

Introduction to Galaxy platform and preparation of FROGS training July 2017

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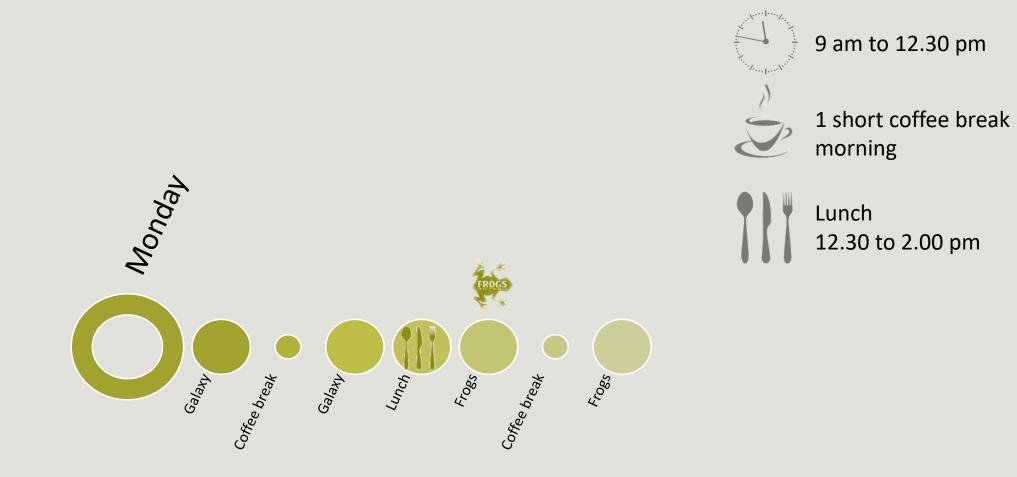


Chitchat time!

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

Objectives

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

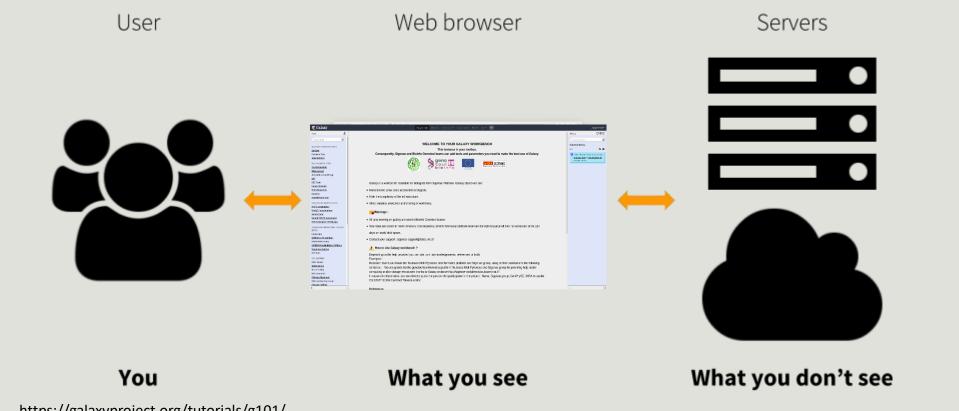


What is Galaxy?

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 must be installed and run on powerful server farms (Cluster).



- Cluster: Many computers tightly connected that work together
- High performance computer:
 - More than 5000 cores н.
 - 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



Exemple of 2 INRA Galaxy platforms

🚍 Galaxy	Analyze Data Workflow Shared Data Visualization - Help - User -					
Tools						
search tools						
search tools	WELCOME TO YOUR GALAXY WORKBENCH					
MANAGE YOUR DATA FILES						
Get Data	This instance is your toolbox.					
Download Data	Consequently, Sigenae and BioInfo Genotoul teams can add tools and parameters you need to make the best					
Jobs statistics	use of Galaxy.					
FILES MANIPULATION						
Text Manipulation						
Filter and Sort	bioinfo Pyrénées-Méditerranée					
Join, Subtract and Group						
GFF						
BED Tools Convert Formats						
Fetch Sequences	Galaxy is a workbench available for biologists from Sigenae Platform. Galaxy objectives are:					
Statistics	Make bioinfo Linux tools accessible to biogists.					
Graph/Display Data						
SEQUENCES MANIPULATION	Hide the complexity of the infrastructure.					
FASTA manipulation	 Allow creation, execution and sharing of workflows. 					
FastQC: fastq/sam/bam						
Illumina fastq Generic FASTQ manipulation	General Science Scienc					
FASTX-Toolkit for FASTQ						
data	 All jobs running on galaxy are sent to BioInfo Genotoul cluster. 					
SAM/BAM MANIPULATION : PICARD (BETA)	• Your data are stored in work/ directory. Consequently, BioInfo Genotoul platform reserves the right to purge all files not					
Conversion	accessed since 120 days on work/ disk space.					
OC/Metrics for sam/bam	Contact your support : sigenae-support@listes.inra.fr					
BAM/SAM Cleaning SAM/BAM manipulation:	- contact your support - signate supportensessingun					
SAMtools	🔥 How to cite Galaxy workbench ?					
Sequences Queries						
VCF Tools	Depending on the help provided you can cite us in acknowledgements, references or both.					
SGS MAPPING	Examples : Research teams any thank the Taulouse Midi Duranees bioinformatics platform and Sigappe group, using in their publications					
BWA - Bowtie Indel Analysis	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					
Variant calling	for providing help and/or computing and/or storage ressources thanks to Galaxy instance http://sigenae-					
SNP annotation	workbench.toulouse.inra.fr".					
RNAseq Alignement	In cases of collaboration, you can directly quote the person who participated to the project : Name, Sigenae group,					
RNAseq Raw Expression	GenPhySE, INRA Auzeville CS 52627 31326 Castanet Tolosan cedex.					
RNAseq Cufflinks	Generatives, Tixka Auzevine CS 32027 31320 Castanet Tolosan Cedex.					
RNAseq Expression Analysis	References					
RNAseq Analyse Expression SARtools	X. SIGENAE [http://www.sigenae.org/]					
sRNAseq	A. OLOLIME [http://www.sigende.org/]					
Phylogenetic graphical						
representation	Sigenae e-learning platform					
METAGENOMICS						
FROGS - Find Rapidly Otu	If you need more training about bioinformatic and Galaxy, please connect to Sigenae e-learning platform					
with Galaxy Solution	If you need there is the base of the base to the control of the base of the base of the base with the base of the					

Some of the tools have a direct access to the e-learning platform of sigenae. Those tools will have this 🥏 in the help

Your Turn!

CONNECT TO OUR GALAXY WORKBENCH

Exercise

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

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 site indique : « Please enter your Genotoul LDAP password »	e. Le
Utilisateur :		
Mot de passe :		
	Annuler OK	

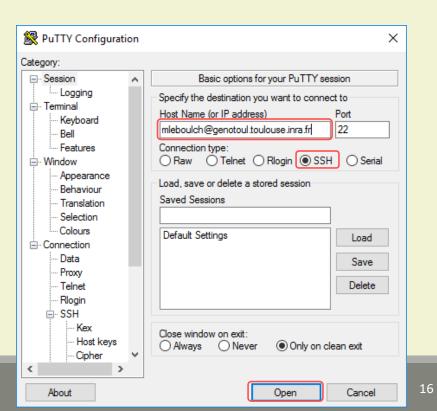
Exercise

• A second time, in the dropdown menu « User » > « Login ».

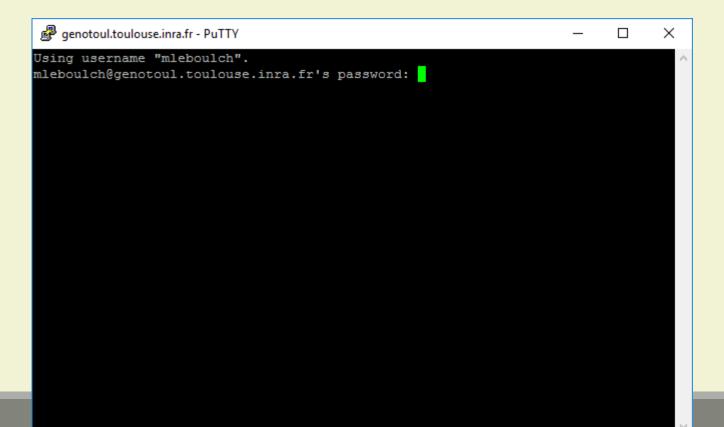
= Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	Using 0 bytes
Tools	Login	History 2 ¢
search tools	Register	search datasets
	WELCOME TO YOUR GALAY ORKBENCH	Unnamed history
MANAGE YOUR DATA FILES	This instance is sollox.	0.6
<u>Get Data</u> Download Data	Consequently, Sigenae and Bioline photoul teams can add tools and	1 This history is empty. You can load
Jobs statistics	parameters you need to make the best use of Galaxy.	your own data or get data from an
FILES MANIPULATION		external source
Text Manipulation		
Filter and Sort		
Join, Subtract and Group		
GFF		
BED Tools	Galaxy is a workbench available for biologists from Sigenae Platform. Galaxy	
Convert Formats	objectives are:	
Fetch Sequences	Make bioinfo Linux tools accessible to biogists.	
Statistics Graph/Display Data	· Make bonno Entax tools accessible to biogists.	
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Illumina fastq	Warnings :	
Generic FASTQ manipulation	_0 warnings .	
FASTX-Toolkit for FASTQ data	All jobs running on galaxy are sent to BioInfo Genotoul cluster.	
SAM/BAM MANIPULATION : PICARD (BETA)	Your data are stored in work/ directory. Consequently, BioInfo Genotoul platform	
Conversion	reserves the right to purge all files not accessed since 120 days on work/ disk space.	
<u>QC/Metrics for sam/bam</u>		
BAM/SAM Cleaning SAM/BAM manipulation: SAMtools	 Contact your support : sigenae-support@listes.inra.fr 	
SAM/BAM manipulation: SAMtools Sequences Queries	٨	
VCF Tools	🔥 How to cite Galaxy workbench ?	
SGS MAPPING	Depending on the help provided you can cite us in acknowledgements, references or	
BWA - Bowtie	both.	
Indel Analysis	Examples :	
Variant calling	Research teams can thank the Toulouse Midi-Pyrenees bioinformatics platform and	
SNP annotation	Sigenae group, using in their publications the following sentence : "We are grateful	
RNAseq Alignement	to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigenae group	
<	for providing help and/or computing and/or storage ressources thanks to Galaxy	> ×

- 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.

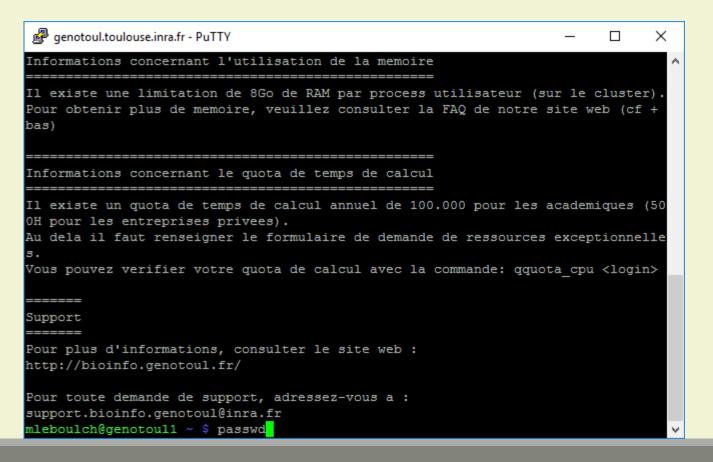
- Launch PuTTY.
- In the following window, you must enter your host name which is:
 - YourGenotoulName@genotoul.toulouse.inra.fr
- The connection type must be SSH.
- Click on « Open » .



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



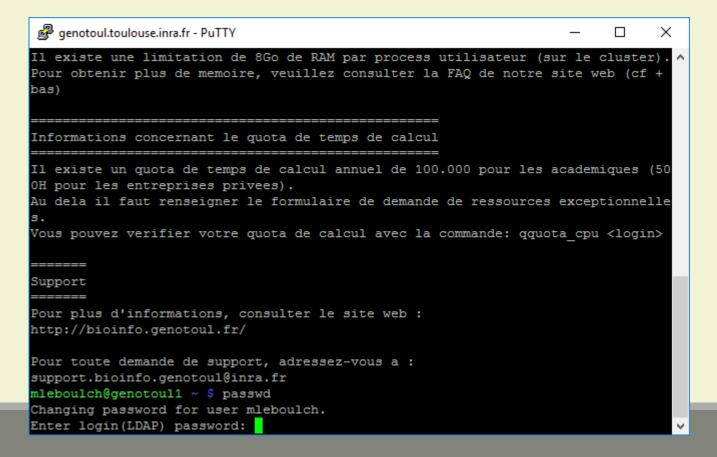
Type « passwd » and hit « Enter ».



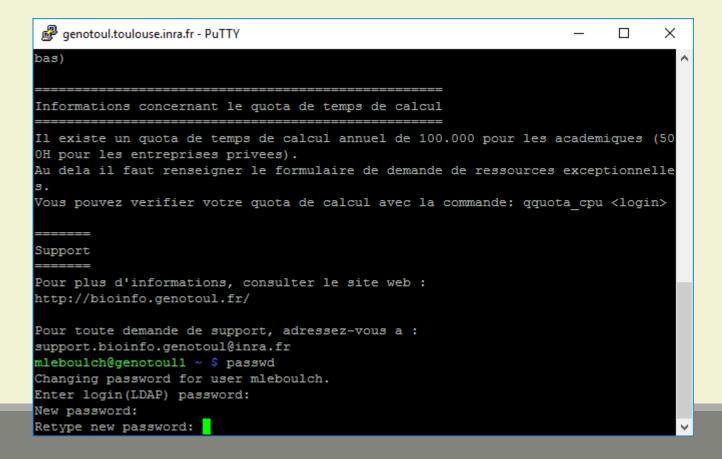
Enter your current password and hit « Enter ».

```
🖉 genotoul.toulouse.inra.fr - PuTTY
                                                                     ×
                                                                _
Il existe une limitation de 8Go de RAM par process utilisateur (sur le 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 100.000 pour les academiques (50
OH pour les entreprises privees).
Au dela il faut renseigner le formulaire de demande de ressources exceptionnelle
Vous pouvez verifier votre quota de calcul avec la commande: gquota cpu <login>
_____
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
mleboulch@genotoul1 ~ $ passwd
Changing password for user mleboulch.
Enter login(LDAP) password:
```

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



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



Galaxy MAIN MENU 201 1 0 WELCOME TO YOUR GALAXY WORKBENCH Unnamed history This instance is your toolbox. Get Data Consequently, Sigenae and BioInfo Genotoul teams can add tools and parameters you need to make the best use of Galaxy. Download Data your own data or get data from an geno toul Σ LA RÉGION OCCITANIE toul Pyrénées-Méditerranée Text Manipulation bioinfo Filter and Sort Join, Subtract and Group GFF BED Tools Galaxy is a workbench available for biologists from Sigenae Platform. Galaxy objectives are: Fetch Sequences Make bioinfo Linux tools accessible to biogists. Statistics DATASETS • Hide the complexity of the infrastructure. **AVAILABLE** Allow creation, execution and sharing of workflow RESULTS VISUALISATION HISTORY FASTA manifulation AND Warnings : Illumina fastq All jobs running on galaxy are sent to BioInfo TOOL PARAMETER WINDOW Generic FASTO manipulation FASTX-Toolkit for FASTQ data • Your data are stored in work/ directory. Consequently, Biolnfo Genotoul platform reserves the right to purge all files not accessed since 120 days on work/ disk space. QC/Metrics for sam/bam Contact your support : sigenae-support@listes.inra.fr BAM/SAM Cleaning SAM/BAM manipulation: SAMtools A How to cite Galaxy workbench ? Sequences Queries VCF Tools Depending on the help provided you can cite us in acknowledgements, references or both. Examples : BWA - Bowtie Research teams can thank the Toulouse Midi-Pyrenees bioinformatics platform and Sigenae group, using in their publications the following Indel Analysis sentence : "We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees and Sigenae group for providing help and/or computing and/or storage ressources 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, INRA Auzeville **RNAseq Alignement** CS 52627 31326 Castanet Tolosan cedex. **RNAseq Raw Expression RNAseq Cufflinks** References

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

	= Galaxy	
	Tools	1
	search tools	0
	MANAGE YOUR DATA FILES	
Search a tool by name.	<u>Get Data</u>	
	Download Data	
	Jobs statistics	
	FILES MANIPULATION	
	Text Manipulation	
	Filter and Sort	

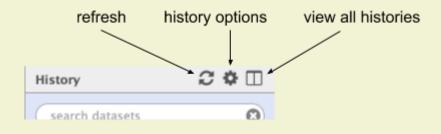
Manipulate Histories

Your Turn!

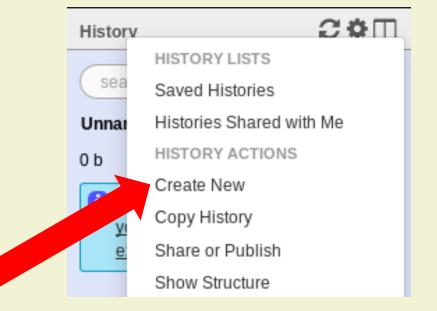
CREATE THE 4 HISTORIES NEEDED FOR THE FROGS FORMATION

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).

Don't use special

characters or

accents!

- Enter « multiplex ».
- Hit « Enter » to validate.

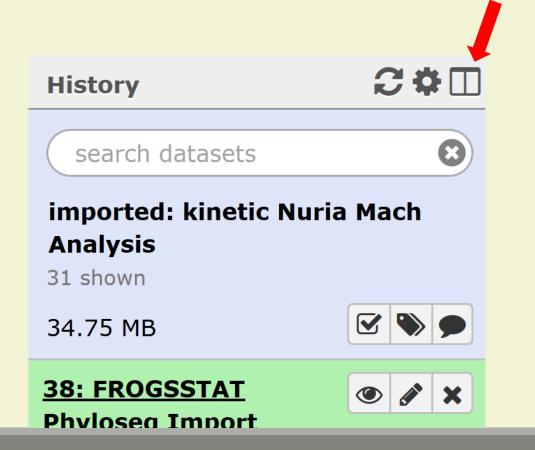


Exercise

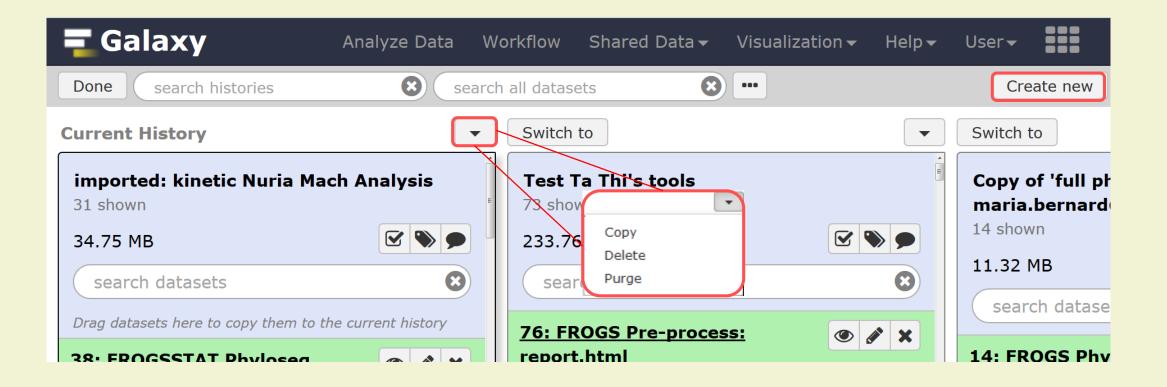
- Create histories named:
 - **454**
 - merged
 - temp
- Switch to the history named « multiplex » as current history.
- Go back to the main interface.

How to list all histories?

• To view all histories, click on this icon.



Explore the « View all histories » section



Switch current history

≡ G ^{≥1} <i>X</i> y	Analyze Data Workflow Shared	Data → Visualization → Help → User →	Using 2.3 GB
Done search histories	Search all datasets	©	Create new
Current History	Switch to	Switch to	
Historique 454	Historique	Historique. 2	o a din
0 b	0 b	0 b	l g his
search datasets	search datasets	Search datasets	©iries.
Drag datasets here to copy them to the current history	This history is empty	1 This history is empty	
1 This history is empty			

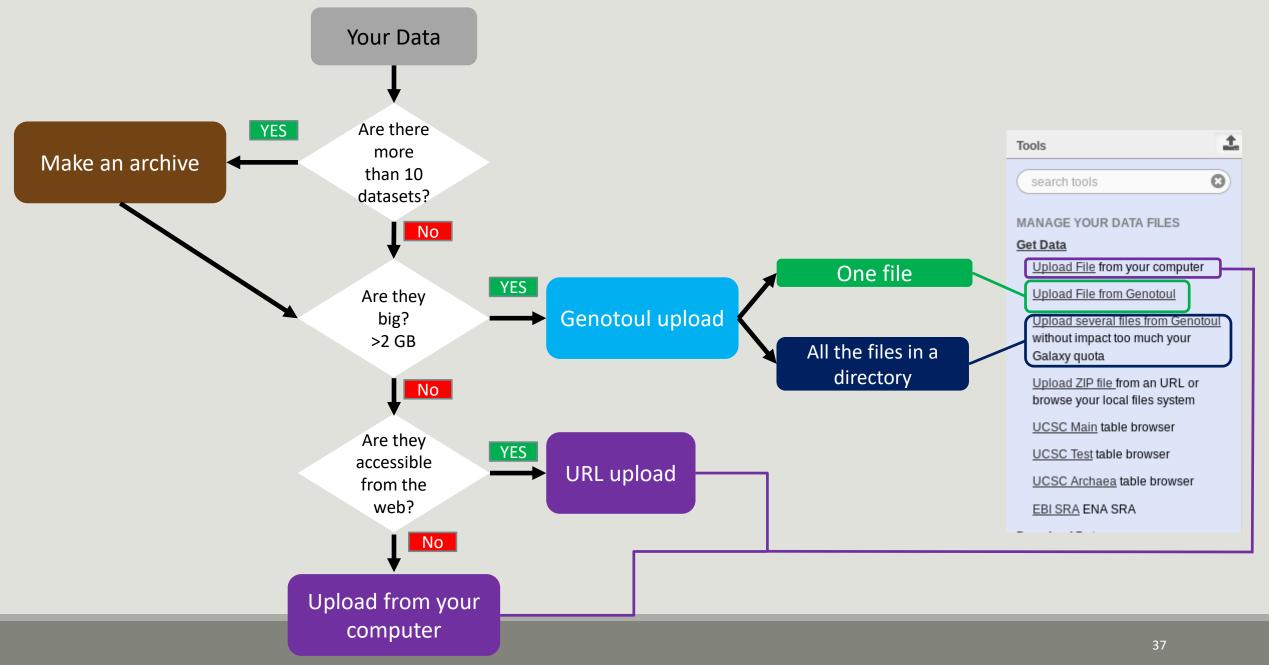
- Switch to the history named « multiplex » as current history.
- Click on "Done" to go back to the main interface.

Data import

How to import your data to Galaxy

- 5 ways to upload your data to Galaxy:
 - By SRA identifiers (not presented today)
 - From your computer
 - By URL
 - From Genotoul Bioinfo clusters
 - Shared by other users of Galaxy

How to choose your upload method?

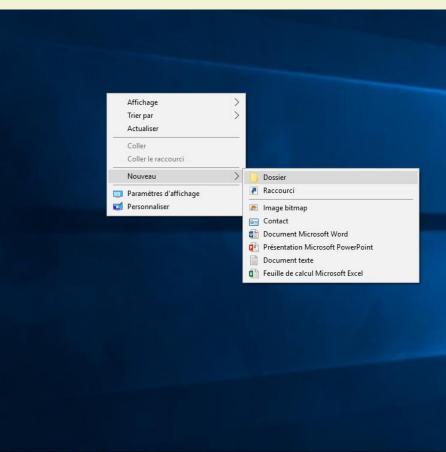


Your Turn!

PREPARE FILES

Create a directory

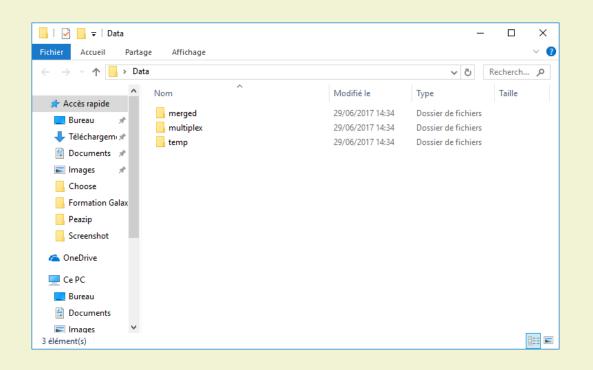
- Create a new directory named « Data » on your desktop
 - Right click on your desktop
 - « New » > « Folder »
 - Name the folder « Data »



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Create a directory

- Inside this directory create 3 new directories named:
 - merged
 - multiplex
 - temp



Download data to multiplex

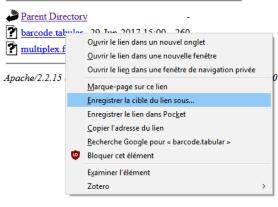
- Click on this URL: <u>http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/Dataset/multiplex/</u>
 - 1) Right click on « barcode.tabular ».
 - 2) Click on save target as.
 - In the new window browse to the directory <u>Data</u> on your desktop and go to the <u>multiplex</u> directory.
 - 4) Save the file in the multiplex directory.
 - 5) Do the same with « multiplex.fastq ».

Index of /~formation/15_FROGS × +

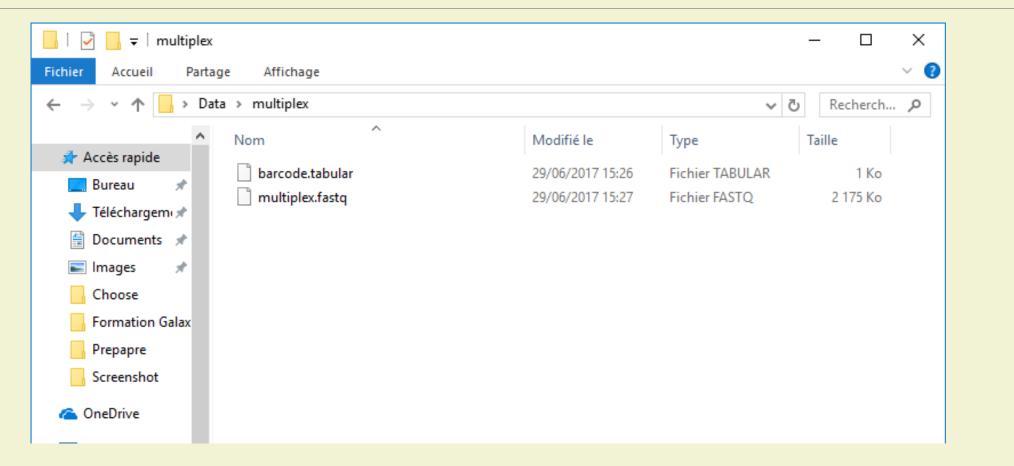
🗧 🛈 genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/Dataset/multiplex/

Index of /~formation/15_FROGS/FROGS_ini/DATA/Dataset/multiplex

<u>Name</u> <u>Last modified</u> <u>Size</u> <u>Description</u>



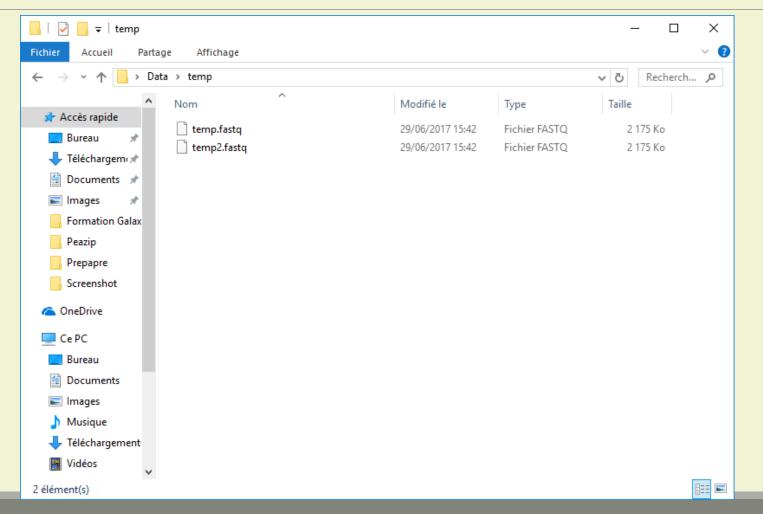
Download data to multiplex



Download data to temp

- Click on this URL: <u>http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/Dataset/temp/</u>
- Do the same as previously for the file temp.fastq and temp2.fastq and save it in the temp directory in the data directory.

Download data to temp

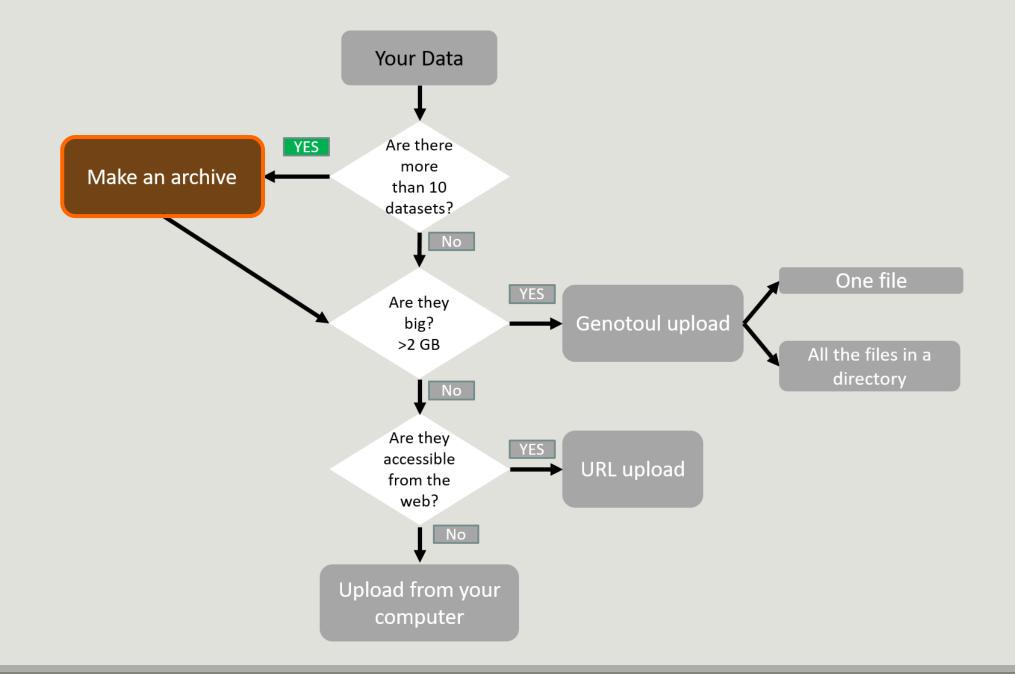


Download data to multiplex

- Click on this URL: <u>http://genoweb.toulouse.inra.fr/~formation/15_FROGS/FROGS_ini/DATA/Dataset/merged/</u>
- Do the same as previously for the 9 files on the website and save it in the merged directory in the data directory.

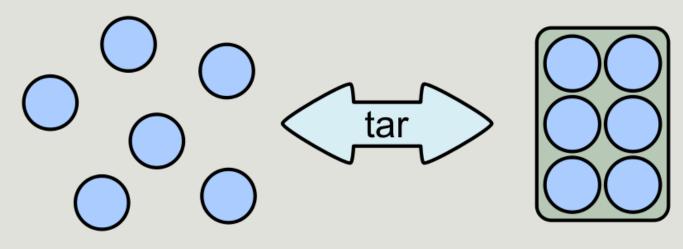
Download data to merged

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🕂 Téléchargem 🖈	100_10000seq_sampleA3.fastq	29/06/2017 15:45	Fichier FASTQ	9 629 Ko	
🚆 Documents 🖈	100_10000seq_sampleB1.fastq	29/06/2017 15:45	Fichier FASTQ	9 482 Ko	
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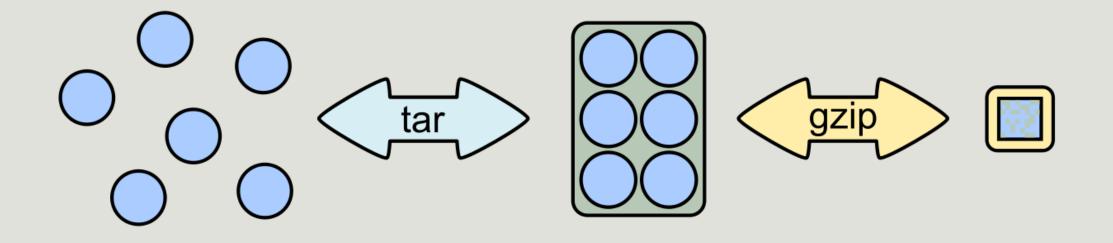
Create a Tar file

- 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



- PeaZip 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.peazip.org/</u>

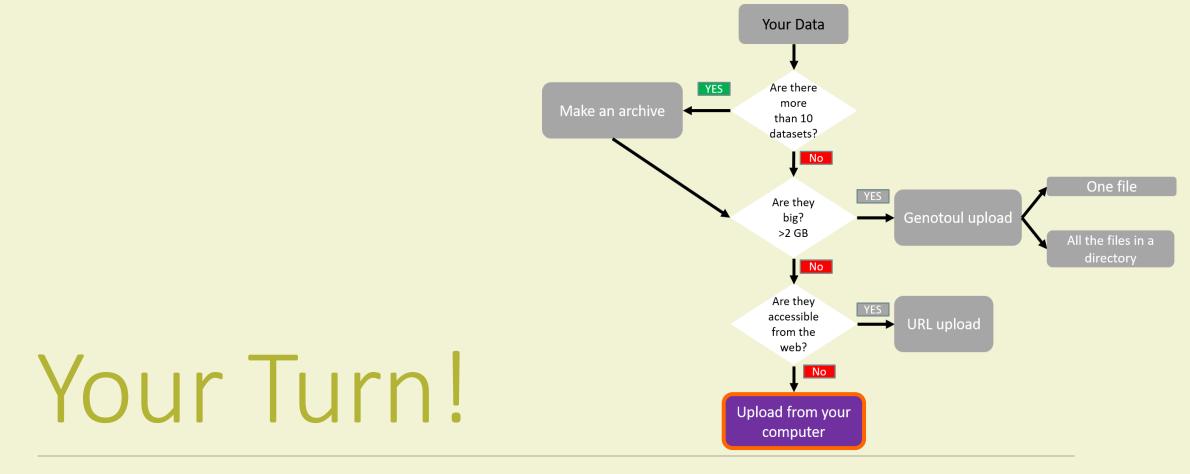


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🖆 Documents 🖈	100_10000seq_sampleB1.fastq	29/06/2017 15:45	Fichier FASTQ	9 482 Ko	
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Peazip	100_10000seq_sampleC1.fastq	29/06/2017 15:45	Fichier FASTQ	9 489 Ko	
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		100_10000seq_sa	mpleB3.fastq	.fastq 9.2 MB 0	1	2017-06-29 15:45:18 A		top\Data\merged\1	00_10000seq_sampleB3.fa	istq	
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											is ticked.
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	launched window	W. ⊧ (20%)	0 dir(s), 9 file(s), 83.	7 MB Potential compres	ssion 50%	6		~	🗸 OK 📉 🗙 Can	icel	F 4

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🔮 Documents 🖈	100_10000seq	_sampleB1.fastq	29/06/2017 15:45	Fichier FASTQ	9 482 Ko		
📰 Images 🛛 🖈	📄 100_10000seq	_sampleB2.fastq	29/06/2017 15:45	Fichier FASTQ	9 481 Ko		
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10 élément(s) 1 élément s	électionné 4,27 Mo	Pronriétés					



UPLOAD FILES FROM YOUR COMPUTER

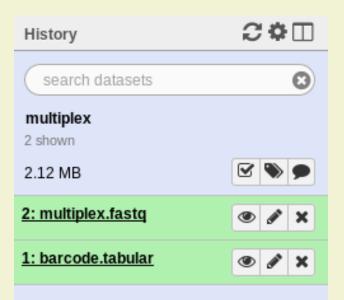
- In Galaxy, your current history must be multiplex.
- Click on the « Get Data » tool.
- Upload file from your computer.

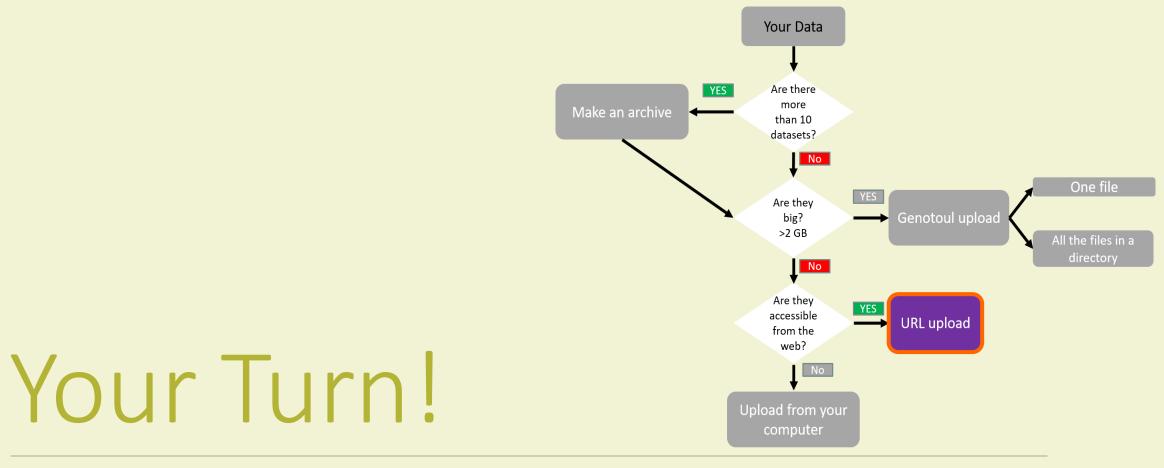
▲ For files smaller than 2 GB

Tools	1
search tools	
MANAGE YOUR DATA FILES	
Get Data	
<u>Upload File</u> 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	

	i ii oiii web oi	r upload from disk
<u>Regular</u>	Composite	
		C. Duran Classica harms
		Click here to choose a file on your hard drive.
		Click here to choose a file on your hard drive.
		Click here to choose a file on your hard drive.
	īype (set all):	Click here to choose a file on your hard drive.
	īype (set all):	Click here to choose a file on your hard drive. Upload one of the two files in the multiplex directory.

Download from web or upload from disk The datatype of a file is the Regular Composite extension of the file: You added 2 file(s) to the queue. Add more files or click 'Start' to proceed. Туре Name Size Genome Settings Status .fasta = fasta Q barcode.tabular 260 b tabular Ŧ ٥ 匬 unspecified (?) v. .fastq = fastq2.1 MB v Q multiplex.fastq ٥ 凬 fastq unspecified (?) .tar = tar 1. Select the type of file (Do not leave on Auto-Detect!). 3. Begin upload. Do no not trust blindly 2. Select your other files the same way. the auto-detect! Type (set all): Q Genome (set all): Auto-detect w unspecified (?) w. Paste/Fetch data Choose local file Pause Reset Start Close





UPLOAD FILE FROM AN URL

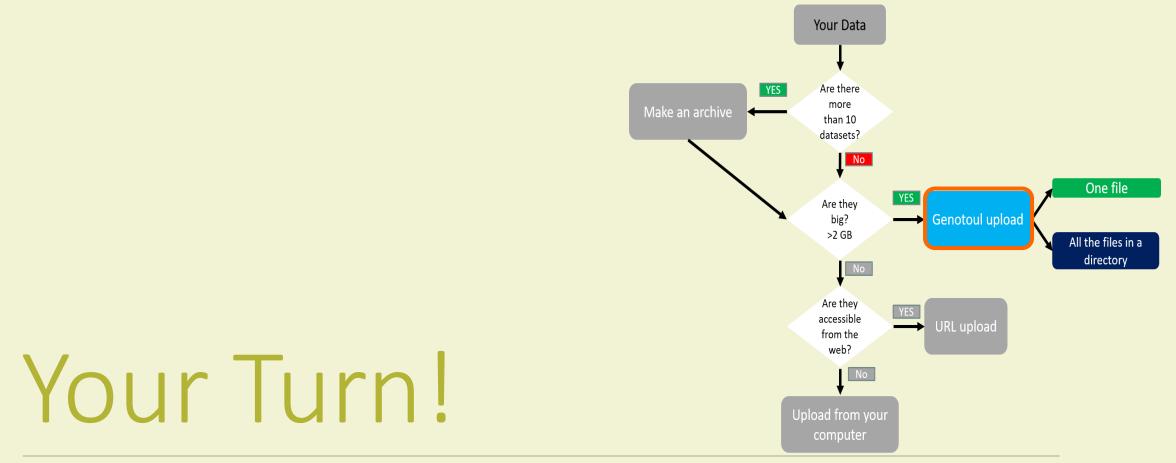
Upload file from URL

- 1. Switch to 454 history as current history.
- Go to Get Data > Upload File from your computer
- 3. Click on Paste/Fetch Data
- Copy the address of the file: <u>http://genoweb.toulouse.inra.fr/~formation/1</u> <u>5 FROGS/FROGS ini/DATA/454.fastq</u>
- 5. Change the type!
- 6. Click on Start.
- 7. You can put one address per line for multiple uploads.

	<u>Composite</u>						
		Yi	ou added 1 file(s) to the que	eue. Add more files or click	Start' to proceed.		
	Name	Size	Туре	Genome	Setting	js Statu	ıs
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		-		L in this box (one per line).	rou can also ulrecuy	paste the contents o	n a nic.
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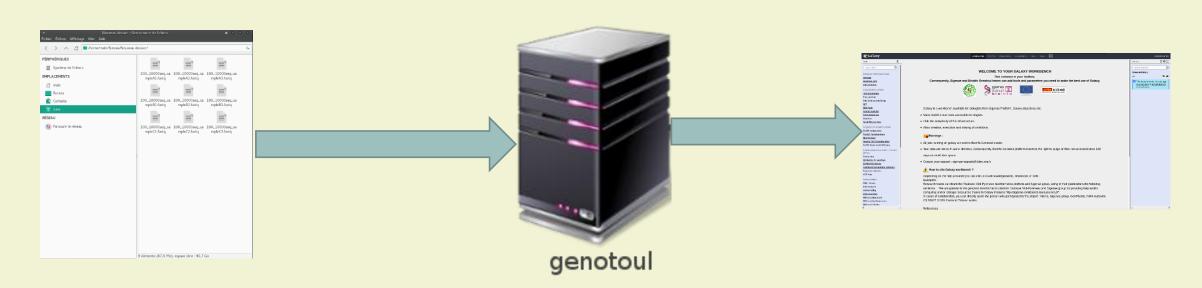
Upload file from URL

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454 1 shown	
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<u>1:</u>	• / ×
http://genoweb.toulouse.inr /~formation/15_FROGS/FRO /DATA/454.fastq	



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.

, File Edit View Transfer Server Bookr		FileZilla	≙ 0 0
₩ × ■	Image: Second	Connection	
Local site: /home/malo/Bureau/Nouveau do	ssier/	Remote site:	
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Filename	Filesize Filetype 🗸 Last modified	Filename Filesize Filesize	e 🗸 Last modified
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100_10000seq_sample.tar.gz	4,773,706 gz-file 06/28/2017 05: 66,157,532 fastq-file 06/27/2017 10:	Not connected to any server	
sampleA_R2.fastq sampleA_R1.fastq	66,157,532 fastq-file 06/27/2017 10: 66,157,532 fastq-file 06/27/2017 10:		
100_10000seq_sampleC3.fastq	9,714,424 fastq-file 06/16/2015 10:		
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100_10000seq_sampleC1.fastq	9,716,445 factorfile p6615/2015 10:		
100_10000seq_sampleB3.fastq	9,707,364 fax Qur P66 6/2015 10:	The server	
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] 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:		
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			Queue: empty

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- Host: genotoul.toulouse.inra.fr
- Port: 22
- Protocol: SFTP
- Logon Type: Normal
- User: your Genotoul login
- Password: your password

<i>y</i>	Site Manager 🔶 O O					
elect Entry:	General Advanced Transfer Settings Charset					
My Sites Genotoul	Host: genotoul.toulouse.inra.fr Port: Protocol: SFTP - SSH File Transfer Protocol Yes Yes					
	Logon Type:Ask for passwordUser:mleboulchPassword:					
	Background color: None 🗸 Comments:					
New Site New Folder						
New Bookmark Rename						
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File Edit View Transfer Server Bookmarks Help				
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sftp://mleboulch@genotoul.toulouse.inra.fr - FileZilla

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Ƴ File Edit View Transfer Server Bookma	arks Heln		sttp://mleboulch@genoto	ultoulouse.inra.fr - FileZilla		≜ 0 0 C
	1 🛛 🗽 🗊 🎞 🛱	🥺 🦚				
Host: Username:	Password:	Port: G	Quickconnect -			
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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:				
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				ct the nple.tar.gz file and ollowing the arrow.		
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▲ 0 0 0

Change file attributes

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

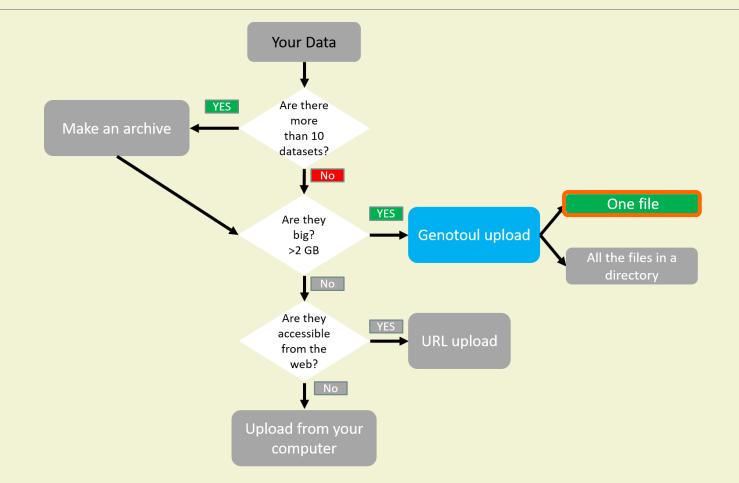
≜ 0

0

Owner perk	issions					
Read	✓ Write	✓ Execute				
Group perm	ssions					
✓ Read	🗌 Write	🖌 Execute				
Public permi	sions					
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Numeric valu	e: 755					
	an x at any positio ne original files ha					
🕑 Recurse i	into subdirectorie	25				
 Apply 	to all files and dir	ectories				
 Apply to files only 						
 Apply to directories only 						
	— Cancel	✓ 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 Hel	lp		si p#micboaren@genoted		- 0 0	Ĭ
₩ •		🗽 🔍 🇉 🔍 :	o 🔥				
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6	 Data merged 				Formation temp		
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 100_100 100_100 100_100 	000seq_sampleb2.rastq 9, 000seq_sampleB1.fastq 9, 000seq_sampleA3.fastq 9, 000seq_sampleA2.fastq 9,	707,921 Tastq-file 709,480 fastq-file 859,424 fastq-file 863,209 fastq-file		ssing the	 100_10000seq_sample.tar.gz temp 	4,773,706 gz-file 06/29/2017 06:04:35 PM Directory 06/29/2017 06:01:32 PM	
10 files Tot	tal size: 92,628,372 bytes				1 file and 1 directory. Total size: 4,773,706 bytes		_
Server/Loc	- -		Direction Remot	a filo	, <u> </u>	Size Priority Status	
Server/Loc	at me		Direction Remot	r ne		Size Priority Status	
Queued file	Eailed transfers Successful transfe	ers (3)				🔓 🕐 Queue: empty 🗣	•

▲ 0 0 0

= Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	Using 808.6 MB
Tools	Upload File from Genotoul (Galaxy Version 1.0.0)	History 2 🌣 🗆
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> <u>external source</u>
Upload several files from Gen of without impact too much your	✓ Execute	
Galaxy quota	t it does	
<u>Upload ZIP file</u> from an URL or browse your local files system	This prevallows 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	Path to file Switch to merged history.	
UCSC Archaea table browser	This must be an absolute	
EBI SRA ENA SRA	valid path : /work/Linu invalid path : /home/L Next go to Get Data > Upload File from Genotoul.	
Download Data	invalue paul monier investige to det Data > oproad the norm denotodi.	
Jobs statistics		
FILES MANIPULATION	To use this tool and to maintain the confidentiality of yours directories: 1. Create a "galaxy" directory in your work : mkdir galaxy	
Text Manipulation Filter and Sort	2. chmod a+x /work/LinuxUserName	
Join, Subtract and Group		
GFF	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		
Statistics	🚯 Thanks to the fact that this tool requires you to enter your filepath (without "browse" button), you can manage your data privacy.	
<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.	
<u>FastQC: fastq/sam/bam</u> Illumina fastq	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)	👍 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	 Version Galaxy Tool : V1.0	
QC/Metrics for sam/bam	Version Galaxy root : V1.0	
<		m >

🚍 Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	Using 808.6 MB
Tools	Upload File from Genotoul (Galaxy Version 1.0.0)	History 2 🌣 🗆
search tools	Path to file	search datasets
MANAGE YOUR DATA FILES <u>Get Data</u> <u>Upload File</u> from your computer <u>Upload File from Genotoul</u> <u>Upload several files from Genotoul</u> without impact too much your	Path must be like : /work/USERNAME/somew.ere/afile Path must be like : /work/USERNAME/somew.ere/afile File type tar.gz ■ Don't forget to change the Datatype!	merged 0 b This history is empty. You can <u>load</u> your own data or <u>get data from an</u> <u>external source</u>
Galaxy quota <u>Upload ZIP file</u> from an URL or	What it does Image: Constraint of the stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.	
browse your local files system <u>UCSC Main</u> table browser <u>UCSC Test</u> table browser <u>UCSC Archaea</u> table browser <u>EBI SRA</u> ENA SRA <u>Download Data</u>	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	
Jobs statistics FILES MANIPULATION Text Manipulation Filter and Sort	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	
<u>Join, Subtract and Group</u> <u>GFF</u> <u>BED Tools</u>	Example : drwxr-x-x 4 smaman sigenae 16384 mar 9 14:15 /work/smaman 3. chmod a+r /work/LinuxUserName/dataGalaxy.fasta	
Convert Formats Fetch Sequences Statistics Graph/Display Data SEQUENCES MANIPULATION	 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: Add "x" rights to "others" on /work/LinuxUserName/ and on galaxy/ 	
FASTA manipulation FastQC: fastq/sam/bam	It is not useful that "others" have "r" rights of these directories.	
Illumina fastq Generic FASTQ manipulation FASTX-Toolkit for FASTQ data	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)	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.	III >

Path to file

/work/mleboulch/Formation

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

Path to file

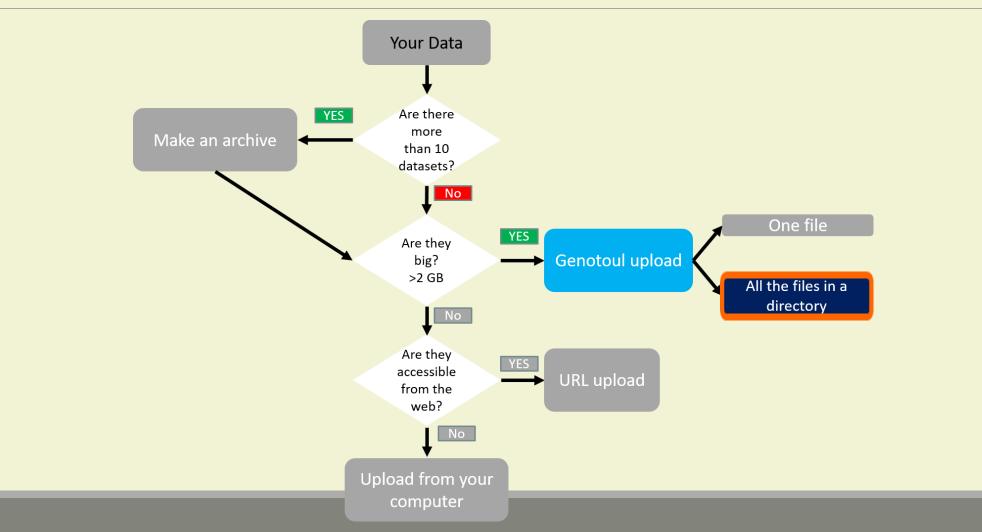
/work/mleboulch/Formation/100_10000seq_sample.tar.gz

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

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

I be a constraint of the co	= Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -		Using 813.2 MB
Lock column Lock column </td <td>Tools</td> <td></td> <td>History</td> <td>℃‡⊡</td>	Tools		History	℃ ‡⊡
Image: Province of the standard and the regular data data data data data data data da	search tools		search datasets	8
General (Second and Control and Contrel and Control and Contrel and Contrel and Con				
liphics the sum of comparing Improve comparing		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.		
Automation Bernahone <	Upload File from your computer			
Identify and life, or any or all states of the order	Upload File from Genotoul			• / ×
biology with Real groups LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser LCSC fund table browser	without impact too much your			<u>.tar.gz</u>
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Join Subtract and Group GFF BED Tools SED Tools Store Streams Statistics				
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FastQC: fastq/sam/bam Illumina fastq Generic FASTQ manipulation ILIUMINA fasTQ FASTX-Toolkit for FASTQ data ILIUMINA fastq SAM/BAM MANIPULATION : PICARD ILIUMINA fastq Conversion ILIUMINA fastq QCMetrics for sam/bam ILIUMINA fastq	-			
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FASTX-Toolkit for FASTQ data SAM/BAM MANIPULATION : PICARD (BETA) Conversion Q/Metrics for sam/bam				
SAM/BAM MANIPULATION : PICARD (BETA) Conversion QC/Metrics for sam/bam				
(BETA) Conversion C/Metrics for sam/bam	FASTX-Toolkit for FASTQ data			
Conversion QC/Metrics for sam/bam				
QC/Metrics for sam/bam				
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Upload files from Genotoul



∽ File Edit View Transfer Server Bookmarks Help	sftp://mleboulch@genotou	.toulouse.inra.fr - FileZilla	± 0 0 0
	: 🔗 🚯		
Host: Username: Password:	Port: Quickconnect 💌		
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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)			🔒 🎯 Queue: empty 🔹 🖷



Host: Username:		uickconnect 💌			
Status: Directory listing of "/work/mleboulch/ Status: Directory listing of "/work/mleboulch/ Status: Retrieving directory /work/mleboulch/For Status: Directory listing of "/work/mleboulch/For Status: Directory listing of "/work/mleboulch/For Status: Directory listing of "/work/mleboulch/For Status: Retrieving directory /work/mleboulch/For Status: Listing directory /work/mleboulch/For Status: Directory listing of "/work/mleboulch/For Status: Directory listing of "/work/mleboulch/For Status: Directory listing of "/work/mleboulch/For	/Formation" successful mleboulch/Formation/temp" rmation/temp /Formation/temp" successful mleboulch/Formation/temp" rmation/temp				
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10 files. Total size: 92,628,372 bytes			2 files. Total size: 4,452,756 bytes		
Server/Local file	Direction Remot	te file	***	Size Priority Status	
Queued files Failed transfers Successful t	transfers (3)				
				🔒 🞯 Queue: empty	••

Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	Using 813.2
is 🚺	Upload several files from Genotoul without impact too much your Galaxy quota (Galaxy Version 1.0.1)	History 2 ¢
search tools	Path to your directory which contains several files	search datasets
NAGE YOUR DATA FILES	/work/mleboulch/Formation/temp	temp
Data	Path must be like : /work/USERNAME/somewhere/	0 b
pload File from your computer	✓ Execute	This history is empty. You can <u>loa</u>
load File from Genotoul	1 What it does	your own data or get data from a external source
ad several files from Genotoul ut impact too much your ky quota	This program allows you to use a file stored in your genotoul work directory and optimize Galaxy work space by creating symlinks.	
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 Iwork/YOUR_USER_NAME/directory	
<u>C Main</u> table browser		
C Test table browser	valid path : /work/LinuxUserName/directory invalid path : /home/LinuxUserName/work/directory	
C Archaea table browser		
RA ENA SRA	A To use this tool and to maintain the confidentiality of yours directories:	
ad Data		
istics	1. Create a "galaxy" directory in your work : mkdir galaxy	
ANIPULATION	2. chmod a+x /work/LinuxUserNap	
nipulation	Example : drwxr-xx 4	
d Sort	Go back to Galaxy and switch to temp history.	[]
tract and Group	Thanks to the fact that this to	
	For example, if your data to down	
<u>b</u>	Add "x" rights to "others" on Work Go to Get Data > Upload Several files from Genotoul	
Formats quences		
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- splay Data	Thus, Galaxy can access and rea Paste the address into field.	
CES MANIPULATION		
anipulation		
fastq/sam/bam	Version Galaxy Tool : V1.0 Versions of bioinformatics tools us Be careful all the files from the directory will be	
astq		
FASTQ manipulation	uploaded!	
Toolkit for FASTQ data	E-learning available : Yes.	
M MANIPULATION : PICARD		
	Please cite :	
ion	Depending on the help provided you can cite us in acknowledgements, references or both.	
ics for sam/bam	Examples : Acknowledgements We wish to thank the SIGENAE group for	

= Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	l	Jsing 819.5 MB
Tools		History	2¢⊡
search tools	1 job has been successfully added to the queue - resulting in the following datasets:	search datasets	0
MANAGE YOUR DATA FILES	1: Upload several files from Genotoul	temp	
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.	3 shown	
Upload File from your computer		4.25 MB	
Upload File from Genotoul		3: Upload several files from Genotoul (temp2)	● # ×
<u>Upload several files from Genotoul</u> without impact too much your Galaxy quota		2: Upload several files from Genotoul (temp)	• / ×
Upload ZIP file from an URL or browse your local files system		1: Upload several files from Genotoul	● / ×
UCSC Main table browser			
UCSC Test table browser			
UCSC Archaea table browser	 Click on execute. 		
EBI SRA ENA SRA			
Download Data	 All the files from the directory are uploaded. 		
Jobs statistics	An the mes norm the uncetory are uploaded.		
FILES MANIPULATION			
<u>Text Manipulation</u> <u>Filter and Sort</u>			
Join, Subtract and Group			
GFF			
BED Tools			
Convert Formats			
Fetch Sequences			
<u>Statistics</u> <u>Graph/Display Data</u>			
SEQUENCES MANIPULATION FASTA manipulation			
FastQC: fastq/sam/bam			
Illumina fastq			
Generic FASTQ manipulation			
FASTX-Toolkit for FASTQ data			
SAM/BAM MANIPULATION : PICARD			
(BETA)			
Conversion			
<u>QC/Metrics for sam/bam</u>			
<			>

Upload by Genotoul



10 GB 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.

Share a History

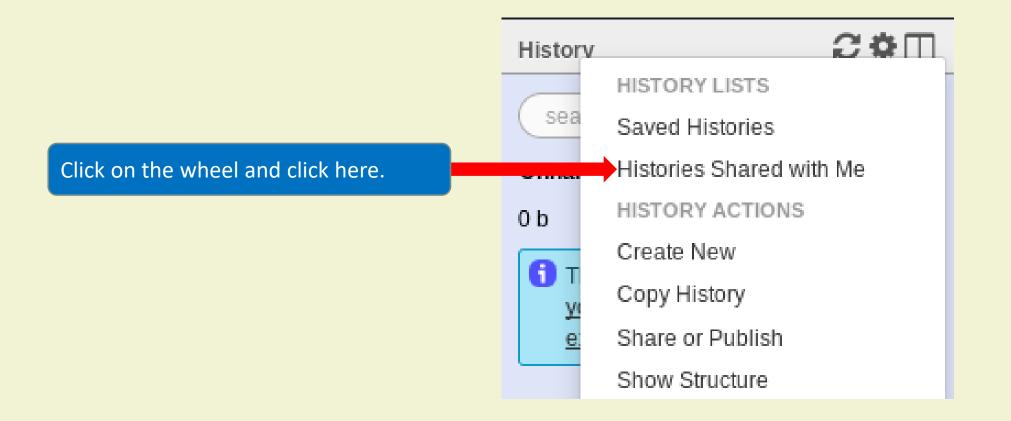
Share a history

- 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



🚍 Galaxy

Using 841.3 MB

Tools

(search tools

MANAGE YOUR DATA FILES

- <u>Get Data</u>
- 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

<u>Illumina fastq</u>

Generic FASTQ manipulation FASTX-Toolkit for FASTQ data

SAM/BAM MANIPULATION : PICARD

(BETA) Conversion

Conversion

QC/Metrics for sam/bam

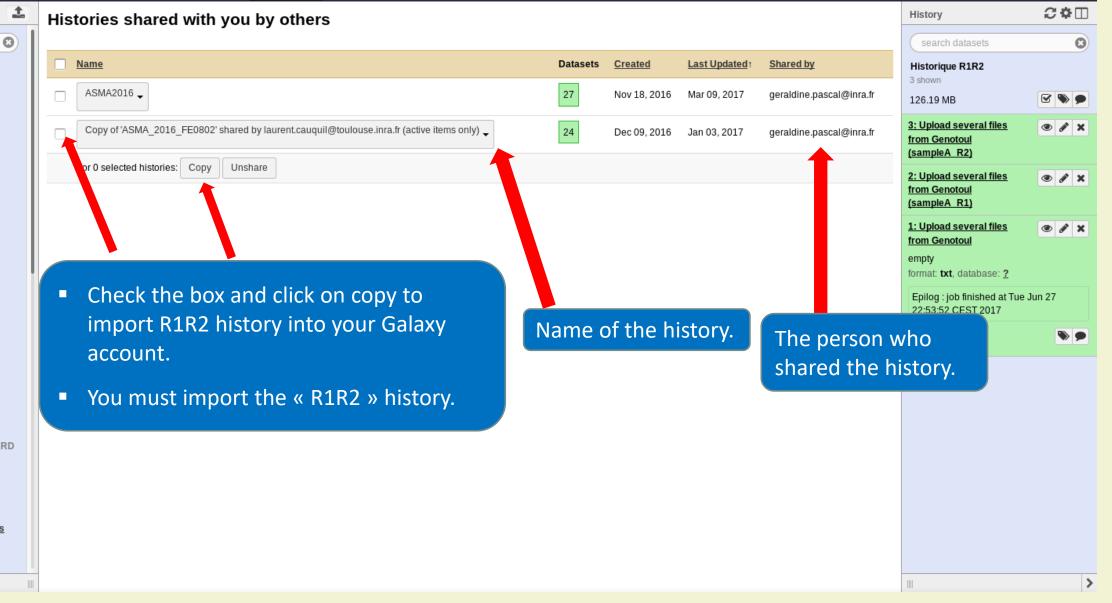
BAM/SAM Cleaning

SAM/BAM manipulation: SAMtools

Sequences Queries

VCF Tools

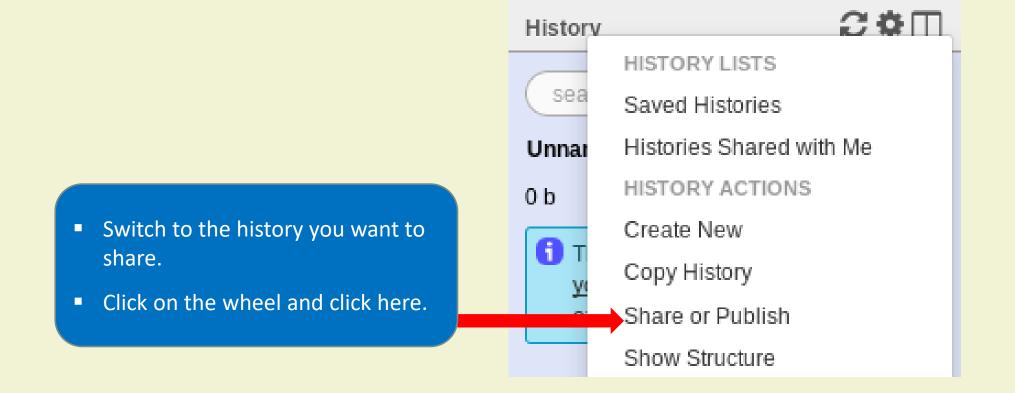
<



Your Turn!

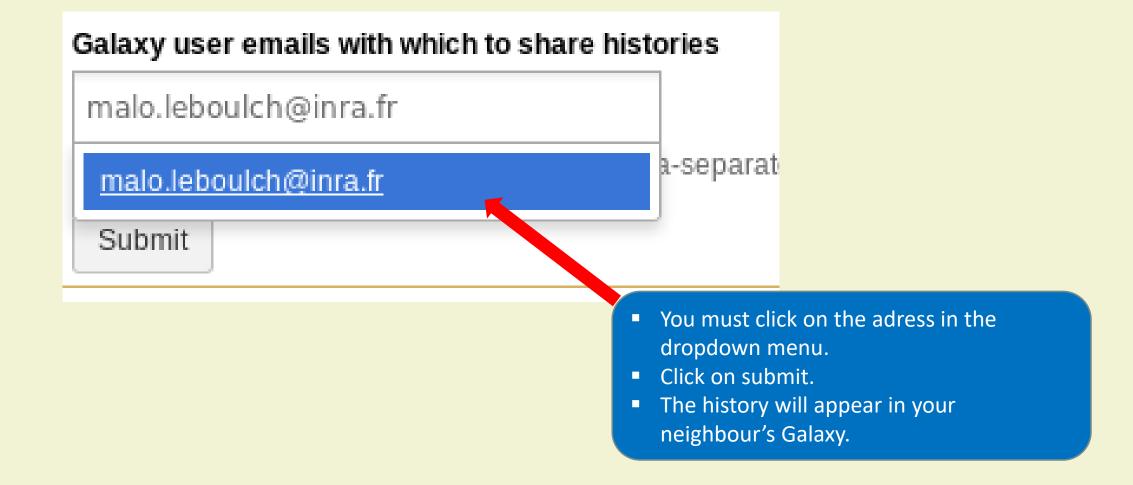
SHARE A HISTORY WITH YOUR NEIGHBOUR

Share a history



Galaxy	Analyze Data Workflow Shared Data → Visualization → Help → User →		Using 841.3 N
ools 1	Share or Publish History 'Historique R1R2'	History	C 🕈
search tools		search datasets	
ANAGE YOUR DATA FILES	Make History Accessible via Link and Publish It	Historique R1R2	
et Data	This history is currently restricted so that only you and the users listed below can access it. You can:	3 shown	
ownload Data	Make History Accessible via Link	126.19 MB	2
bbs statistics	Generates a web link that you can share with other people so that they can view and import the history.	3: Upload several files	۲
	Cenerates a web link that you can share with other people so that they can view and import the history.	from Genotoul	
LES MANIPULATION ext Manipulation	Make History Accessible and Publish	(sampleA_R2)	
Iter and Sort	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.	2: Upload several files	۲
bin, Subtract and Group		from Genotoul (sampleA_R1)	
FF	Share History with Individual Users		
ED Tools		1: Upload several files from Genotoul	۲ ک
onvert Formats	You have not shared this history with any users.	empty	
etch Sequences	Share with a user	format: txt , database: <u>?</u>	
atistics			a hua 07
raph/Display Data	Back to Histories List	Epilog : job finished at Tu 22:53:52 CEST 2017	e Jun 27
EQUENCES MANIPULATION		0 2	•
STA manipulation			
astQC: fastq/sam/bam			
umina fastq			
eneric FASTQ manipulation	Click on « share with a user ».		
STX-Toolkit for FASTQ data			
AM/BAM MANIPULATION : PICARD			
ETA)			
onversion			
C/Metrics for sam/bam			
AM/SAM Cleaning			
AM/BAM manipulation: SAMtools			
equences Queries			
CF Tools			

= Galaxy	Analyze Data Workflow Shared Data - Visualization - Help - User -	ι	lsing 841.3 MB
Tools	Share 1 histories	History	2≎⊡
search tools	Histories to be shared:	search datasets	0
MANAGE YOUR DATA FILES	History Name Number of Datasets	Historique R1R2	
Get Data	Historique R1R2 3	3 shown	
Download Data	Galaxy user emails with which to share histories	126.19 MB	2 🃎 🗩
Jobs statistics	Select a user	3: Upload several files	• / ×
FILES MANIPULATION	Enter a Galaxy user email the sess or a comma-separated list of addresses if sharing with multiple users	from Genotoul (sampleA_R2)	
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	Enter an email address from a Galaxy	from Genotoul	
Convert Formats		empty	
Fetch Sequences Statistics	user.	format: txt , database: <u>?</u>	
Graph/Display Data		Epilog : job finished at Tue 22:53:52 CEST 2017	9 Jun 27
SEQUENCES MANIPULATION		02	۰ ا
FASTA manipulation			
FastQC: fastq/sam/bam			
<u>Illumina fastq</u>			
Generic FASTQ manipulation			
FASTX-Toolkit for FASTQ data			
SAM/BAM MANIPULATION : PICARD (BETA)			
Conversion			
QC/Metrics for sam/bam			
BAM/SAM Cleaning			
SAM/BAM manipulation: SAMtools			
Sequences Queries			
VCF Tools			
<			

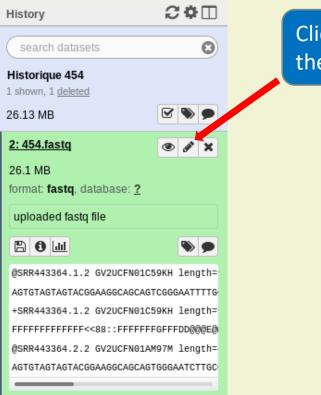


Manipulate datasets

Your Turn!

RENAME A DATASET

• Switch to 454 history.



Click here to display attributes and change the name.

Attributes Convert Format Datatype Permissions
Edit Attributes
Name:
http://genoweb.toulouse.inra.fr/~formatio Change the name here and call it « 454.fastq ».
Info:
uploaded fastq file
Annotation / Notes:
Add an annotation or notes to a dataset; annotations are available when a history is viewed.
Database/Build:
unspecified (?)
Save
Auto-detect
This will inspect the dataset and attempt to correct the above column values if they are not accurate.

Attributes Convert Format Datatype Permissions
Edit Attributes
Name: http://genoweb.toulouse.inra.fr/~formatio Info: uploaded fastq file uploaded fastq file
Annotation / Notes:
Database/Build: unspecified (?) Save Auto-detect This will inspect the dataset and attempt to correct the above column values if they are not accurate.

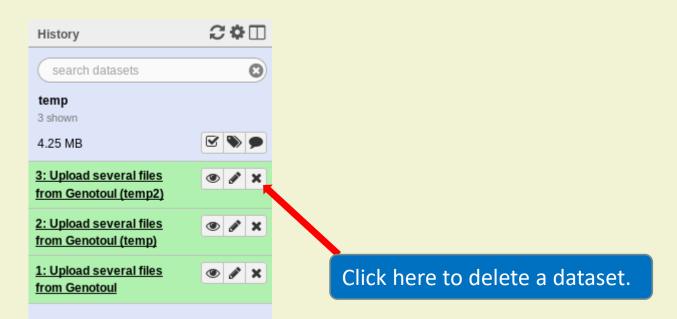
- Do the same with the merged history:
 - Switch to the merged history.
 - Change the name of the file to «100_10000seq_sample.tar.gz ».

Your Turn!

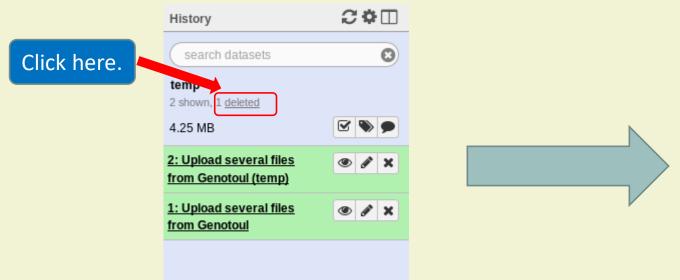
DELETE A DATASET

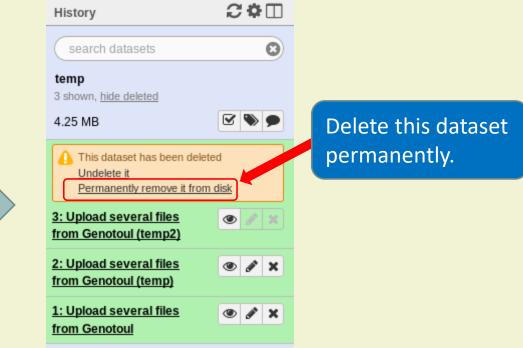
Delete a dataset

Switch to temp history.



Delete a dataset

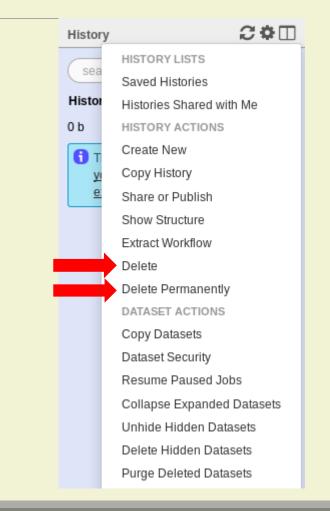




Nothing is deleted in Galaxy until you delete it permanently (=purge).

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 ».



Done search histories			search all datasets		8		
irrent History	-	Switch to	-	Switch to	-	Switch to	
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2 shown 126.19 MB		2 shown 2.12 MB		1 shown 26.13 MB		1 shown 83.8 MB	
search datasets	8	search datasets	8	search datasets	8	search datasets	
Drag datasets here to copy them to the	current history	2: barcode.tabular	● 🖋 🗙	<u>1: 454.fastq</u>	• / ×	<u>1:</u>	۲
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ormai: fastq , database: <u>?</u>		uploaded tabular file		uploaded fastq file			
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- GGTTCCGTCAATTTCTTTGAGTTTCAGCCTT							

Galaxy support

- Mail: <u>sigenae.support@listes.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 webbased genome analysis tool for experimentalists". Current Protocols in Molecular Biology. 2010 Jan; Chapter 19:Unit 19.10.1-21.

• Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, Zhang Y, Blankenberg D, Albert I, Taylor J, Miller W, 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 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, INRA Auzeville CS 52627 31326 Castanet Tolosan cedex.