

#### Formation FROGS juillet 2019

Géraldine Pascal, Laurent Cauquil

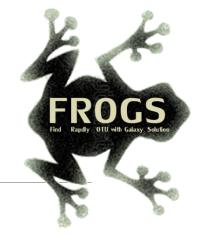
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# Training on Galaxy: Metagenomics July 2019

# Find, Rapidly, OTUs with Galaxy Solution

FRÉDÉRIC Escudié\* and LUCAS AUER\*, MARIA BERNARD, LAURENT CAUQUIL, SARAH MAMAN, MAHENDRA MARIADASSOU, SYLVIE COMBES, GUILLERMINA HERNANDEZ-RAQUET, GÉRALDINE PASCAL & MALO LE BOULCH

\*THESE AUTHORS HAVE CONTRIBUTED EQUALLY TO THE PRESENT WORK.





# Introduction to Galaxy platform and preparation of FROGS training July 2019

MALO LE BOULCH, SARAH MAMAN, GÉRALDINE PASCAL

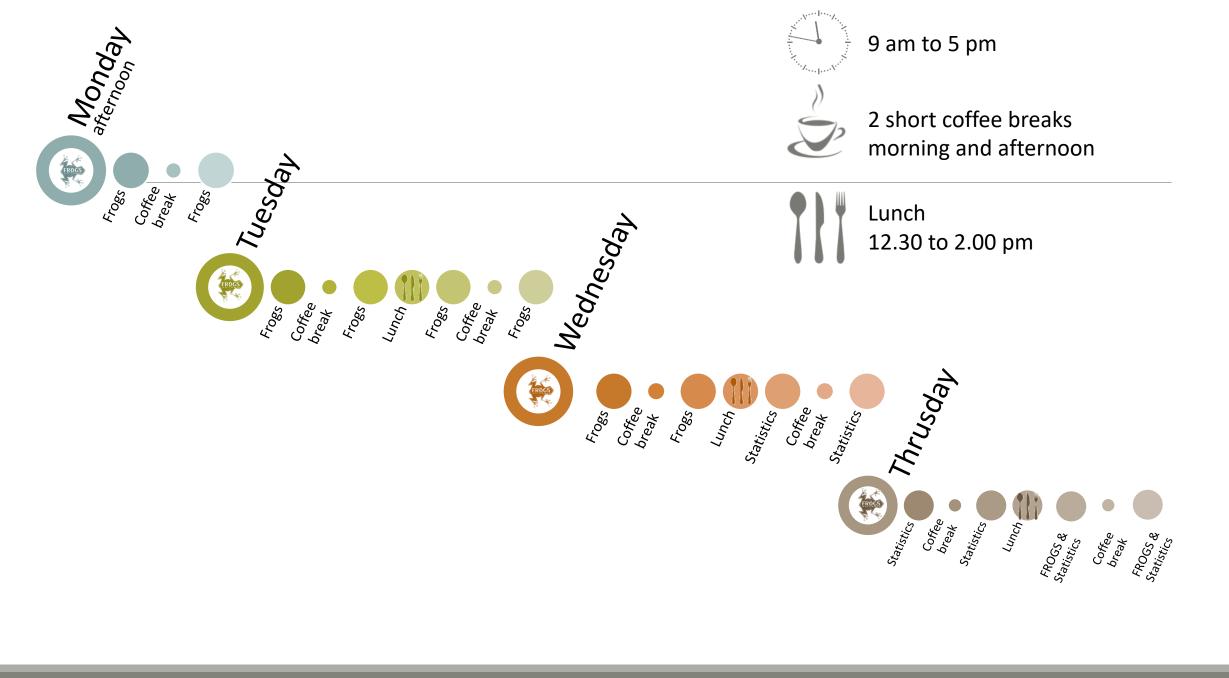


### Chitchat time!

- 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?
- 16S/ITS ?
- Your background ?



## Objectives of the 1<sup>st</sup> part

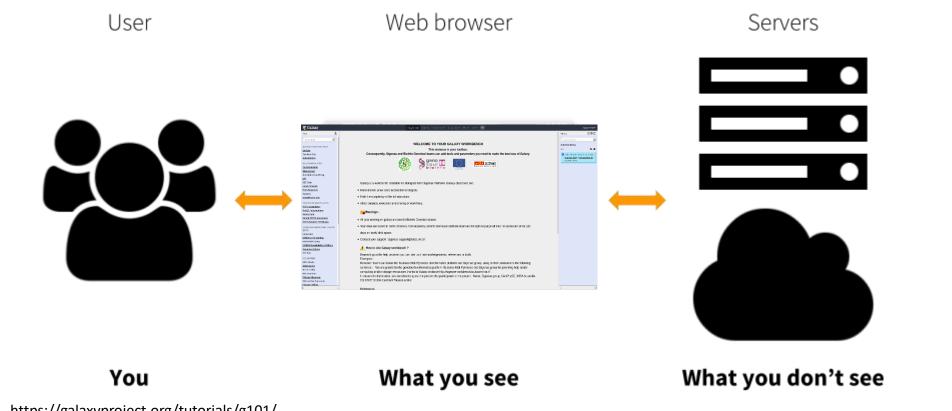
- Learn the basics of Galaxy
- Being independent when using it
- Prepare the datasets for FROGS formation

# 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?

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

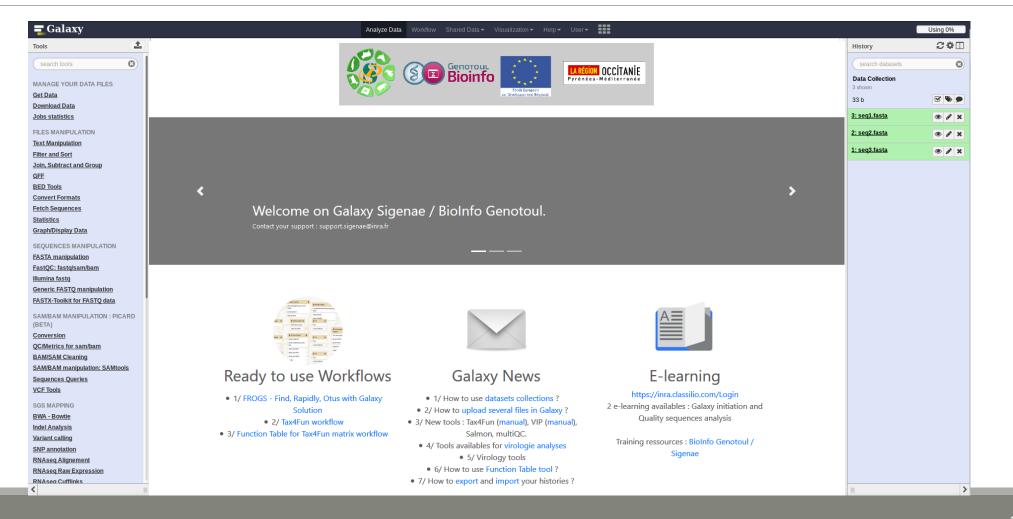
⚠ The different platforms of Galaxy are not connected together

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

## Exemple of 2 INRA Galaxy platforms

📲 Galaxy / Migale	Analyze Data Workflow Shared Data - Visualization - Help - User -
Tools	
search tools	Bienvenue sur le portail Galaxy de la plateforme Migale. Pour tous renseignements, demandes ou remarques, veuillez contacter galaxy-help@jouy.inra.fr
Migale Tools	
Get Data	
Send Data	
Lift-Over	micipile
Gene Annotation	
Gene Prediction	Plateforme de BioInformatique - INRA Jouy en Josas
Text Manipulation	
Filter and Sort	
Join, Subtract and Group	
GFFtools	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
Convert Formats	Center for Comparative Genomics and Bioinformatics. L'utilisateur peut réaliser quatre grands types d'opérations :
Extract Features	- manipulation de fichiers : ajout ou suppression de colonnes, trier les fichiers, concaténer plusieurs fichiers, comparaison de listes,
Fetch Sequences	- opérations sur les données : sommer, moyenner, soustraire, calculer la couverture d'une région déterminée,
Fetch Alignments	- analyse de séquences : calculer des corrélations, utiliser des outils d'EMBOSS, aligner les données de séquençage,
Get Genomic Scores	- visualisation des données : afficher des alignements multiples, générer des graphiques,
Statistics	Contact: <u>galaxy-help@jouy.inra.fr</u>
Graph/Display Data	
Phenotype Association	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.
<u>Sequence Alignment/Pairwise</u> <u>Alignment</u>	Une Foire Aux Questions autour de Galaxy a été mise en place sur le site web de la plateforme Migale.
Metagenomic analyses	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.
Metagenomics FROGS	
Metagenomics Qiime	SCIENCE & MIRAC
Metagenomics Mothur	
FASTA manipulation	
NGS: QC and manipulation	
NGS: Assembly	This project is supported in part by NSE_NUCPI and the Huck Institutes of the Life Sciences
NGS: Mapping	This project is supported in part by <u>NSF</u> , <u>NHGRI</u> , and <u>the Huck Institutes of the Life Sciences</u> .
NGS: RNA Analysis	
NGS: SAM Tools	
NGS: Peak Calling	
SNP/WGA: Data; Filters	
<u>Variant Analysis</u>	
NGS: Picard	
NGS: Variant analysis	
Workflows	
All workflows	

## Exemple of 2 INRA Galaxy platforms



# Your Turn!

CONNECT TO OUR GALAXY WORKBENCH

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.



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 : <u>http://bioinfo.genotoul.fr/index.php/ask-for/create-an-account/</u>



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

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

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

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

The first time in this pop-up window:

~	Authentification requise 🔷 🔿	0
and the second	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 »	e
Utilisateur :		
Mot de passe :		
	Annuler OK	

#### • And a second time, in the browser:

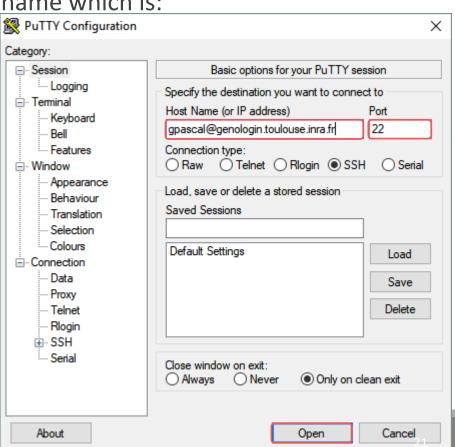
<b>=</b> Galaxy	Analyze Data	Workflow	Shared Data 🕶	Visualization 🔻	Help 🕶	User∓	•••	Using 0 bytes
This Galaxy instance has been configured such that only users who are logged in may use it.								
Login								
Username / Email Address: Password:								
Login								

- In order to change your password, you need to download PuTTY: <u>http://www.putty.org/</u>
- 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.

- Launch PuTTY.
- In the following window, you must enter your host <u>name which is:</u>

YourGenotoulName@genologin.toulouse.inra.fr

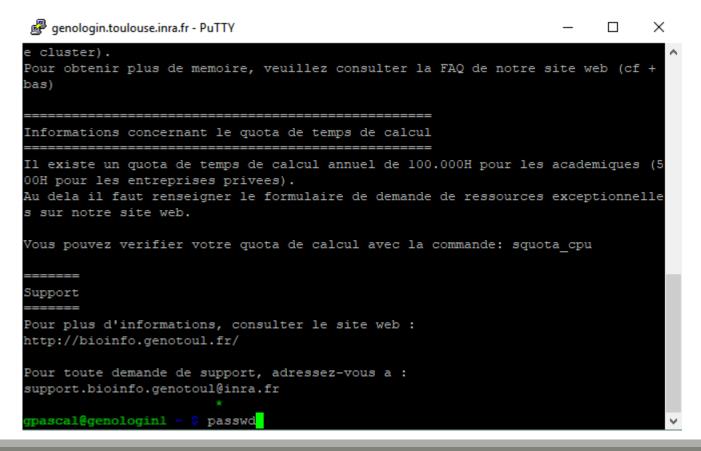
- The connection type must be SSH.
- Click on « Open » .



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



Type « passwd » and hit « Enter ».



Enter your current password and hit « Enter ».

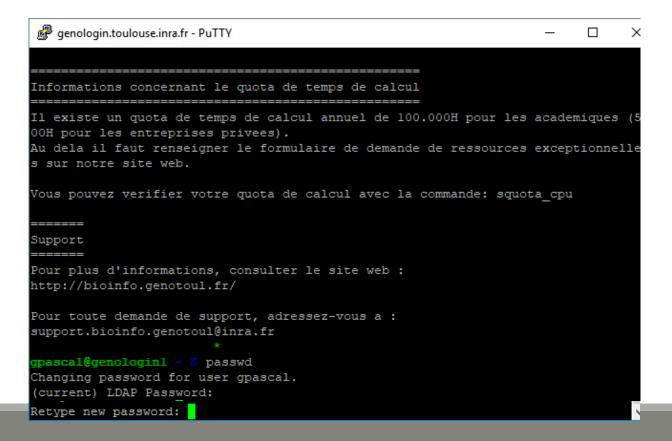
🥵 genologin.toulouse.inra.fr - PuTTY		—	$\times$
bas)			^
Informations concernant le quota de temps de calcul			
Il existe un quota de temps de calcul annuel de 100.000H po 00H pour les entreprises privees). Au dela il faut renseigner le formulaire de demande de ress s sur notre site web.			
Vous pouvez verifier votre quota de calcul avec la commande	e: squot	ta_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@genologinl ~ \$ passwd			
Changing password for user gpascal. (current) LDAP Password:			~

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

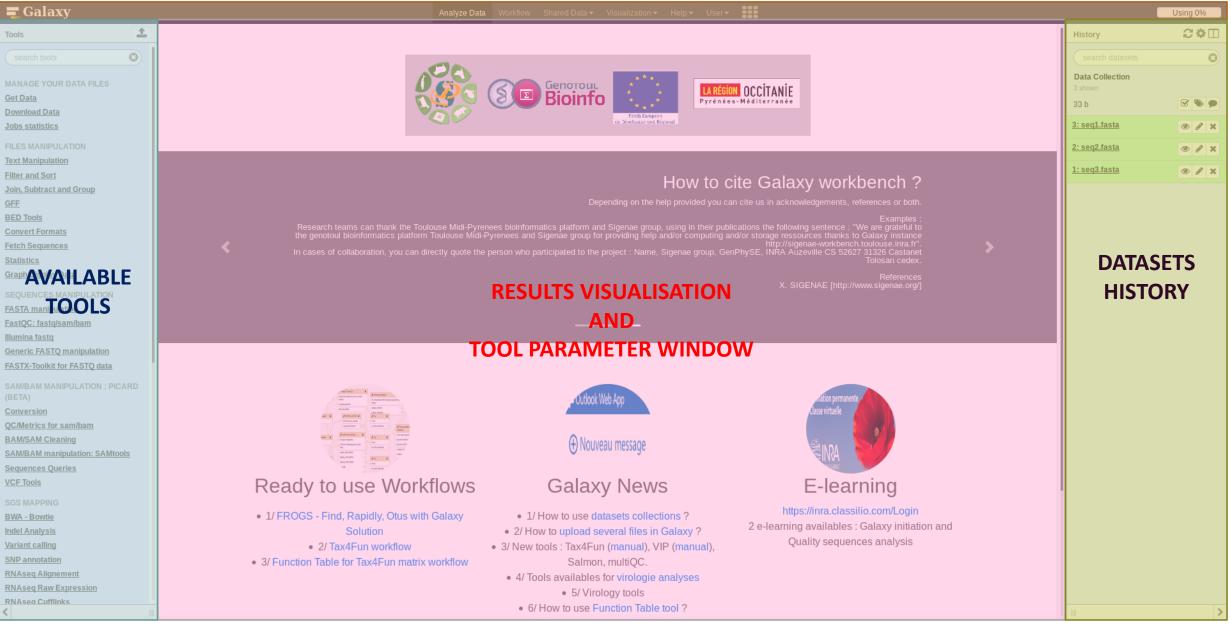
Benologin.toulouse.inra.fr - PuTTY	_		×
			^
Informations concernant le quota de temps de calcul			
Il existe un quota de temps de calcul annuel de 100.000H pour les 00H pour les entreprises privees). Au dela il faut renseigner le formulaire de demande de ressources s sur notre site web.		-	
Vous pouvez verifier votre quota de calcul avec la commande: squot	a_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 *			
<b>gpascal@genologinl ~ \$</b> passwd Changing password for user gpascal. (current) LDAP Password: New LDAP password:			~



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



#### MAIN MENU



# 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

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

	<b>=</b> Galaxy		
	Tools	1	
Search a tool by name.	Search tools MANAGE YOUR DATA FILES Get Data Download Data Jobs statistics FILES MANIPULATION Text Manipulation		
	Filter and Sort		

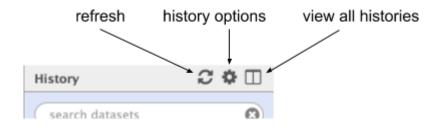
# Manipulate Histories

# Your Turn!

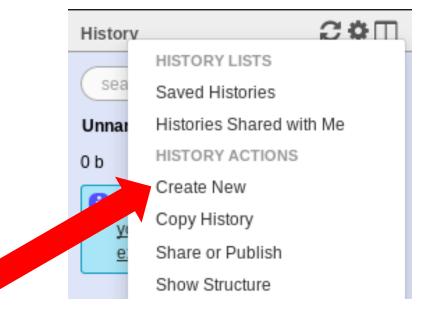
CREATE THE 4 HISTORIES NEEDED FOR THE FROGS FORMATION

To create a new history:

Click on the wheel.

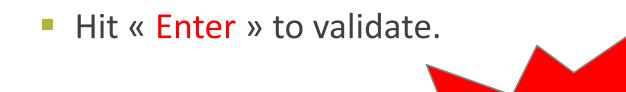


Click on « create new ».



### To rename a history:

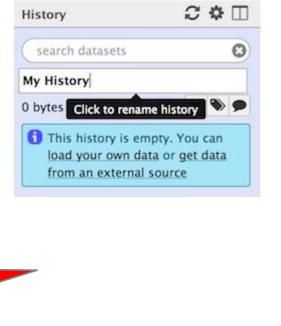
- Click on the history name (at the top).
- Enter « multiplex ».



Don't use special

characters or

accents!



#### Exercise

- Create histories named:
  - 454 or 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.

History	₽\$□
search datasets	8
imported: kinetic Nu Analysis 31 shown	ıria Mach
34.75 MB	
<u>38: FROGSSTAT</u> Phyloseg Import	• * *

## Explore the « View all histories » section

<b>=</b> Galaxy	Analyze Data	Workflow	Shared Data <del>-</del>	Visualization <del>-</del>	Help <del>-</del>	User 🗸 📕
Done search histories	Se Se	earch all datas	ets 😢	•••		Create new
Current History		- Switch	to		•	Switch to
imported: kinetic Nuria Ma 31 shown 34.75 MB search datasets	ch Analysis 🕑 🍋 🗩	<b>Test</b> 73 sho 233.7 sea	6 Copy Delete			Copy of 'full ph maria.bernard 14 shown 11.32 MB
Drag datasets here to copy them to the S& FROGSSTAT Phylosed	he current history	76: FF report	ROGS Pre-proces	<u>s:</u> @ ø	<pre>   × </pre>	search datase

#### Switch current history

	Analyze Data Workflow Shared Data 👻 Visualization 👻 Help 🗨	- U	Jser <del>-</del>	Using 2.3 C	GΒ
Done search histories	search all datasets			Create ne	ew
Current History	Switch to	•	Switch to	-	្
Historique 454	Historique		Historique 2		.oadir
0 b	0ь		0 b	>	ıg his:
search datasets	search datasets		search datasets	8	tories
Drag datasets here to copy them to the current history	1 This history is empty	וור	1 This history is empty		:
1 This history is empty					

- 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

- 5 ways to upload your data to Galaxy:
  - From your computer

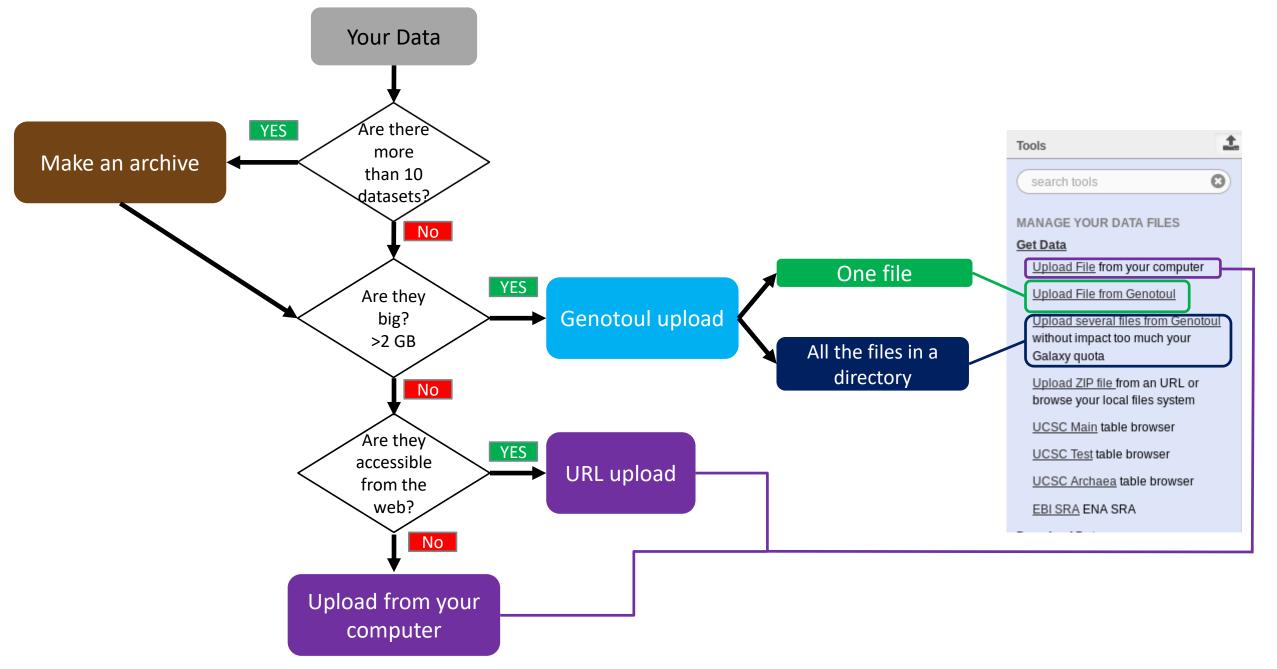


- From Genotoul Bioinfo clusters
- Shared by other users of Galaxy





#### How to choose your upload method?



# Your Turn!

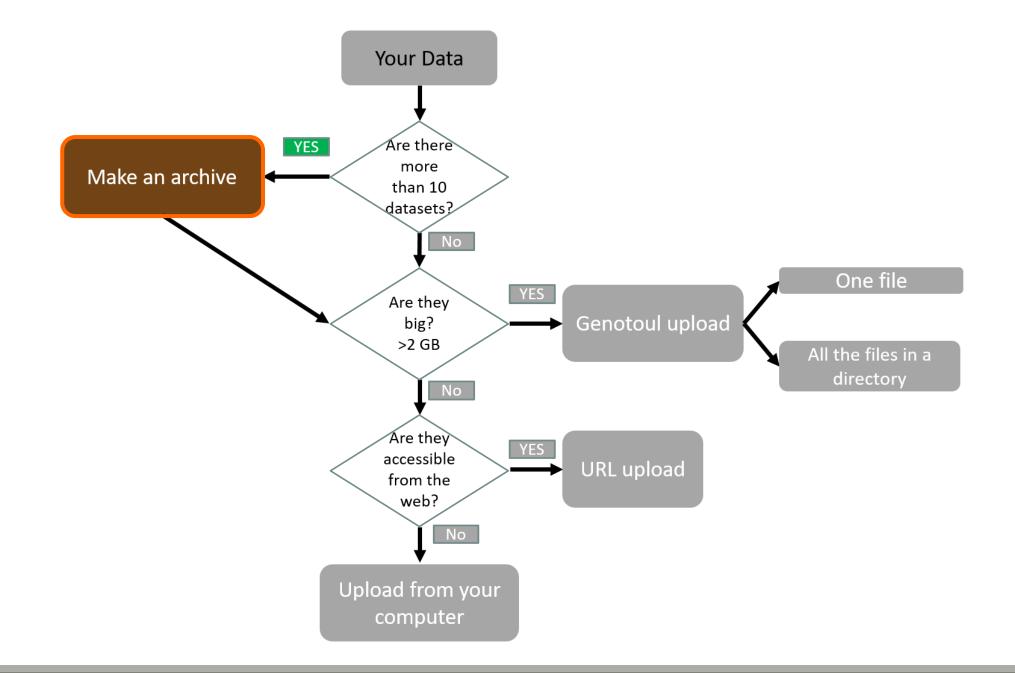
PREPARE FILES

#### Formation data

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

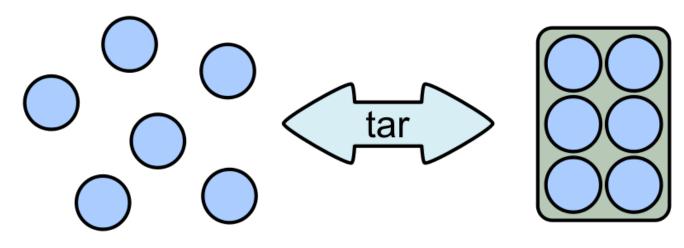
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	ata		ٽ ~	Recherch.	<i>p</i>
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<ul> <li>Bureau</li> <li>Téléchargemente</li> <li>Documents</li> <li>Images</li> <li>Choose</li> <li>Formation Galax</li> <li>Peazip</li> </ul>	merged multiplex temp	29/06/2017 14:34 29/06/2017 14:34 29/06/2017 14:34	Dossier de fichiers Dossier de fichiers Dossier de fichiers		
Screenshot					

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



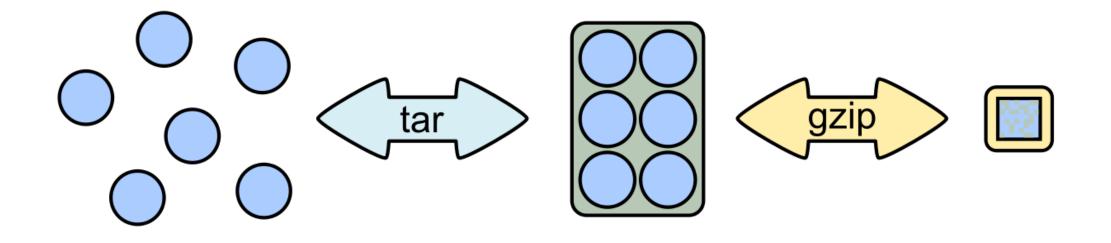
#### Create a Tar file

- 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: <u>http://www.7-zip.org/</u>



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

📙 🔄 📙 🚽 🛛 merged						- 🗆	×
Fichier Accueil Partag	ge Affichage						$\sim$
← → ∽ ↑ 🔒 → Dat	a > merged				~ Ū	Rechercher dans : merged	Q
^	Nom	Modifié le	Туре	Taille			
📌 Accès rapide	100_10000seq_sampleA1.fastq	04/04/2018 10:37	Fichier FASTQ	9 632 Ko			
📃 Bureau 🛛 🖈	100_10000seq_sampleA2.fastq	04/04/2018 10:37	Fichier FASTQ	9 633 Ko			
🕂 Téléchargem 🖈	100_10000seq_sampleA3.fastq	04/04/2018 10:37	Fichier FASTO	9 629 Ko			
🚆 Documents 🖈	100_10000seq_sampleB1.fastq	04/04/2018 10:37	Fichier FASTQ	9 482 Ko			
📰 Images 🛛 🖈	100_10000seq_sampleB2.fastq	04/04/2018 10:37	Fichier FASTQ	9 481 Ko			
Formation Galax	100_10000seq_sampleB3.fastq	04/04/2018 10:37	Fichier FASTQ	9 480 Ko			
Musique	100_10000seq_sampleC1.fastq	04/04/2018 10:37	Fichier FASTQ	9 489 Ko			
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Select all files and right click on it > 7-Zip > Add to archive . . .

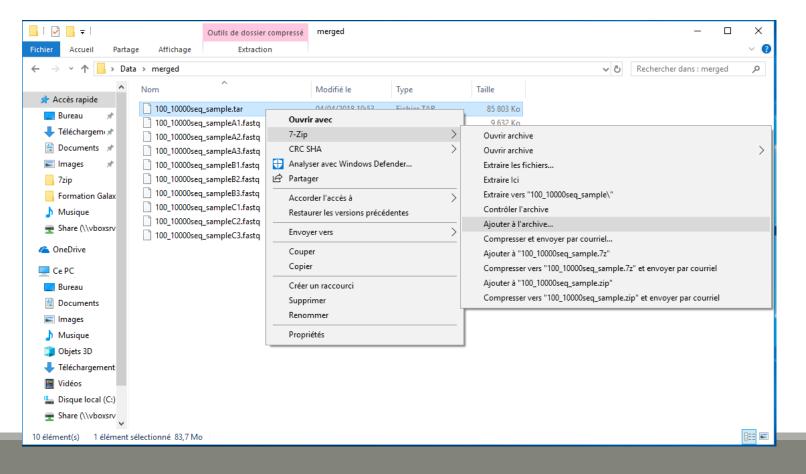
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📃 Bureau				>	Ajouter à l'archive				
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Musique		Couper			Compresser vers "m	nerged.7z" et envoyer par co	urriel		
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- Change the name of the archive to:
- « 100\_10000seq\_sample.tar »
- Choose « tar » as archive format .
- Click on OK .

Ajouter à l'archive		×
Archive : C:\Users\Malo\Desktop\Data\merged\ 100_10000seq_sample.tar		<b>~</b>
Format de l'archive : 🛛 🗸 🗸	Mode de mise à jour :	Ajouter et remplacer les fich $ \smallsetminus $
Niveau de compression : Aucune $\sim$	Mode de chemin :	Nom de chemin relatif $\sim$
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Taille du dictionnaire :	Compresser des fich	
Taille des mots : V	Effacer les fichiers a	après compression
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Nombre de threads CPU : V 1	Entrez le mot de passe	
Mémoire pour la compression : 1 MB	Entrez le mot de passe	à nouveau :
Mémoire pour la décompression : 1 MB		
Diviser en volumes, octets :	Afficher le mot de pa	asse
Paramètres :	Méthode de chiffremen	t : ~
NTFS Emmagasine liens symboliques Emmagasine liens solides	OK Ann	uler Aide

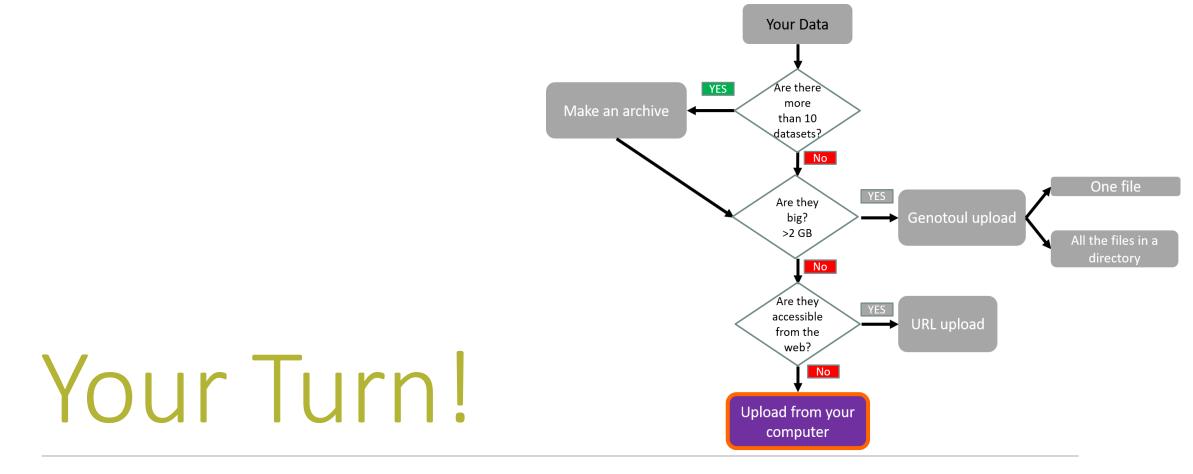
Select the newly created archive and right click on it > 7-Zip > Add to archive . . .



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

Archive : C:\Users\Malo\De	sktop\Data\merged\ mple.tar.gz	N		×
Format de l'archive :	gzip	~	Mode de mise à jour :	Ajouter et remplacer les fict $ \smallsetminus $
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Diviser en volumes, octets :			Afficher le mot de p	Dasse
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🕂 Téléchargemi		100_10000sec	q_sampleA1.fastq	04/04/2018 10:37	Fichier FASTQ	9 632 Ko			
Documents	*	📄 100_10000sec	q_sampleA2.fastq	04/04/2018 10:37	Fichier FASTQ	9 633 Ko			
📰 Images	*	📄 100_10000sec	q_sampleA3.fastq	04/04/2018 10:37	Fichier FASTQ	9 629 Ko			
7zip		📄 100_10000sec	q_sampleB1.fastq	04/04/2018 10:37	Fichier FASTQ	9 482 Ko			
Formation Ga	lax	🗋 100_10000sec	q_sampleB2.fastq	04/04/2018 10:37	Fichier FASTQ	9 481 Ko			
💧 Musique		🗋 100_10000sec	q_sampleB3.fastq	04/04/2018 10:37	Fichier FASTQ	9 480 Ko			
Share (\\vbox		🗋 100_10000sec	q_sampleC1.fastq	04/04/2018 10:37	Fichier FASTQ	9 489 Ko			
	SIV	🗋 100_10000sec	q_sampleC2.fastq	04/04/2018 10:37	Fichier FASTQ	9 487 Ko			
i OneDrive		🗋 100_10000sec	q_sampleC3.fastq	04/04/2018 10:37	Fichier FASTQ	9 487 Ko			
💻 Ce PC									
📃 Bureau									
🔮 Documents									
📰 Images									
👌 Musique									
🧊 Objets 3D									
🕂 Téléchargeme	ent								
📑 Vidéos									
🏪 Disque local (	C:)								
🛖 Share (\\vbox	srv 🗸								
11 élément(s) 1 élé	ément s	électionné 4,27 Mo							:== 



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

Tools	1
search tools	3)
MANAGE YOUR DATA FILES	
<u>Get Data</u>	
Upload File from your computer	
Upload File from Genotoul	
Upload several files from Genotou	1
without impact too much your	
Galaxy quota	
<u>Upload ZIP file</u> 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 from web or upload from disk

Regular	<u>Composite</u>	
		& Drop files here
		Click here to choose a file on your hard drive.
		Upload one of the two files in the multiplex directory.
Ţ	ype (set all):	Auto-detect <b>v Q</b> Genome (set all): unspecified (?) <b>v</b>
		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

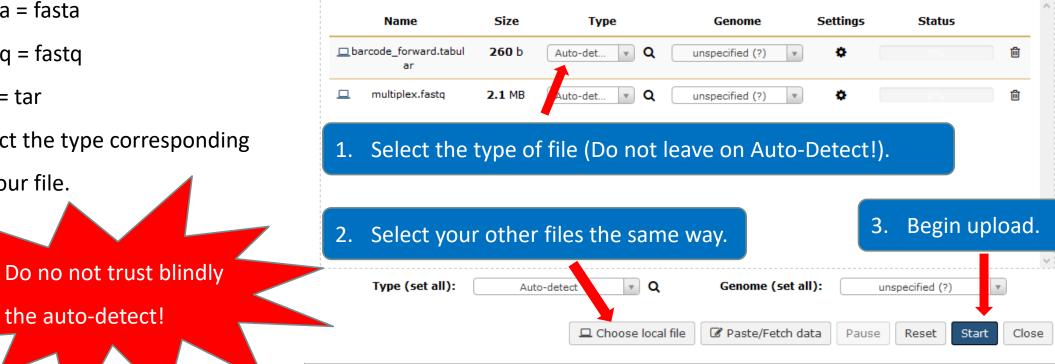
the auto-detect!

to your file.

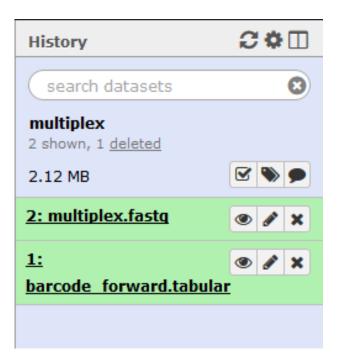
#### Download from web or upload from disk

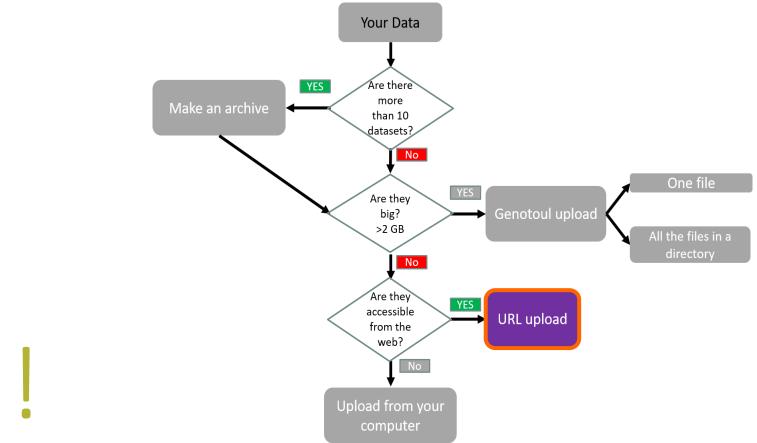
Regular Composite

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



#### Upload local files





## Your Turn!

UPLOAD FILE FROM AN URL

## Upload file from URL

- 1. Switch to 454 or 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/454.fastq

#### Or

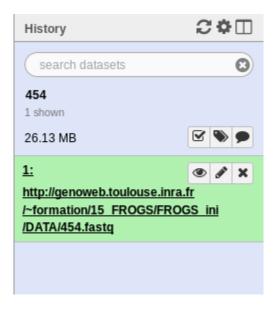
http://genoweb.toulouse.inra.fr/~formation/15\_FROGS/FROGS \_\_ini/DATA/ITS.tar.gz

- 1. Change the type!
- 2. Click on Start.
- 3. You can put one address per line for multiple uploads.

#### Download from web or upload from disk

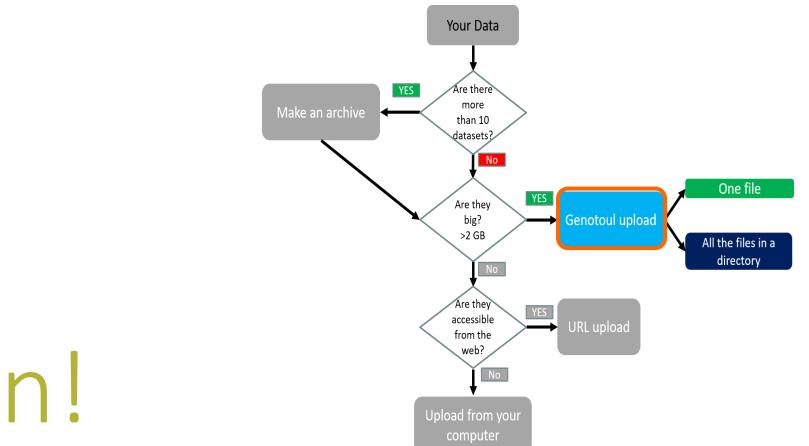
Regular	<u>Composite</u>						
		You ad	ided 1 file(s) to the queue. A	dd more files or click 'Start'	to proceed.		
	Name	Size	Туре	Genome	Settings	Status	
C	New File	76 b	Auto-detect 🔻 🗨	unspecified (?)	• •	0%	圃
	You can tell Ga	laxy to download data from	m web by entering URL in th	nis box (one per line). You ca	an also directly paste th	e contents of a file.	
http://ge	enoweb.toulouse.ii	nra.fr/~formation/15_FRO	GS/FROGS_ini/DATA/454.1	astq			
http://	genoweb.toulou	use.inra.fr/~formation,	/15_FROGS/FROGS_ini/	DATA/ITS.tar.gz			<b>~</b>
Ţ	ype (set all):	Auto-detect	▼ Q	Genome (set all):	unspecifie	d (?) 🔻	
			□ Choose	local file 🕜 Paste/Fe	etch data Pause	Reset	urt Close

#### Upload file from URL



OR

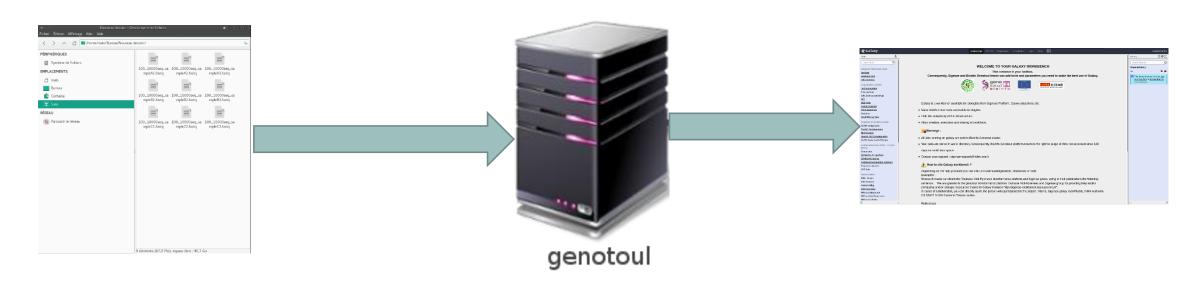
History	C	Ф				
search datasets			8			
ITS 1 shown 156.91 MB		•	•			
1:      Attp://genoweb.toulouse.inra.fr /~formation/15 FROGS /FROGS ini/DATA/ITS.tar.gz						



## Your Turn!

#### UPLOAD FILES TO GENOTOUL AND LINK IT TO GALAXY

#### Objectives



Transfer your files to your Genotoul account and link the file to Galaxy.

Preparation

- 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/



✓ File Edit View Transfer Server Book			FileZilla	≜ O O
Host:   Username:	118 😣 🕵 🍤 🗉 <table-cell> 🖉 Password:</table-cell>	Port: Quickconnect	Connection	
.ocal site: /home/malo/Bureau/Nouveau do	ossier/		Remote site:	
- 1				
🕀 📙 bin			i	
	Filesize Filetype 🗸 L	ast modified	Filename	Filesize Filetype 🗸 Last modified
	Thesize Thetype 🗸 L	ast mouneu	Thename	Thesize Therype 👻 Last modified
100_10000seq_sample.tar.gz	4,773,706 gz-file 06	5/28/2017 05:		
sampleA_R2.fastq		5/27/2017 10:		Not connected to any server
sampleA_R1.fastq	66,157,532 fastq-file 06	5/27/2017 10:		
100_10000seq_sampleC3.fastq	9,714,424 fastq-file 06	5/16/2015 10:		
] 100_10000seq_sampleC2.fastq	9,714,107 fastq-file 06	5/16/2015 10:		
] 100_10000seq_sampleC1.fastq	9,716,445 fastq-file	5/16/2015 10:		
100_10000seq_sampleB3.fastq	9,707,364 fast Qur Po	5/2015 10: 56/2015 10:		The server
] 100_10000seq_sampleB2.fastq	9,707,921 fastq-file 06	5/16/2015 10:		
100_10000seq_sampleB1.fastq	9,709,480 fastq-file 06	5/16/2015 10:		
] 100_10000seq_sampleA3.fastq	9,859,424 fastq-file 06	5/16/2015 10:		
] 100_10000seq_sampleA2.fastq	9,863,209 fastq-file 06	5/16/2015 10:		
] 100_10000seq_sampleA1.fastq	9,862,292 fastq-file 06	5/16/2015 10:		
2 files. Total size: 224,943,436 bytes			Not connected.	
Server/Local file		Direction Remote file	····	Size Priority Status
Server Eved me		on cellon Remote ne		Size Filolity Status
			Upload advancement	
Failed transform	transfors			
ueued files Failed transfers Successful	t transiers			
				Queue: empty

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Host:	Username: Password:	Port: Quickconnect 👻		
Status: Status: Status:	Listing directory usung of "homerniebouch" work Directory listing of "/work/mleboulch" successful Retrieving directory listing of "/work/mleboulch/Formation" Listing directory /work/mleboulch/Formation Directory listing of "/work/mleboulch/Formation" successful Deleting 2 files from "/work/mleboulch/Formation" Disconnected from server			
Local site:	/home/malo/Bureau/Data/	~	Remote site: /work/mleboulch/Formation	~
	Data     merged		Image: Imag	
Filename	Filesize Filetype 🗸		Filename	Filesize Filetype 🗸 Last modified Per
 temp multiple merged	,		Empty director	y listing
3 directori	ies		Empty directory.	
Server/Lo	ocal file	Direction Remote file		Size Priority Status
Queued fi	Failed transfers         Successful transfers (2)			🔓 🞯 Queue: empty 🔹 👁

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Hos	Username:	Password:	Port:	Quickconnect -			
Status: Listin Status: rect Status: tie		uccessful leboulch/Formation" nation ormation" successful					
Local site: /hom	ne/malo			~	Remote site: /work/mleboulch/Formation		~
	Data merged				mleboulch     Formation		ļ
Filename		Filesize Filetype 🗸	Last modified		Filename	Filesize Filetype 🗸 Last modified	Per
Temp multiplex merged Directory 06/29/2017 05: Directory 06/29/2017 05: Directory 06/29/2017 05: To connect to Genotoul click on this icon.				Empty directo	ory listing		
3 directories Server/Local file	2		Direction Remo	te file	Empty directory.	Size Priority Status	
Queued files	Failed transfers Successful tra	ansfers (2)				🔒 🞯 Queue: empty	• •

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Host: genologin.toulouse.inra.fr 

S

- Port: 22
- Protocol: SFTP
- User: your Genotoul login
- Logon Type: Ask for password
- Click on connect.

Password: your password 

,		Site Manager				≜	0
elect Entry:		Gene	eral	Advanced	Transfe	er Settings	)
Formation		Protocol:	SFTP - SSH File Transfer Protocol				
🖳 Genotoul		Host:	geno	login.toulouse.inr	a.fr	Port:	22
		Logon Type:	Ask f	for password			•
		User:	mleb	oulch			
		Password:					
		_					
		Background	olor:	None 🔻			
		Comments:					
New Site	New Folder						
New Bookmark	Rename						
Delete	Duplicate						



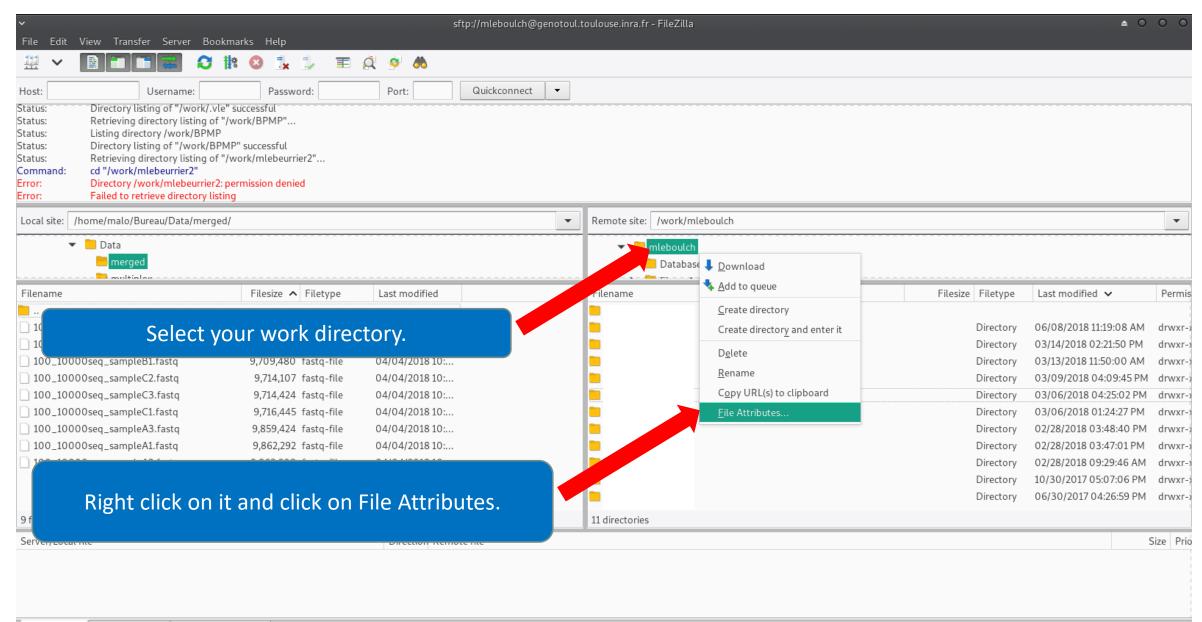
∽ File Edit View Transfer Server Bookmarks Help	nleboulch@genotoul.toulouse.inra.fr - FileZilla		≜ 0 0 0
A v   🖹 🗂 🗮   😂 🎠 🕹 📜   王 🍳 🔗 🙈			
Host: Username: Password: Port: Quickconnect -			
Status:       Connecting to genotoul.toulouse.inra.fr         Status:       Connected to genotoul.toulouse.inra.fr         Status:       Retrieving directory listing         Status:       Listing directory /home/mleboulch         Status:       Directory listing of "/home/mleboulch" successful			
Local site: /home/malo/Bureau/Data/	Remote site: /home/mleboulch		~
□ □ / ⊕ □ bin			
Filename Filesize Filetype 🗸 Last modified	Filename	Filesize Filetype 🗸	· Last modified F
temp         Directory         06/29/2017 05:		4,162 xbel-file	03/30/2017 02:26:33 PM -r
	recently-used.xbel	4,102 xberne 615 File	
multiplex         Directory         06/29/2017 05:           merged         Directory         06/29/2017 05:	viminfo	542 File	02/14/2017 09:59:45 AM -r 06/01/2017 11:08:10 AM -r
merged Directory 06/29/2017 05:	.bashrc	542 File	02/14/2017 09:59:45 AM -r
		226 File	05/15/2017 03:39:59 PM -r
	bash_profile bash_history	17,308 File	06/23/2017 11:15:47 AM -r
	: Xauthority	4,608 File	06/23/2017 11:15:47 AM -r
		+,008 The Directory	10/21/2016 04:37:06 PM In
Double click on work directory to access it.	z work	Directory	10/21/2016 04:37:06 PM Ir
Double click off work directory to access it.	AIC-prefs	Directory	02/14/2017 10:04:44 AM di
	ssh	Directory	01/10/2017 02:28:16 PM di
	pki	Directory	03/30/2017 02:56:02 PM dr
	pathway-tools	Directory	06/01/2017 10:45:23 PM di
	gaome2	Directory	02/01/2017 06:14:17 PM di
	gconfd	Directory	03/30/2017 02:26:51 PM di
	gconf	Directory	03/30/2017 09:08:21 AM dr
	dbus	Directory	02/01/2017 06:12:40 PM di
	.config	Directory	04/25/2017 04:13:46 PM dr
		Directory	
3 directories	Selected 1 directory.		
Server/Local file Direction Remote file		Size Priority Status	
Queued files     Failed transfers     Successful transfers			
		(	🔒 🕐 Queue: empty 🛛 🔍 🗨

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Host:	Username: Password: Port: Quickconnect -					
Status:DiscontStatus:RetrievStatus:ListingStatus:DirectoStatus:RetrievStatus:Listing	ing 2 mes from / work/mebouldin/ormation nected from server ing directory listing of "/work/mleboulch" directory /work/mleboulch" successful ing directory listing of "/work/mleboulch/Formation" directory /work/mleboulch/Formation ory listing of "/work/mleboulch/Formation" successful					
	/malo/Bureau/Data/	~	e site: /work/mleboulch/			~
	Data merged		mleboulch Formation			
Filename	Filesize Filetype 🗸 Last modified		e		Filesize Filetype 🗸 Last modified	Per
 temp multiplex merged	<ul> <li>Directory 06/29/2017 05:</li> <li>Create new directory with right click &gt; Create directory.</li> <li>Name it « Formation ».</li> <li>Go inside this directory next.</li> </ul>		<ul> <li>Download</li> <li>Add files to queen view/Edit</li> <li><u>Create director</u></li> <li>Create director</li> <li>Create new fil</li> <li>Refresh</li> <li>Delete</li> <li>Rename</li> <li>Copy URL(s) t</li> <li>File permission</li> </ul>	ory ory and enter it ile to clipboard		
3 directories			directory.			
Server/Local file	Direction Remote file				Size Priority Status	
Queued files	Failed transfers   Successful transfers (2)				🔒 🕜 Queue: empty	

∽ File Edit View Transfer Server Bookmarks Help	sftp://mleboulch@genotou	ıl.toulouse.inra.fr - FileZilla	<b>≜</b> ○ ○ ○
	š 🧐 🚳		
Host: Username: Password: Status. Listing directory momentable	Port: Quickconnect 💌		
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" successful         Status:       Retrieving directory listing of "/work/mleboulch/Formation"         Status:       Listing directory /work/mleboulch/Formation         Status:       Directory listing of "/work/mleboulch/Formation         Status:       Directory listing of "/work/mleboulch/Formation			
Local site: /home/malo/Bureau/Data/	×	Remote site: /work/mleboulch/Formation	~
/ 		Imation	
Filename Filesize Filetype 🗸	Last modified	Filename	Filesize Filetype 🗸 Last modified Per
<ul> <li></li> <li>temp</li> <li>Directory</li> <li>multiplex</li> <li>Directory</li> </ul>	06/29/2017 05: 06/29/2017 05:	Empty directory listing	
merged Directory	and drop it follo	directory and drag owing the arrow. The merge directory.	
Server/Local file	Direction Remote file	···· /	Size Priority Status
			Size Honry Status
Queued files Failed transfers Successful transfers			🔒 🕜 Queue: empty 🛛 🔹 🗨

File Edit View Transfer Conver Beelmarks	. Lisla		srtp://mtebouicn@genoto	ultoulouse.inra.fr - FileZilla		1000
File Edit View Transfer Server Bookmarks	о пер 🔕 🏂 🐌   🎞 🕰	A (A)				
Host: Username:	Password:	Port: Q	uickconnect -			
Status.         Eising uneccipy work/miebouch/r of Command:         put "/home/malo/Bureau/Data/temp/te Status:           Status:         File transfer successful, transferred 2, Status:         File transfer successful, transferred 2, Status:           Status:         Retrieving directory listing of "/work/n Status:         Listing directory /work/mleboulch/For Status:           Directory listing of "/work/mleboulch/For         Directory listing of "/work/mleboulch/For	emp2.fastq <sup>**</sup> temp2.fastq" emp2.fastq => remote:/work/ 226,378 bytes in 1 second 226,378 bytes in 1 second neboulch/Formation" mation	'mleboulch/Formation/te	emp/temp2.fastq			
Local site: /home/malo/Bureau/Data/merged/			~	Remote site: /work/mleboulch/Formation		~
Data				The bould bound bou		
Filename	Filesize Filetype 🗸	Last modified		Filename	Filesize Filetype 🗸 Last	modified Pe
💼 a				· · ·		
100_10000seq_sample.tar.gz	4,773,706 gz-file	06/28/2017 05:		📒 temp	Directory 06/29	9/2017 06:01:32 PM drv
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:				
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:				
D 100_10000seq_sampleA1.fastq	9,862,292 fastq-file	06/16/2015 10:				
				nple.tar.gz file and		
Selected 1 file. Total size: 4,773,706 bytes			drag and drop it fo	ollowing the arrow.		
Server/Local file		Dire	Double click on th	e merge directory.	Size Priority Status	
				e merge uncetory.		
Queued files Failed transfers Successful tr	ransfers (2)					Queue: empty 🔹 👁



#### Change file attributes

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

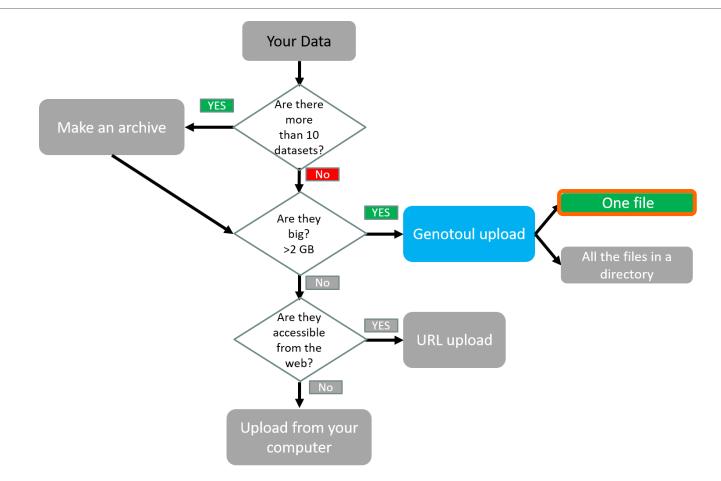
**≜** 0.

0

Owner perk	issions							
✓ Read	✓ Write	✓ Execute						
Group perm	ssions							
✓ Read	🗌 Write	🖌 Execute						
Public permi	sions							
💌 Read	Write	🖌 Execute						
Numeric valu	e: 755							
	an x at any positio ne original files ha							
🖌 Recurse i	into subdirectorie	25						
<ul> <li>Apply to all files and directories</li> </ul>								
<ul> <li>Apply</li> </ul>	<ul> <li>Apply to files only</li> </ul>							
<ul> <li>Apply</li> </ul>	<ul> <li>Apply to directories only</li> </ul>							
	— Cancel V OK							

- 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.

#### Upload files from Genotoul



∽ File Edit View Transfer Server Bookmarks Help	ul.toulouse.inra.fr - FileZilla	≜ 0 0 0
Host: Username: Password: Port: Quickconnect		
Status:       /work/mleboulch/Formation/temp/temp2.fastq.to.755         Status:       /work/mleboulch/Formation/temp/temp2.fastq.to.755         Status:       Retrieving directory listing of "/work/mleboulch/Formation"         Status:       Directory listing of "/work/mleboulch/Formation" successful         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"         Status:       Directory listing of "/work/mleboulch/Formation/temp         Status:       Directory listing of "/work/mleboulch/Formation/temp <t< th=""><th></th><th></th></t<>		
Local site: /home/malo/Bureau/Data/merged/	Remote //work/mleboulch/Formation	~
Data     merged	Formation     temp	l
Filename Filesize Filetype 🗸 Last modified	Filename Filesize Filetype V	Last modified     Per
Select this text and copy it by pressing the keyboard keys Ctrl+C.	<ul> <li></li> <li>100_10000seq_sample.tar.gz</li> <li>4,773,706 gz-file</li> <li>Directory</li> </ul>	06/29/2017 06:04:35 PM -rw 06/29/2017 06:01:32 PM drw:
100_10000seq_sampleB2.tastq       9,707,921 tastq-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	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)		Ŷ ⑦ Queue: empty

<b>=</b> Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	Using 808.6 MB
Tools	Upload File from Genotoul (Galaxy Version 1.0.0) <ul> <li>Options</li> <li>Options</li></ul>	History
search tools 😢	Path to file	search datasets
MANAGE YOUR DATA FILES		merged
<u>Get Data</u>	Path must be like : /work/USERNAME/somewhere/afile	0 b
Upload File from your computer	File type	1 This history is empty. You can <u>load</u>
Upload File from Genotoul	tar.gz	<u>your own data</u> or <u>get data from an</u> external source
Upload several files from Gen	✓ Execute	
without impact too much your Galaxy quota		
Upload ZIP file from an URL or	t it does This purpose to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.	
browse your local files system	This preventions you to use a me stored in your genotodi work directory and optimize Galaxy work space by creating symmixs.	
UCSC Main table browser	Path to file Switch to merged history.	
UCSC Test table browser	This must be an absolute	
UCSC Archaea table browser		
EBI SRA ENA SRA	<ul> <li>Valid path : /work/Link Invalid path : /home/L</li> <li>Next go to Get Data &gt; Upload File from Genotoul.</li> </ul>	
Download Data	next go to oct bata v oproda i ne nem cenetean	
Jobs statistics		
FILES MANIPULATION	To use this tool and to maintain the confidentiality of yours directories:	
Text Manipulation	1. Create a "galaxy" directory in your work : mkdir galaxy 2. chmod a+x /work/LinuxUserName	
Filter and Sort Join, Subtract and Group		
<u>GFF</u>	Example : drwxr-xx 4 smaman sigenae 16384 mar 9 14:15 /work/smaman	
BED Tools	3. chmod a+r /work/LinuxUserName/dataGalaxy,fasta	
Convert Formats		
Fetch Sequences	1 Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.	
<u>Statistics</u> <u>Graph/Display Data</u>	For example, if your data to download in Galaxy are: /work/LinuxUserName/galaxy/data.fasta:	
SEQUENCES MANIPULATION	1. Add "x" rights to "others" on /work/LinuxUserName/ and on galaxy/	
FASTA manipulation	It is not useful that "others" have "r" rights of these directories.	
FastQC: fastq/sam/bam		
<u>Illumina fastq</u>	2. Add "r" rights (only) to "others" on data.fasta file.	
Generic FASTQ manipulation	Thus, Galaxy can access and read data.fasta but all other files in those directories will not be accessible or readable.	
FASTX-Toolkit for FASTQ data		
SAM/BAM MANIPULATION : PICARD (BETA)	A 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 fatsq files uploaded will not be listed among available datasets in Galaxy tools.	
Conversion		
QC/Metrics for sam/bam	Version Galaxy Tool : V1.0	
<	Versions of bioinformatics tools used : No bioinformatique tool used.	×

<b>=</b> Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	Using 808.6 MB	
Tools	Upload File from Genotoul (Galaxy Version 1.0.0)  COptions	History C C	נ
search tools	Path to file	search datasets	Ì
MANAGE YOUR DATA FILES Get Data Upload File from your computer Upload File from Genotoul	Path must be like : /work/USERNAME/somewwere/afile File type tar.gz	merged 0 b This history is empty. You can <u>load</u> your own data or get data from an <u>external source</u>	]
Upload several files from Genotoul without impact too much your Galaxy quota <u>Upload ZIP file</u> from an URL or browse your local files system	Execute     Don't forget to change the Datatype!     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.		
UCSC Main table browser UCSC Test table browser UCSC Archaea table browser EBI SRA ENA SRA Download Data	Path to file This must be an absolute path to a file located in your genotoul work directory. The path must start with <i>work/YOUR_USER_NAME/blablabla.extension</i> valid path : /work/LinuxUserName/galaxy/file.extension invalid path : /home/LinuxUserName/work/galaxy/file.extension		
Jobs statistics FILES MANIPULATION Text Manipulation Filter and Sort Join, Subtract and Group	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-xx 4 smaman sigenae 16384 mar 9 14:15 /work/smaman		
GFF BED Tools Convert Formats Fetch Sequences	3. chmod a+r /work/LinuxUserName/dataGalaxy.fasta		
Statistics Graph/Display Data SEQUENCES MANIPULATION	<ul> <li>Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.</li> <li>For example, if your data to download in Galaxy are: /work/LinuxUserName/galaxy/data.fasta:         <ol> <li>Add "x" rights to "others" on /work/LinuxUserName/ and on galaxy/</li> </ol> </li> </ul>		
FASTA manipulation FastQC: fastq/sam/bam Illumina fastq Generic FASTQ manipulation FASTX-Toolkit for FASTQ data	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.		
SAM/BAM MANIPULATION : PICARD (BETA) Conversion	A 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 fatsq files uploaded will not be listed among available datasets in Galaxy tools.		
QC/Metrics for sam/bam	Version Galaxy Tool : V1.0 Versions of bioinformatics tools used : No bioinformatique tool used.		>

#### Path to file

/work/mleboulch/Formation

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

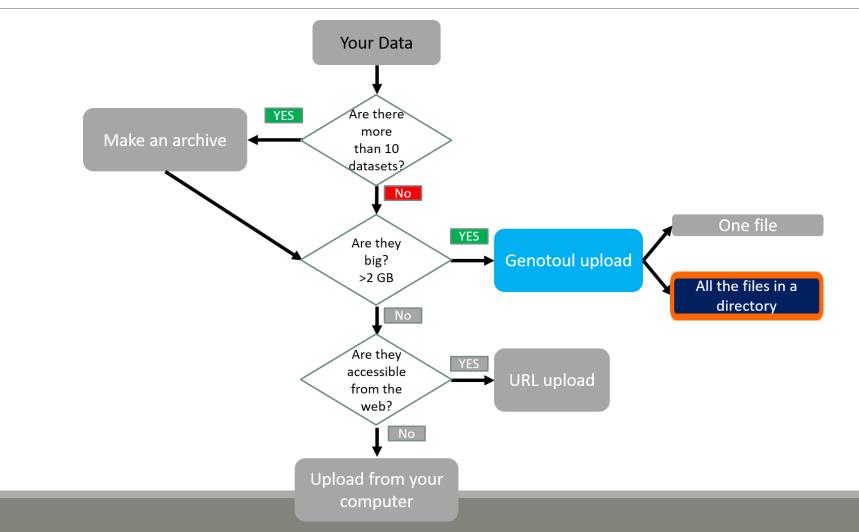
#### Path to file

Awork/mleboulch/Formation/100\_10000seq\_sample.tar.gz
Path must be like : Awork/USERNAME/somewhere/afile

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

<b>=</b> Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -		Using 813.2 MB
Tools		History	<i>C</i> ‡ ⊡
search tools	1 job has been successfully added to the queue - resulting in the following datasets:	search datasets	8
	1: /work/mleboulch/Formation/100_10000seq_sample.tar.gz	merged	
MANAGE YOUR DATA FILES Get Data	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.	1 shown	
Upload File from your computer		4.55 MB	<b>()</b>
Upload File from Genotoul		1: /work/mleboulch	• 🖋 🗙
<u>Upload several files from Genotoul</u> without impact too much your Galaxy quota		<u>/Formation</u> /100 10000seq sample.	.tar.gz
<u>Upload ZIP file</u> 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	After executing the file is imported into Colovy		
BED Tools	After executing, the file is imported into Galaxy.		
<u>Convert Formats</u> <u>Fetch Sequences</u>			
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<u>Graph/Display Data</u>			
SEQUENCES MANIPULATION			
FASTA manipulation			
<u>FastQC: fastq/sam/bam</u> Illumina fastq			
Generic FASTQ manipulation			
FASTX-Toolkit for FASTQ data			
SAM/BAM MANIPULATION : PICARD (BETA)			
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#### Upload files from Genotoul



File Edit View Transfer Server Bookmarks Help	
Host: Username: Password: Port: Port: Quickconnect -	
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10 files. Total size: 92,628,372 bytes	
Server/Local file Direction Remote file Size Priority Status	
Queued files     Failed transfers     Successful transfers (3)	Queue: empty

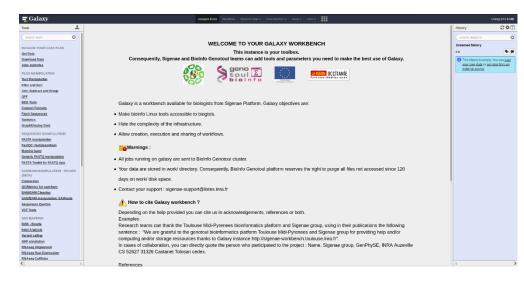
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ad File from your computer	✓ Execute	1 This history is empty. You can <u>l</u>
d File from Genotoul	1 What it does	your own data or get data from external source
several files from Genotoul	This program allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.	
t impact too much your		
ad <u>ZIP file</u> from an URL or	Path to file	
e your local files system	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	
Main table browser		
<u>C Test</u> table browser	valid path : /work/LinuxUserName/directory invalid path : /home/LinuxUserName/work/directory	
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A ENA SRA		
Data	To use this tool and to maintain the confidentiality of yours directories:	
stics	1. Create a "galaxy" directory in your work : mkdir galaxy	
ANIPULATION	2. chmod a+x /work/LinuxUserNan	
nipulation	Example : drwxr-xx 4	
d Sort	<ul> <li>Go back to Galaxy and switch to temp history.</li> </ul>	
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fastq	- uploaded!	
<u>c FASTQ manipulation</u> Toolkit for FASTQ data	Contacts (noms et emails) : sigen	
	E-learning available : Yes.	
AM MANIPULATION : PICARD	Please cite :	
sion	Depending on the help provided you can cite us in acknowledgements, references or both.	
rics for sam/bam	Examples : Acknowledgements We wish to thank the SIGENAE group for	

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	QC/Metrics for sam/bam			
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### Upload by Genotoul





1TB of space

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

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

# Share a History

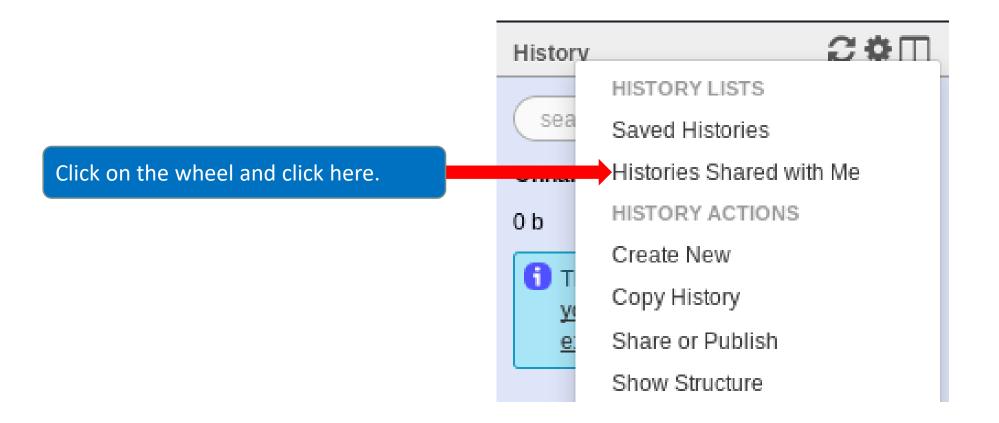
## Share a history

- 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

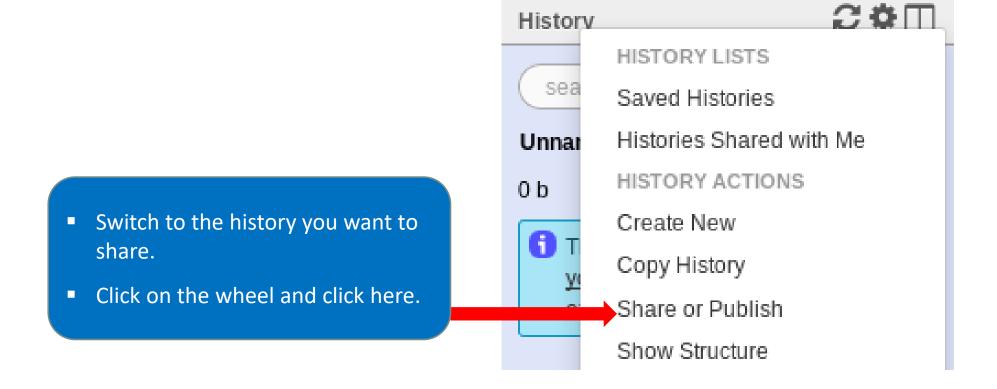


<b>=</b> Galaxy	Analyze Data Workflow Shared Data - Visualization	➡ Help ➡ User	-			ι	Jsing 841.3 MB
Tools	Histories shared with you by others					History	€‡□
search tools						search datasets	8
MANAGE YOUR DATA FILES	Name Name	Datasets	Created	Last Updated	Shared by	Historique R1R2	
<u>Get Data</u>	ASMA2016 🗸	27	Nov 18, 2016	Mar 09, 2017	geraldine.pascal@inra.fr	3 shown 126.19 MB	<b>S</b>
Download Data Jobs statistics FILES MANIPULATION	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	3: Upload several files from Genotoul (sampleA R2)	• # ×
Text Manipulation Filter and Sort Join, Subtract and Group	or 0 selected histories: Copy Unshare				1	2: Upload several files from Genotoul (sampleA_R1)	● # ×
GFF BED Tools Convert Formats						1: Upload several files from Genotoul empty	• / ×
<u>Fetch Sequences</u> <u>Statistics</u> <u>Graph/Display Data</u>	Check the box and click on copy to import P1P2 bistory into your Colory					format: txt, database: ? Epilog : job finished at Tue 22:53:52 CEST 2017	e Jun 27
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<u>Illumina fastq</u> <u>Generic FASTQ manipulation</u> FASTX-Toolkit for FASTQ data	You must import the « R1R2 » history.						
SAM/BAM MANIPULATION : PICARD (BETA)							
Conversion QC/Metrics for sam/bam							
BAM/SAM Cleaning SAM/BAM manipulation: SAMtools							
Sequences Queries VCF Tools							
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# Your Turn!

SHARE A HISTORY WITH YOUR NEIGHBOUR

#### Share a history



search tools       Solution         MANAGE YOUR DATA FILES       Make History A         Get Data       This history is cu         Download Data       Make History A         Jobs statistics       Generates a web         FILES MANIPULATION       Make History A         Filter and Sort       Make the history         Join, Subtract and Group       Make the history	Publish History 'Historique R1R2'       History         Publish History 'Historique R1R2'       search datasets         Publish Link and Publish It       Historique R1R2'         renty restricted so that only you and the users listed below can access it. You can:       126.19 MB         ccessible via Link       3: Upload several files         Ink that you can share with other people so that they can view and import the history.       3: Upload several files         ccessible and Publish       rom Genotoul         raccessible via Link (see above) and publishes the history to Galaxy's Published Histories section, where it is publicly listed and searchable.       2: Upload several files	
search tools       Solution         MANAGE YOUR DATA FILES       Make History A         Get Data       This history is cu         Download Data       Make History A         Jobs statistics       Generates a web         FILES MANIPULATION       Make History A         Text Manipulation       Makes the history         Filter and Sort       Join, Subtract and Group	search datasets         search datasets         renty restricted so that only you and the users listed below can access it. You can:         ccessible via Link         link that you can share with other people so that they can view and import the history.         ccessible and Publish         r accessible via link (see above) and publishes the history to Galaxy's Published Histories section, where it is publicly listed and searchable.	<b>2 8</b>
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Tools	Share 1 histories	History	<i>€</i> ‡ ⊡
search tools	Histories to be shared:	search datasets	8
MANAGE YOUR DATA FILES	History Name Number of Datasets	Historique R1R2	
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Download Data	Galaxy user emails with which to share histories	126.19 MB	2 > >
Jobs statistics	Select a user	3: Upload several files	• 🖋 🗙
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Text Manipulation	Submit		
Filter and Sort		2: Upload several files from Genotoul	• 🖋 🗙
Join, Subtract and Group		(sampleA R1)	
GFF		1: Upload several files	• / ×
BED Tools		from Genotoul	
Convert Formats	Enter an email address from a Galaxy	empty	
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Conversion			
QC/Metrics for sam/bam			
BAM/SAM Cleaning			
SAM/BAM manipulation: SAMtools			
Sequences Queries			
VCF Tools			
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#### Galaxy user emails with which to share histories

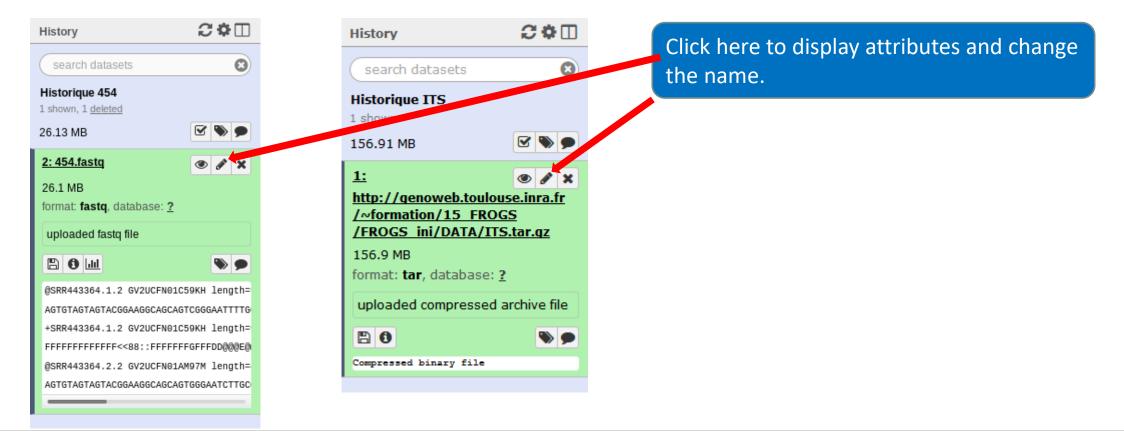


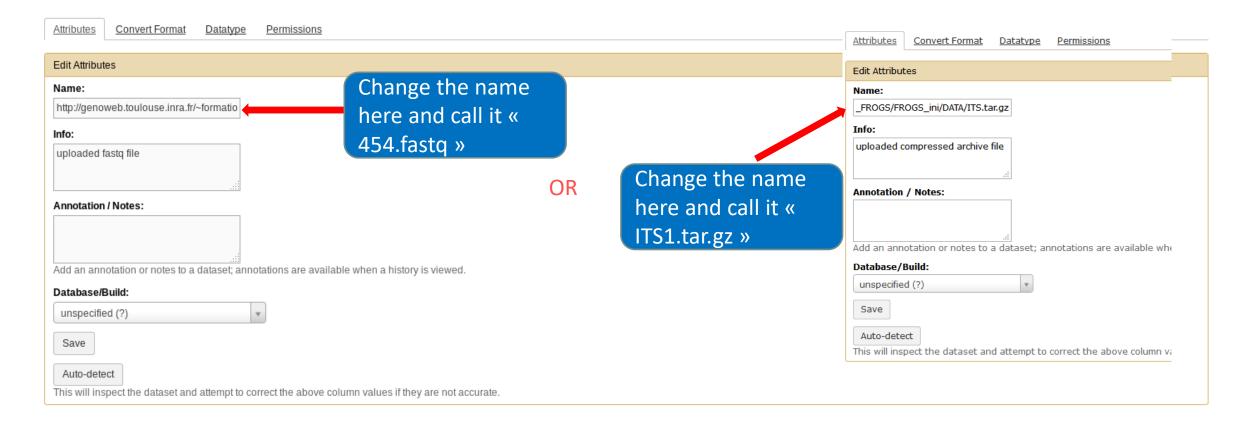
# Manipulate datasets

## Your Turn!

RENAME A DATASET

#### Switch to 454 history or ITS history





Attributes Convert F	t Format Datatype Permissions	
Edit Attributes		
Name: http://genoweb.toulouse Info: uploaded fastq file	If you put the wrong datatype in during the upload, you can change it here.	
Annotation / Notes:	notes to a dataset; annotations are available when a history is viewed.	
Database/Build: unspecified (?) Save Auto-detect This will inspect the data	ataset and attempt to correct the above column values if they are not accurate.	

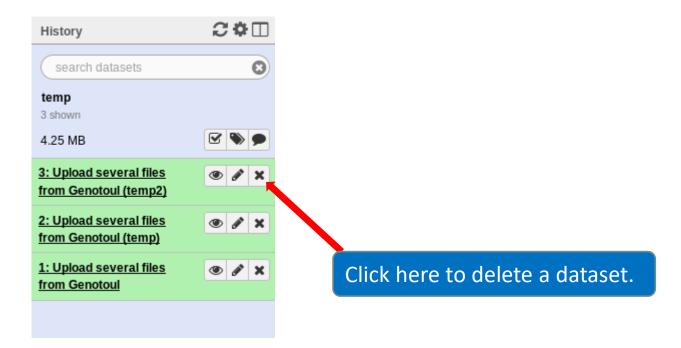
- Do the same with the merged history:
  - Switch to the merged history.
  - Change the name of the file to «100\_10000seq\_sample.tar.gz ».

## Your Turn!

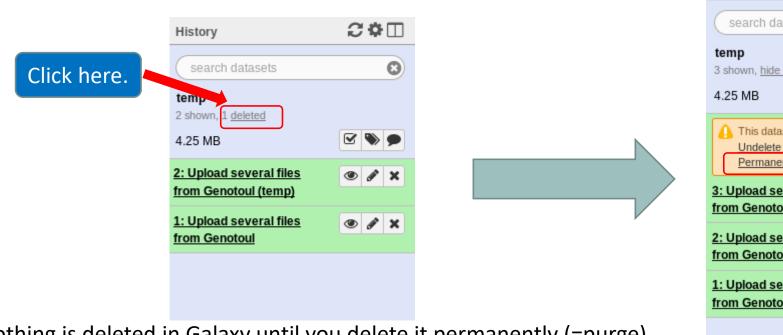
DELETE A DATASET

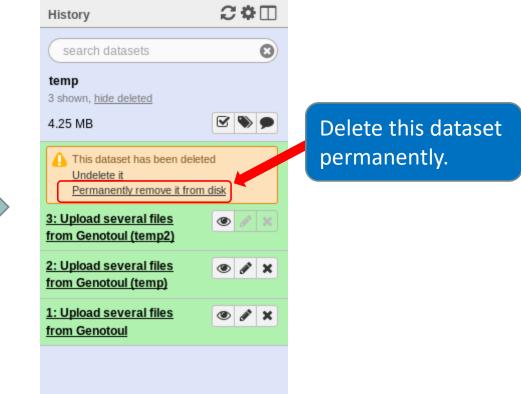
#### Delete a dataset

• Switch to temp history.



#### Delete a dataset

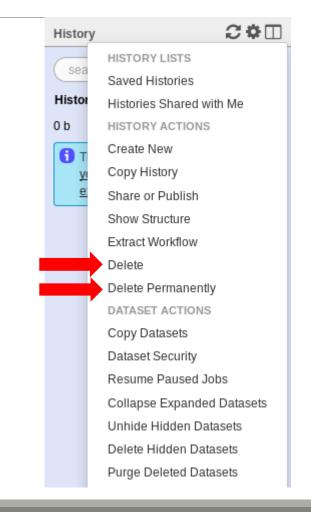




Nothing is deleted in Galaxy until you delete it permanently (=purge).

## 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	•	Switch to	-	Switch to	-
multiplex 2 shown, 1 <u>deleted</u>		merged 1 shown		<b>454</b> 1 shown		Historique R1R2 2 shown, 1 <u>deleted</u>	
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search datasets		search datasets	8	search datasets		( search datasets	
Drag datasets here to copy them to the		1:		<u>1: 454.fastq</u>		<u>3: sampleA_R2</u>	
2: multiplex.fastq	• / ×	<u>100 10000seq_sample.tar.qz</u>	• 🖋 🗙	<u>1. 434.1050</u>	• / ×		
<u>1: barcode_forward.tabular</u>	• / ×					<u>2: sampleA_R1</u>	(e) A

#### One word about data collections

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



History	2 O 🗆	History	201	History	C ♥ □		History	200
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		4: patient4.fg		4: patient4.fo			Undelete da	
3: patient3.fr		3: patient3.fq		3: patient3.fo			Permanenti	y delete datasets
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## Others tools available on galaxy

- Text Manipulation
- Filter and Sort
- FASTA manipulation

### Galaxy support

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

### How to cite Galaxy?

Goecks, J, Nekrutenko, A, Taylor, J and The Galaxy Team. "Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences." Genome Biol. 2010 Aug 25;11(8):R86.

Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. "*Galaxy: a web-based genome analysis tool for experimentalists*". Current Protocols in Molecular Biology. 2010 Jan; Chapter 19:Unit 19.10.1-21.

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 Kent WJ, Nekrutenko A. "Galaxy: a platform for interactive large-scale genome analysis." Genome Research. 2005 Oct; 15(10):1451-5.

## How to cite Genotoul Galaxy workbench?

Research teams can thank the Toulouse Midi-Pyrenees 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 <a href="http://sigenae-workbench.toulouse.inra.fr">http://sigenae-workbench.toulouse.inra.fr</a>".

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