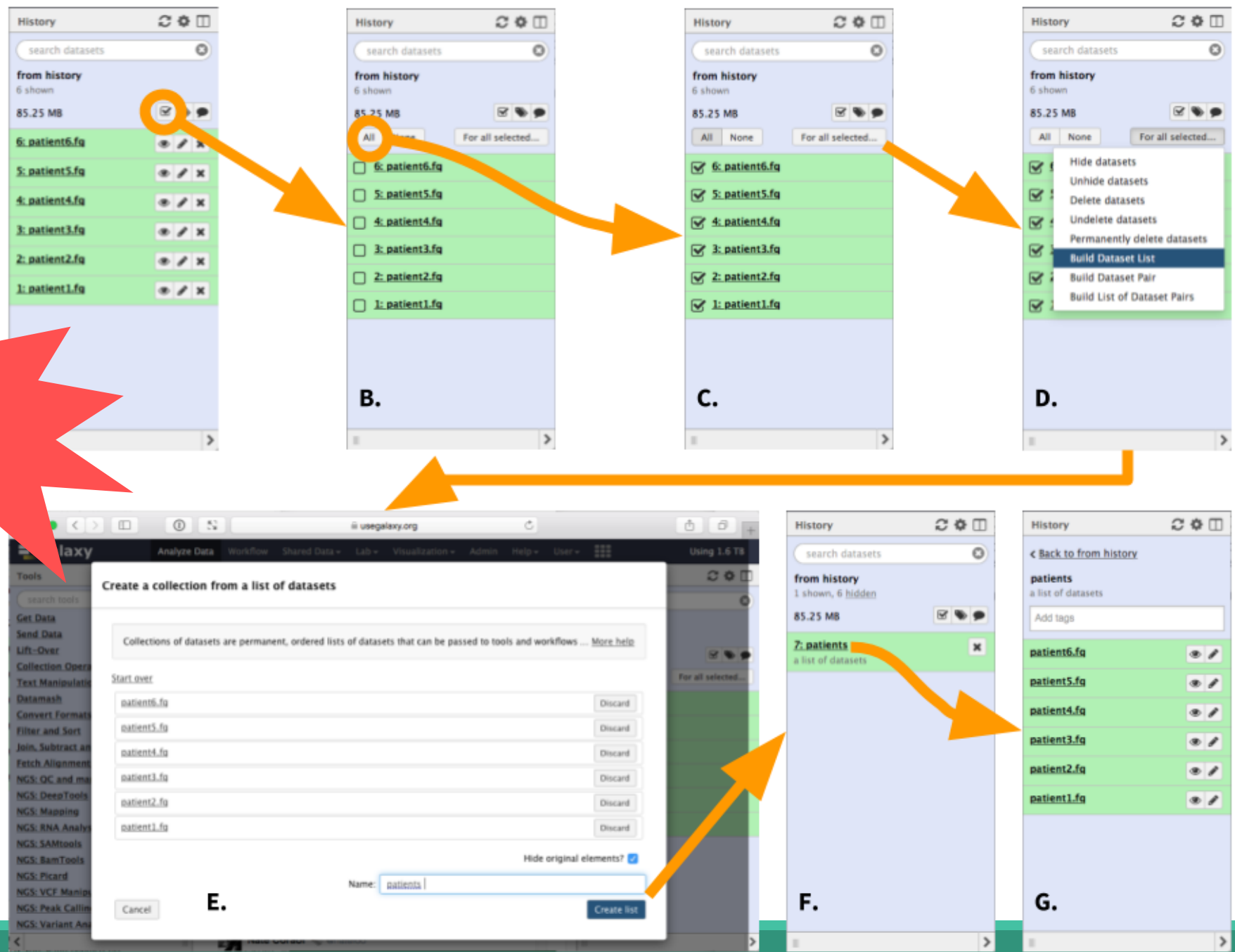
2: sampleA_R1

One word about data collections

- Used to perform the same analysis on multiple files.
- Gather multiple datasets in one collection.



Doesn't work with FROGS!



Other tools available on Galaxy

- Text Manipulation
- Filter and Sort data
- FASTA manipulation

Galaxy support

- Mail: support.sigenae@inrae.fr
- If you need more training about bioinformatics and Galaxy, please connect to Sigenae e-learning platform:
<http://sig-learning.toulouse.inra.fr/>

How to cite Galaxy?

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How to cite Genotoul Galaxy workbench?

- Research teams can thank the Toulouse Occitanie bioinformatics platform and Sigenae group, using in their publications the following sentence : "We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigenae group for providing help and/or computing and/or storage resources thanks to Galaxy instance <http://sigenae-workbench.toulouse.inra.fr>".
- In cases of collaboration, you can directly quote the person who participated to the project : Name, Sigenae group, GenPhySE, INRAE Auzeville CS 52627 31326 Castanet Tolosan cedex.