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> galBU-ISCIII

Introduction to Galaxy

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Unidad de Bioinformática
Unidades Centrales Científico Técnicas – SGAFI-ISCIII

22-26 Noviembre 2021, 1^a Edición
Programa Formación Continua, ISCIII

Outline

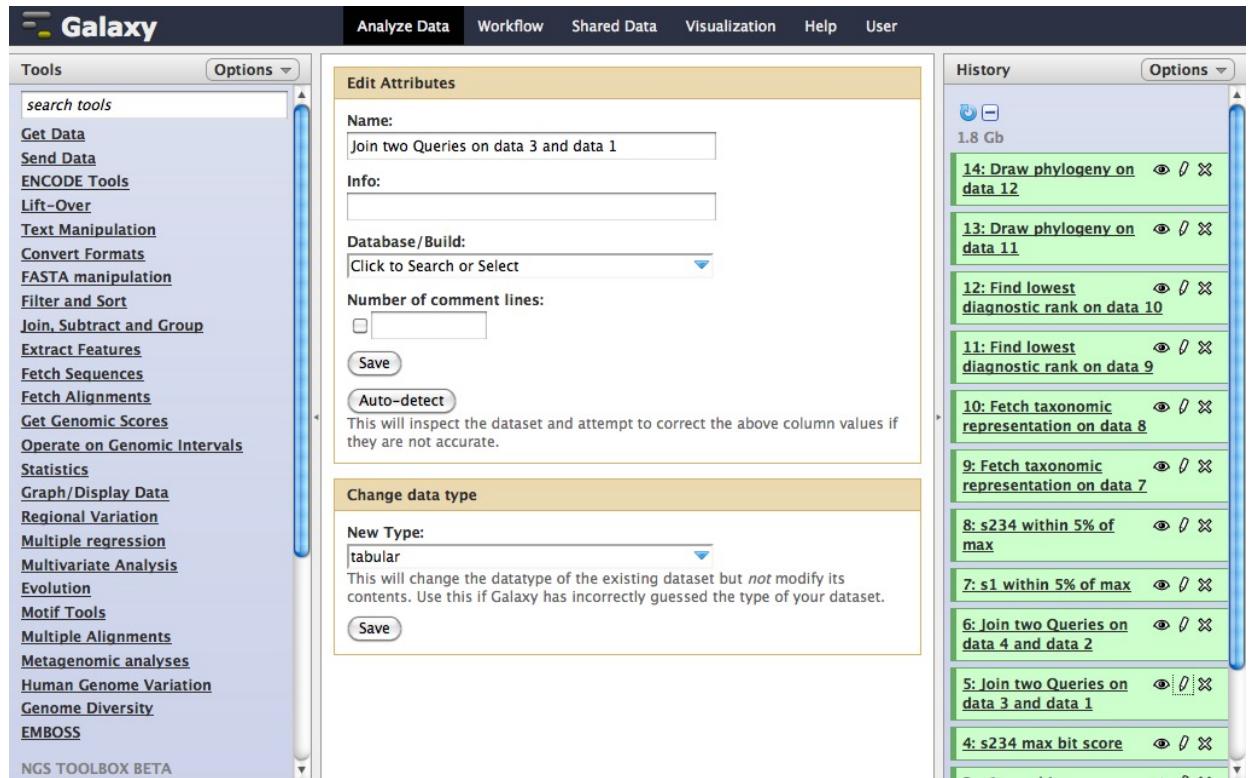
1. What is Galaxy?
2. Why Galaxy?
3. Why NOT Galaxy?
4. How to use Galaxy?

1. What is Galaxy?

<https://galaxyproject.org>



- Web platform
- Easy to use
- Free



The screenshot shows the Galaxy web interface. On the left, a sidebar lists various tools: Get Data, Send Data, ENCODE Tools, Lift-Over, Text Manipulation, Convert Formats, FASTA manipulation, Filter and Sort, Join, Subtract and Group, Extract Features, Fetch Sequences, Fetch Alignments, Get Genomic Scores, Operate on Genomic Intervals, Statistics, Graph/Display Data, Regional Variation, Multiple regression, Multivariate Analysis, Evolution, Motif Tools, Multiple Alignments, Metagenomic analyses, Human Genome Variation, Genome Diversity, EMBOS, and NGS TOOLBOX BETA.

The main area contains two panels: 'Edit Attributes' and 'Change data type'. The 'Edit Attributes' panel has fields for Name (Join two Queries on data 3 and data 1), Info, Database/Build (Click to Search or Select), and Number of comment lines (with a checkbox). It includes Save and Auto-detect buttons, with a note about auto-detection. The 'Change data type' panel has a New Type dropdown set to tabular, with a note about changing the datatype without modifying contents, and a Save button.

On the right, a 'History' panel lists 14 completed analysis steps:

- 14: Draw phylogeny on data 12
- 13: Draw phylogeny on data 11
- 12: Find lowest diagnostic rank on data 10
- 11: Find lowest diagnostic rank on data 9
- 10: Fetch taxonomic representation on data 8
- 9: Fetch taxonomic representation on data 7
- 8: s234 within 5% of max
- 7: s1 within 5% of max
- 6: Join two Queries on data 4 and data 2
- 5: Join two Queries on data 3 and data 1
- 4: s234 max bit score
- 3: Join two Queries on data 2 and data 1
- 2: Find lowest diagnostic rank on data 1
- 1: Draw phylogeny on data 1

Source: <https://commons.wikimedia.org/wiki/File:GalaxyScreenshot.png>

1. What is Galaxy?



Source: https://training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-short/slides.html?utm_source=usegalaxyeu&utm_medium=website&utm_campaign=covid2021#7

1. What is Galaxy?



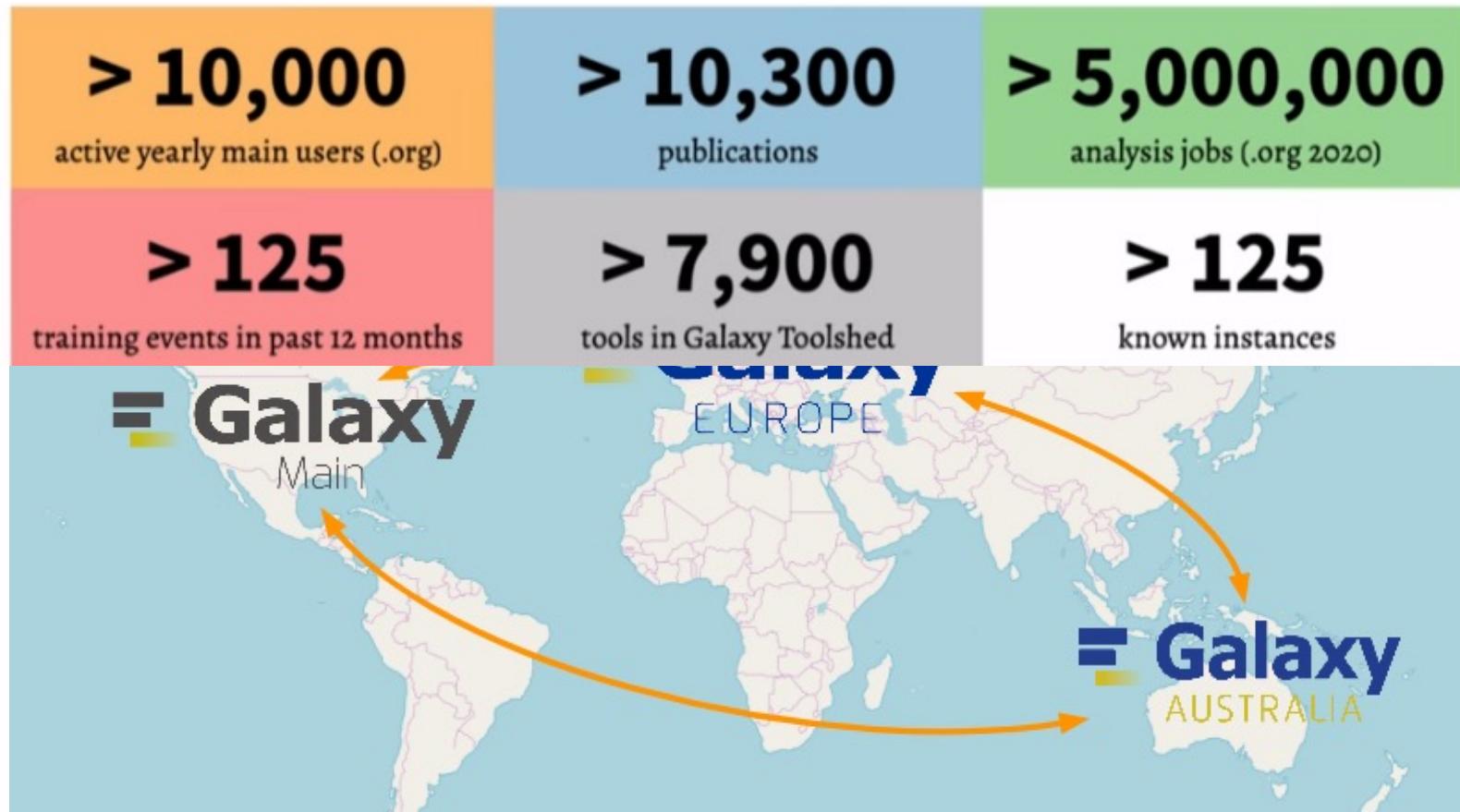
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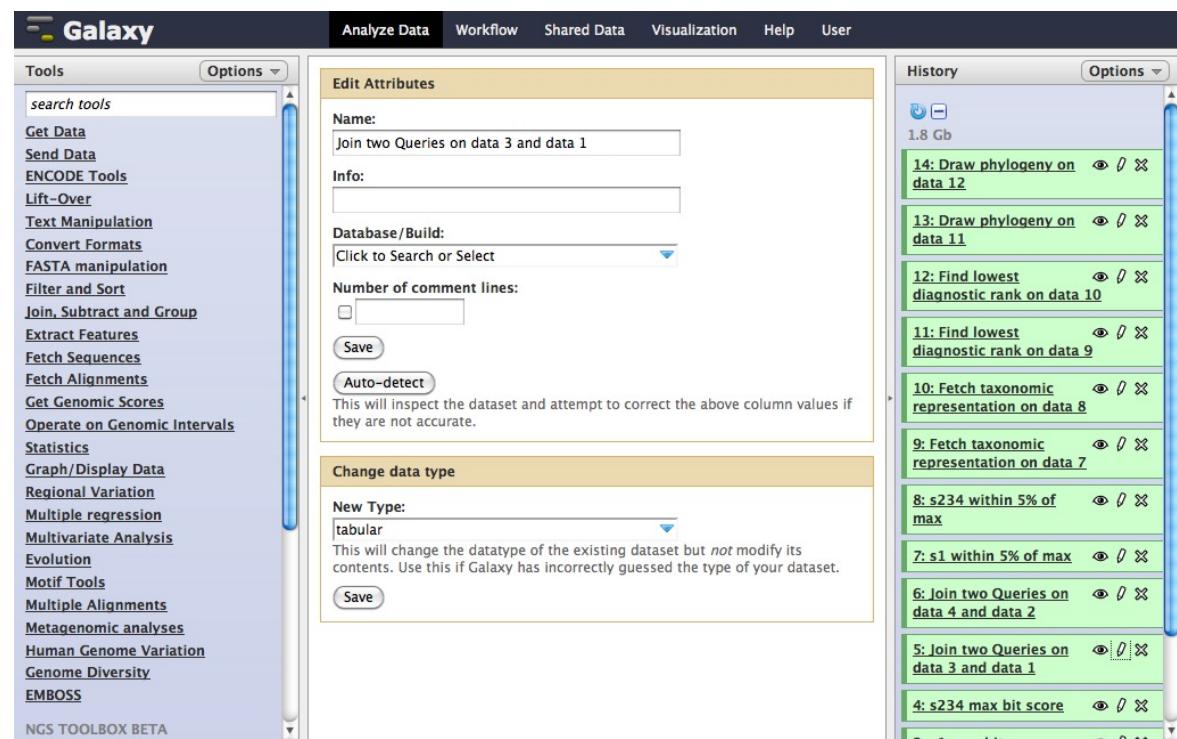
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2. Why Galaxy?

- Easy and accessible:
 - No installation
 - No commands
- Reproducible
- Versatile workflows
- Open source
- Multidisciplinary



The screenshot shows the Galaxy web interface. On the left, a sidebar titled 'Tools' lists various bioinformatics tools: search tools, Get Data, Send Data, ENCODE Tools, Lift-Over, Text Manipulation, Convert Formats, FASTA manipulation, Filter and Sort, Join, Subtract and Group, Extract Features, Fetch Sequences, Fetch Alignments, Get Genomic Scores, Operate on Genomic Intervals, Statistics, Graph/Display Data, Regional Variation, Multiple regression, Multivariate Analysis, Evolution, Motif Tools, Multiple Alignments, Metagenomic analyses, Human Genome Variation, Genome Diversity, and EMBOS. Below this is a section for 'NGS TOOLBOX BETA'. The main area is titled 'Edit Attributes' and contains fields for 'Name' (Join two Queries on data 3 and data 1), 'Info', 'Database/Build' (Click to Search or Select), and 'Number of comment lines'. It also includes an 'Auto-detect' button with a note about inspecting dataset values. A 'Change data type' section shows 'New Type: tabular' with a note about changing datatype without modifying contents. At the bottom right of the main area is a 'Save' button. To the right, a vertical 'History' panel lists 15 workflow steps, each with a preview icon, name, and delete button. The steps include: 14: Draw phylogeny on data 12, 13: Draw phylogeny on data 11, 12: Find lowest diagnostic rank on data 10, 11: Find lowest diagnostic rank on data 9, 10: Fetch taxonomic representation on data 8, 9: Fetch taxonomic representation on data 7, 8: s234 within 5% of max, 7: s1 within 5% of max, 6: Join two Queries on data 4 and data 2, 5: Join two Queries on data 3 and data 1, and 4: s234 max bit score.

3. Why NOT Galaxy?

	UseGalaxy Servers	Public Servers	TlaaS	Academic Clouds	Commercial Clouds	Containers	VMs	Local
Free to use	Yes	Yes	Yes	Yes ¹	No	Yes	Yes	Yes
Uses your local compute infrastructure	No	No	No	No	No	Yes ²	Yes ²	Yes
Datasets total > 250GB (including intermediate)	No	? ⁵	Yes	Yes	Yes	Yes ³	Yes ³	Yes
Computational requirements are similarly large	No	? ⁵	Yes	Yes	Yes	Yes ³	Yes ³	Yes
Share Galaxy objects outside your organization	Yes	Yes	Yes	Yes	Yes	Yes ⁴	Yes ⁴	Yes ⁵
Install custom tools and reference genomes	No	No	Yes ⁵	Yes	Yes	Yes	Yes	Yes
Have absolute data security requirements	No	No	? ⁵	? ⁵	? ⁵	? ⁵	? ⁵	Yes

¹ Depends on provider, and if you are eligible for the service

² These technologies can be deployed on clouds or locally.

³ Depends on the size of the system you are running it on.

⁴ With these technologies you can save the server and share the entire platform with them.

⁵ Depends on configuration.

Source: <https://galaxyproject.org/use/>

3. Why NOT Galaxy?

<https://usegalaxy.eu/>

UseGalaxy Servers	
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Uses your local compute infrastructure	No
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<https://usegalaxy.eu/>

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> 5,000,000
analysis jobs (.org 2020)

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4. How to use Galaxy?

<https://usegalaxy.eu/>

Galaxy Europe Using 0 bytes

Tools search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

COVID-19 Research!

Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the [Galaxy SARS-CoV-2 portal](#). We mirror [all public SARS-CoV-2 data](#) from ENA in a [Galaxy data library](#) for your convenience. The Galaxy community has created [COVID-19 dedicated training materials](#). Please check our [recent activities](#) for more details.

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Nov 18, 2021

History search datasets

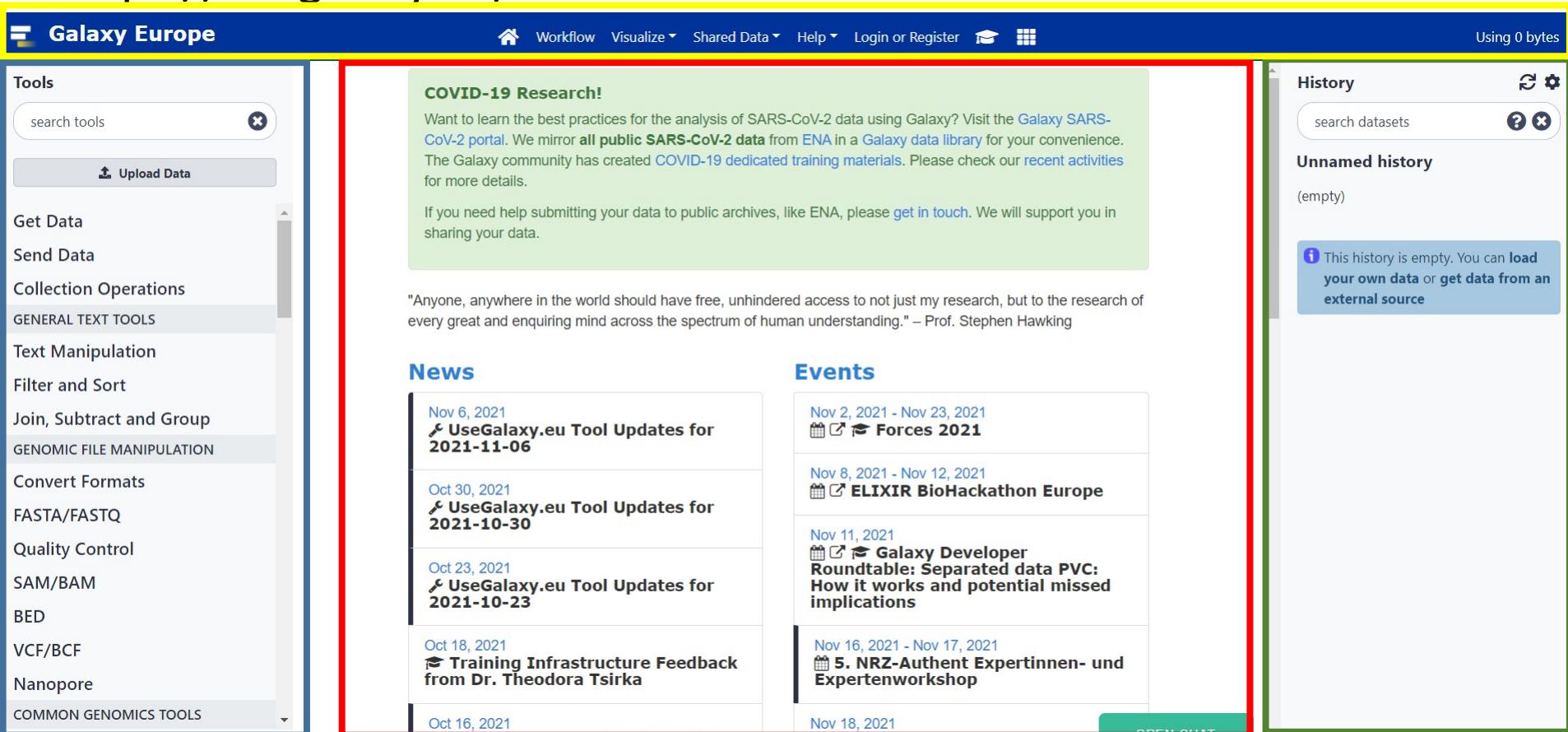
Unnamed history (empty)

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

OPEN CHAT

4. How to use Galaxy?

<https://usegalaxy.eu/>



Galaxy Europe

Workflow Visualize Shared Data Help Login or Register

Using 0 bytes

Tools

search tools

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

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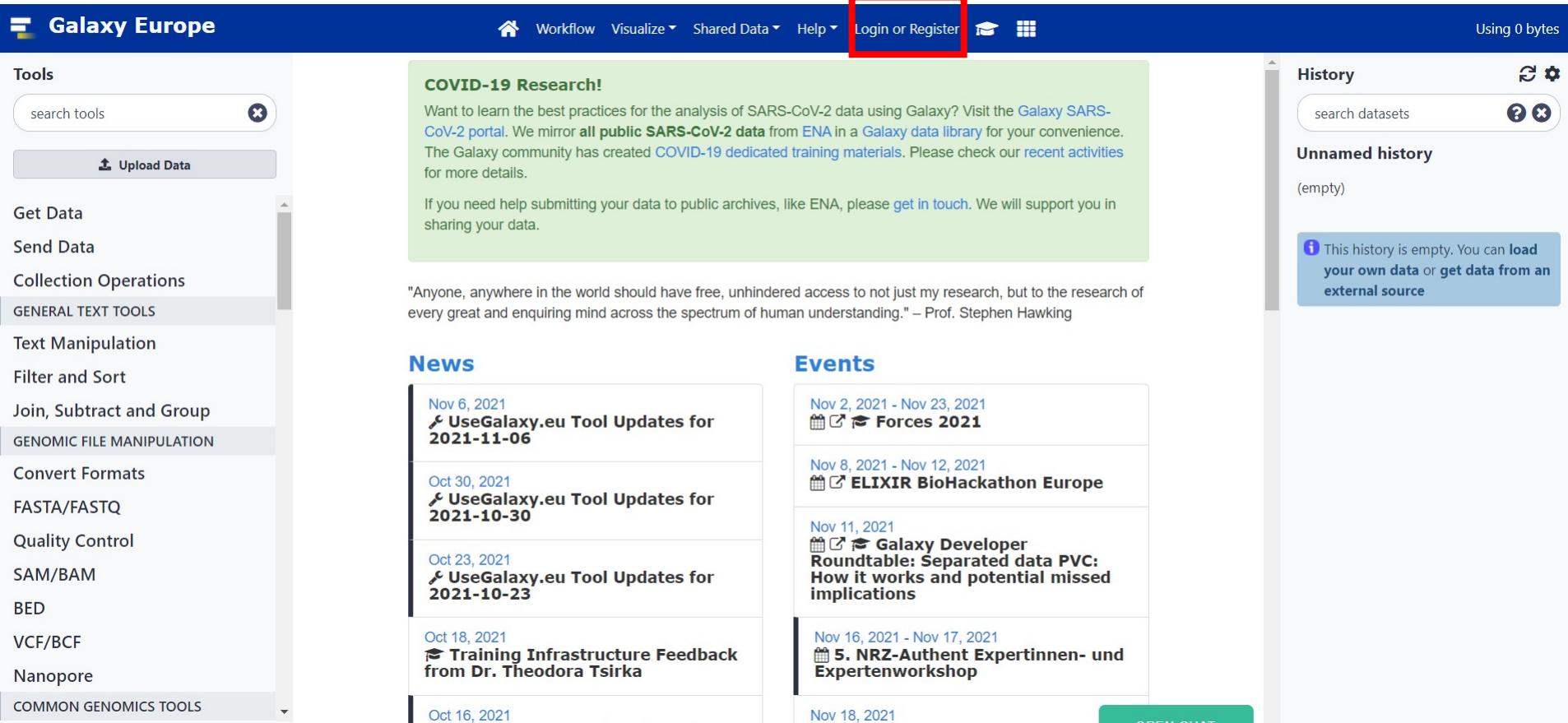
Unnamed history

(empty)

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

4. How to use Galaxy?

<https://usegalaxy.eu/>



The screenshot shows the UseGalaxy.eu homepage. On the left, there's a sidebar with various genomic tools and file manipulation options. The main content area features a COVID-19 Research section, a quote from Stephen Hawking, and news and events sections. A red box highlights the "Login or Register" button in the top navigation bar.

COVID-19 Research!

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History

search datasets [?](#) [X](#)

Unnamed history

(empty)

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

4. How to use Galaxy?

Galaxy Europe



Flujo de Trabajo

Visualizar ▾

Datos Compartidos ▾

Ayuda ▾

Iniciar sesión o Registrarse



Welcome to Galaxy, please log in

Public Name or Email Address

Password

Forgot password? Click here to reset your password.

[Login](#)Don't have an account? [Register here.](#)

COVID-19 Research!

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Oct 23, 2021

[↗ UseGalaxy.eu Tool Updates for 2021-](#)[OPEN CHAT](#)

4. How to use Galaxy?

Galaxy Europe

Flujo de Trabajo Visualizar ▾ Datos Compartidos ▾ Ayuda ▾ Iniciar sesión o Registrarse  

Please register only one account - we provide this service free of charge and have limited computational resources. Multi-accounts are tracked and will be subjected to account termination and data deletion.

Create a Galaxy account

Email Address

Password

Confirm password

Public name

Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes (';', '_', '-').

Already have an account? Log in here.

GDPR

GDPR Compliance Documentation

For UseGalaxy.eu

ToS & PP

- [Privacy Policy](#)
- [Terms of Service](#)

GDPR Documentation

- [Your Rights Under the GDPR](#)
- [Legitimate Interest Analyses](#)
- [Data Storage and Access](#)
- [Data Processing Activities Register](#)

Contact

Bioinformatics Group

contact@usegalaxy.eu

Department of Computer Science

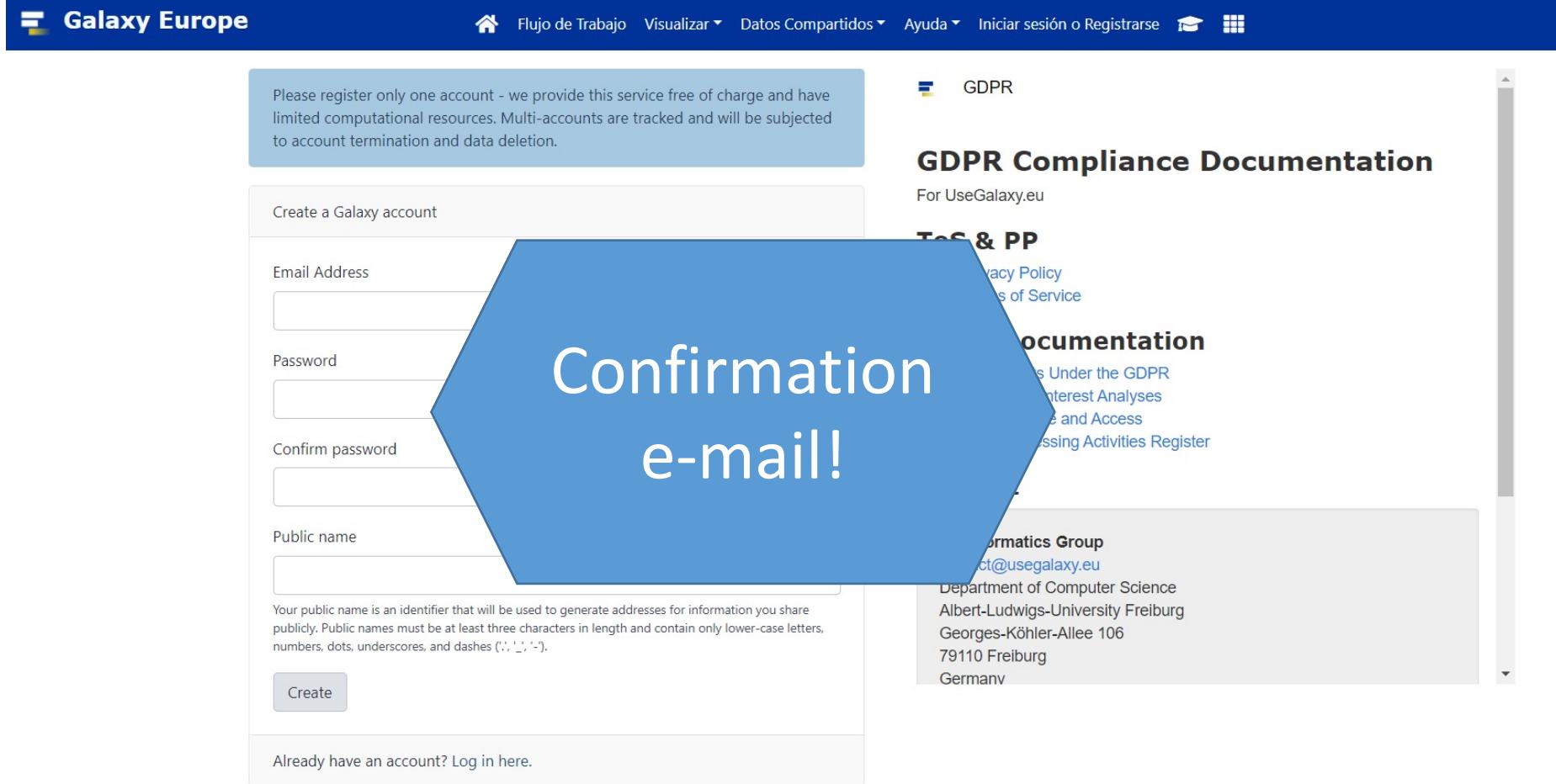
Albert-Ludwigs-University Freiburg

Georges-Köhler-Allee 106

79110 Freiburg

Germany

4. How to use Galaxy?



The screenshot shows the Galaxy Europe account creation interface. A large blue hexagon is overlaid on the page, containing the text "Confirmation e-mail!".

Galaxy Europe

Please register only one account - we provide this service free of charge and have limited computational resources. Multi-accounts are tracked and will be subjected to account termination and data deletion.

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Create

Already have an account? Log in here.

Flujo de Trabajo Visualizar ▾ Datos Compartidos ▾ Ayuda ▾ Iniciar sesión o Registrarse  

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ToS & PP
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Documentation
[Data Protection Under the GDPR](#)
[Interest Analyses](#)
[Data and Access](#)
[Processing Activities Register](#)

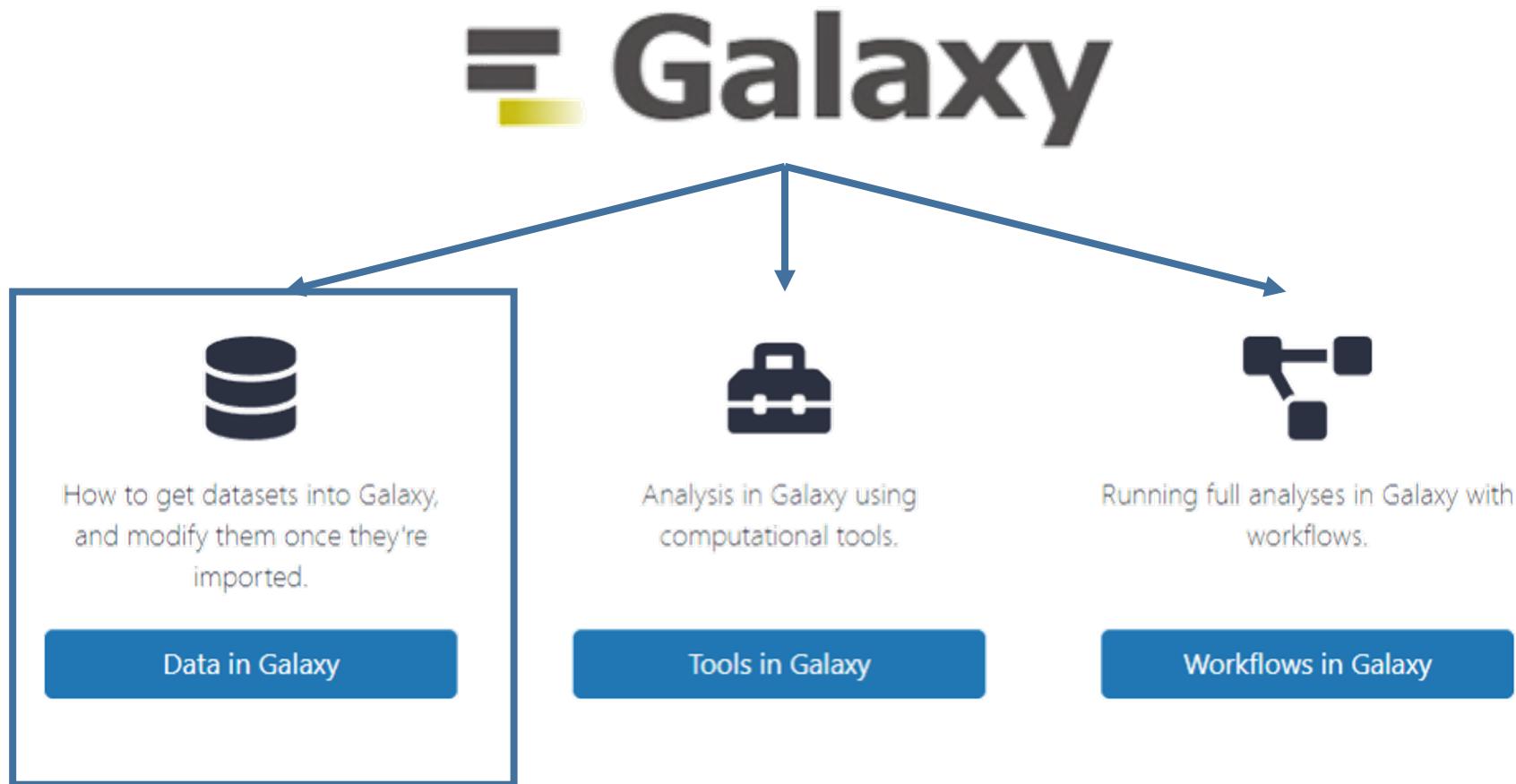
informatics Group
uct@usegalaxy.eu
Department of Computer Science
Albert-Ludwigs-University Freiburg
Georges-Köhler-Allee 106
79110 Freiburg
Germany

4. How to use Galaxy?



Source: <https://usegalaxy.org/welcome/new>

4. How to use Galaxy?





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4.1. Data



Loading in data from your machine or via URL.

Importing via Data Uploader



Use data from sources such as UCSC, SRA, or EMBL.

Retrieving Data from Public Databases



Find and retrieve data shared between Galaxy users.

Obtaining Shared Data



Observing and modifying your data

Data and Metadata in Galaxy.



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Instituto
de Salud
Carlos III

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4.1. Data

<https://usegalaxy.eu/>

Galaxy Europe Using 0 bytes

Tools search tools

Get Data Send Data Collection Operations GENERAL TEXT TOOLS Text Manipulation Filter and Sort Join, Subtract and Group GENOMIC FILE MANIPULATION Convert Formats FASTA/FASTQ Quality Control SAM/BAM BED VCF/BCF Nanopore COMMON GENOMICS TOOLS

COVID-19 Research!
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History search datasets
Unnamed history (empty)
i This history is empty. You can [load your own data](#) or [get data from an external source](#)

OPEN CHAT

4.1. Data

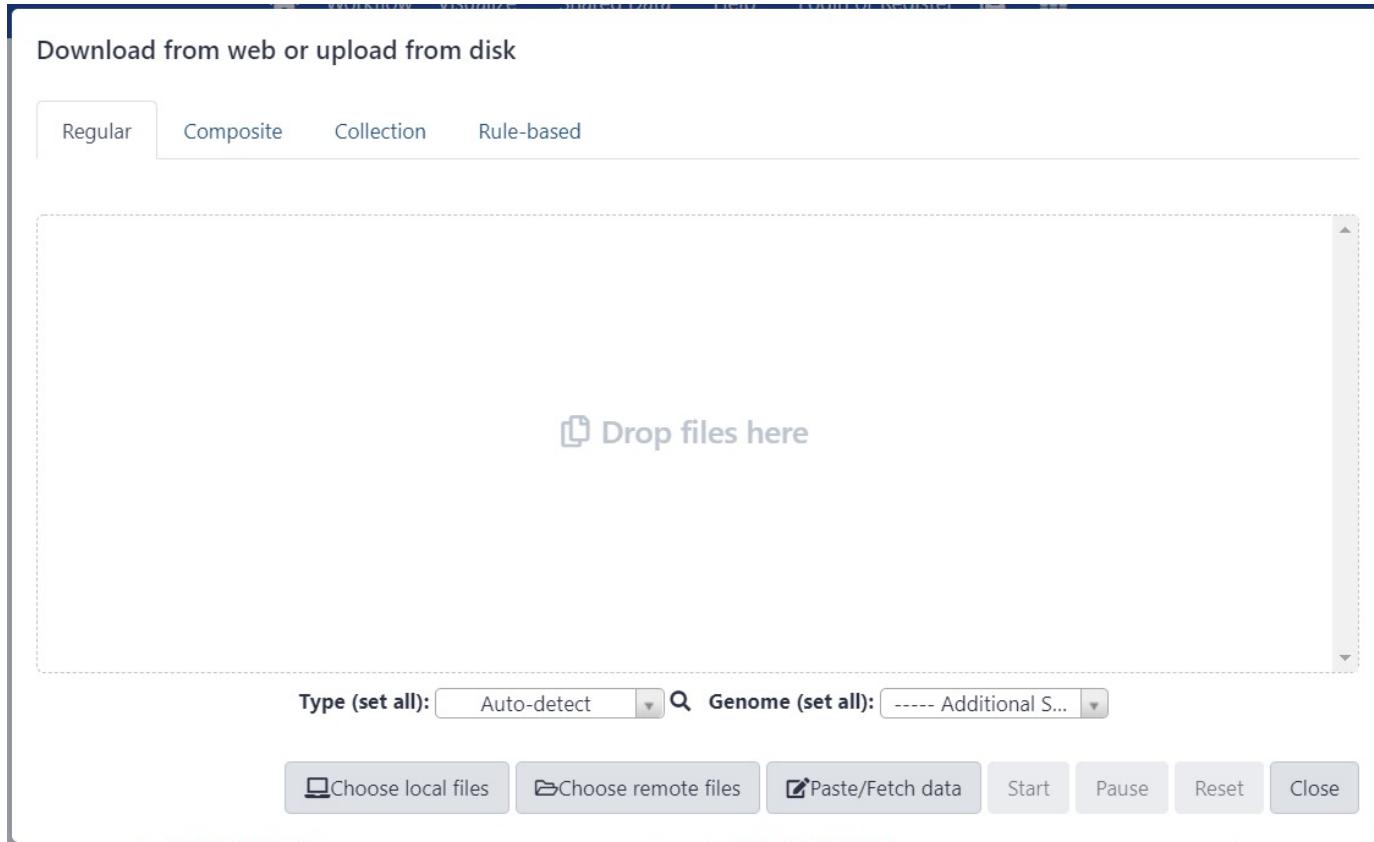
Download from web or upload from disk

Regular Composite Collection Rule-based

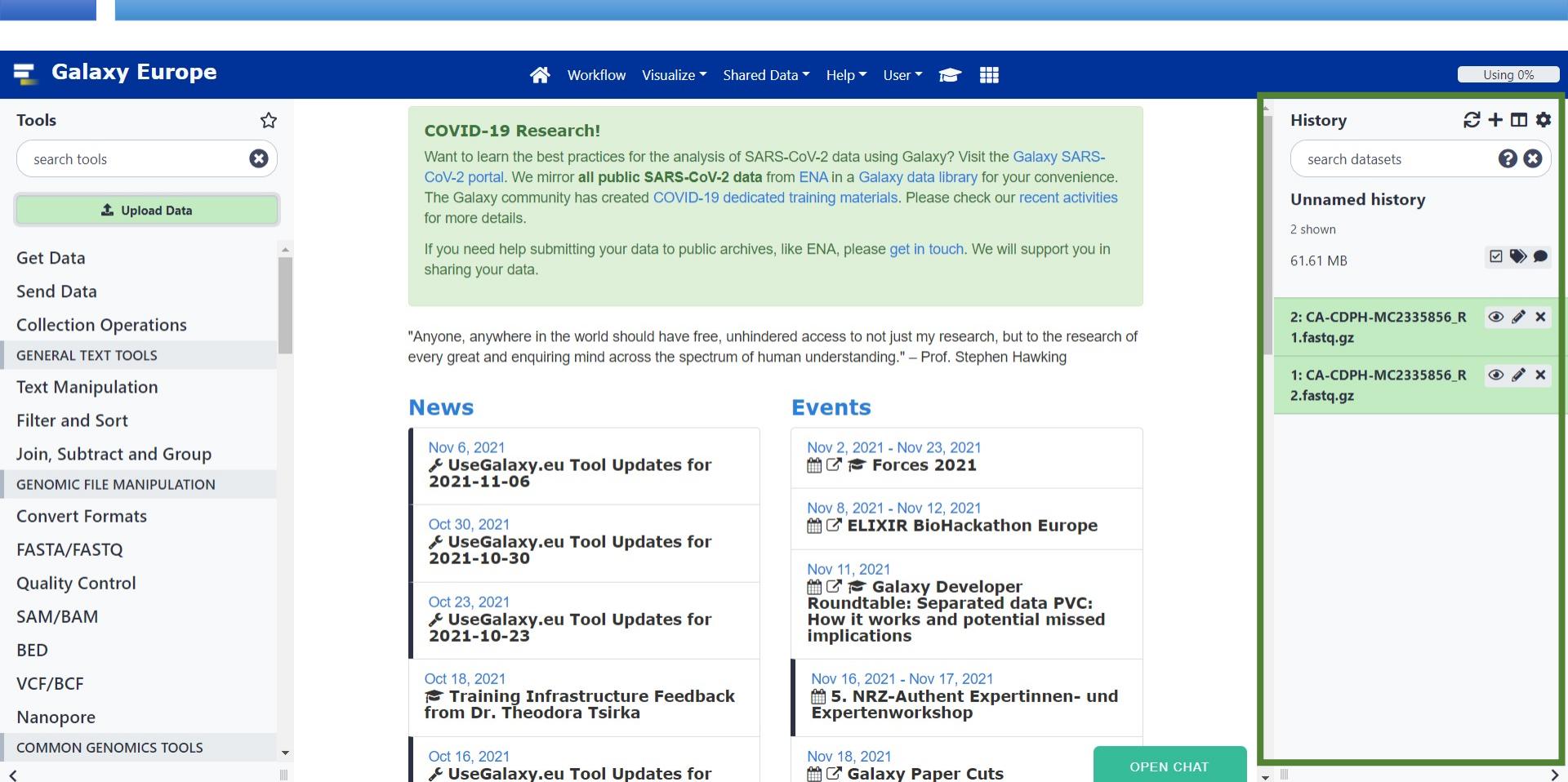
Drop files here

Type (set all): Auto-detect Q Genome (set all): ----- Additional S... ▾

Choose local files Choose remote files Paste/Fetch data Start Pause Reset Close



4.1. Data



The screenshot shows the Galaxy Europe interface. On the left, a sidebar lists various genomic tools and file manipulation options. The main content area features a green box for "COVID-19 Research", news items, events, and a history panel.

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- Nov 16, 2021 - Nov 17, 2021 [5. NRZ-Authent Expertinnen- und Expertenworkshop](#)
- Nov 18, 2021 [Galaxy Paper Cuts](#)

History

search datasets

Unnamed history

2 shown

61.61 MB

2: CA-CDPH-MC2335856_R 1.fastq.gz

1: CA-CDPH-MC2335856_R 2.fastq.gz

OPEN CHAT

4.1. Data

Galaxy Europe Using 0%

Tools 

search tools 

 Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

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Nanopore

COMMON GENOMICS TOOLS

 Workflow Visualize Shared Data Help User  

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 OPEN CHAT

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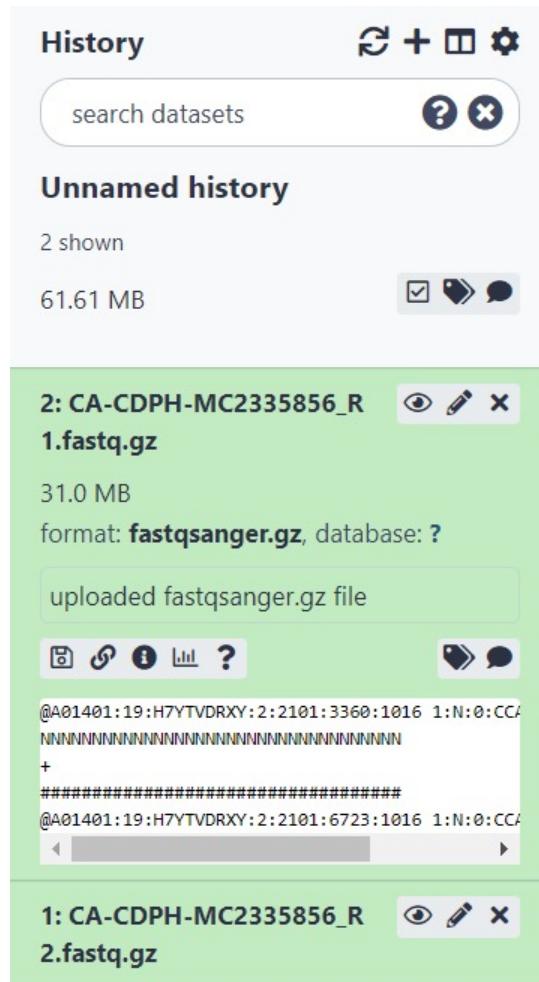
61.61 MB

2: CA-CDPH-MC2335856_R   
1.fastq.gz

1: CA-CDPH-MC2335856_R   
2.fastq.gz

4.1. Data



History ⟳ + ⌂ ⚙

search datasets ? ×

Unnamed history

2 shown

61.61 MB ✓ 🌐 💬

2: CA-CDPH-MC2335856_R eye edit x
1.fastq.gz
31.0 MB
format: **fastqsanger.gz**, database: ?
uploaded fastqsanger.gz file

uploaded fastqsanger.gz file

@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0:CCA
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
+

@A01401:19:H7YTVDRXY:2:2101:6723:1016 1:N:0:CCA

1: CA-CDPH-MC2335856_R eye edit x
2.fastq.gz

4.1. Data

History    

search datasets  

Unnamed history

2 shown

61.61 MB   

2: CA-CDPH-MC2335856_R   
1.fastq.gz

31.0 MB
format: fastqsanger.gz, database: ?
uploaded fastqsanger.gz file

```
@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0:CCA  
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  
+  
#####  
@A01401:19:H7YTVDRXY:2:2101:6723:1016 1:N:0:CCA
```

1: CA-CDPH-MC2335856_R   
2.fastq.gz

4.1. Data

4.1. Data

History    

search datasets  

Unnamed history

2 shown

61.61 MB   

2: CA-CDPH-MC2335856_R   

1.fastq.gz

31.0 MB

format: fastqsanger.gz, database: ?

uploaded fastqsanger.gz file

```
@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0:CCA  
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  
+  
#####  
@A01401:19:H7YTVDRXY:2:2101:6723:1016 1:N:0:CCA
```

1: CA-CDPH-MC2335856_R   

2.fastq.gz

4.1. Data

The screenshot shows the Galaxy History interface. At the top, there's a search bar labeled "search datasets" with a question mark icon and a close button. Below it, the title "Unnamed history" is displayed, followed by "2 shown". A file entry for "2: CA-CDPH-MC2335856_R 1.fastq.gz" is shown, with a size of 61.61 MB and a green status bar indicating it's an uploaded fastqsanger.gz file. The file content preview shows sequence data starting with "@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0:CCA" and ending with "@A01401:19:H7YTVDRXY:2:2101:6723:1016 1:N:0:CCA". Another file entry for "1: CA-CDPH-MC2335856_R 2.fastq.gz" is partially visible below it.

4. How to use Galaxy?





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de Salud
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4.2. Analysis



Understanding the tool form and running any standard tool

Standard Tools and the Tool Form



Easily view your data through graphs and other methods.

Data Visualization Tools



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4.2. Analysis



Understanding the tool form and running any standard tool

Standard Tools and the Tool Form



Easily view your data through graphs and other methods.

Data Visualization Tools

4.2. Analysis

The screenshot shows the Galaxy Europe web interface. At the top, there's a navigation bar with 'Galaxy Europe' logo, user account, and help links. The main area has a 'Tools' sidebar on the left containing links for 'fastqc', 'Upload Data', 'Show Sections', and sections for 'Create a model to recommend tools' and 'Combine FASTA and QUAL into FASTQ'. A large central panel displays a sequence dataset with a warning message: 'This dataset is large and only the first megabyte is shown below.' Below the message are buttons for 'Show all' and 'Save'. The main content area shows a sequence of reads starting with '@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0:CCATCATTAG+AGAGGCAACC'. To the right, there's a 'History' panel showing an 'Unnamed history' entry for 'R1.fastq.gz' (format: fastqsanger.gz) and a 'WORKFLOWS' section listing 'All workflows'.

4.2. Analysis

The screenshot shows the Galaxy Europe web interface. The top navigation bar includes links for 'Flujo de Trabajo', 'Visualizar', 'Datos Compartidos', 'Ayuda', 'Usuario', and a user icon. The main content area is titled 'FastQC Read Quality reports (Galaxy Version 0.73+galaxy0)'. On the left, a sidebar lists various tools: 'fastqc' (selected), 'Upload Data', 'Show Sections', 'Create a model to recommend tools using deep learning', 'FastQC Read Quality reports', 'Combine FASTA and QUAL into FASTQ', 'fastp - fast all-in-one preprocessing for FASTQ files', 'Map with PerM for SOLiD and Illumina', 'Manipulate FASTQ reads on various attributes', 'Create a model to recommend tools using deep learning', and 'FLUJOS DE TRABAJO' (All workflows). The central panel contains sections for 'Raw read data from your current history' (listing '2: CA-CDPH-MC2335856_R1.fastq.gz'), 'Contaminant list' (listing 'No tabular dataset available.'), 'Adapter list' (listing 'No tabular dataset available.'), and 'Submodule and Limit specifying file' (listing 'Nothing selected'). A detailed description for the submodule section states: 'a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter'. Below this is a setting for 'Disable grouping of bases for reads >50bp' with a 'No' toggle switch. A note explains: 'Using this option will cause fastqc to crash and burn if you use it on really long reads, and your plots may end up a ridiculous size. You have been warned! (-nogroup)'. At the bottom, a note about sequence length specifies: 'As long as you set this to a value greater or equal to your longest read length then this will be the sequence length used to create your read groups.' The right side features a 'History' panel showing an 'Unnamed history' entry for '2: CA-CDPH-MC2335856_R1.fastq.gz' and a preview of the FASTQ file content.

4.2. Analysis

The screenshot shows the Galaxy Europe web interface. The top navigation bar includes links for 'Flujo de Trabajo', 'Visualizar', 'Datos Compartidos', 'Ayuda', 'Usuario', and a user icon. A status bar at the top right indicates 'Using 0%'. The left sidebar contains a 'Tools' section with a search bar for 'fastqc', an 'Upload Data' button, and a 'Show Sections' button. Below this are several tool descriptions: 'Create a model to recommend tools using deep learning', 'FastQC Read Quality reports', 'Combine FASTA and QUAL into FASTQ', 'fastp - fast all-in-one preprocessing for FASTQ files', 'Map with PerM for SOLiD and Illumina', 'Manipulate FASTQ reads on various attributes', 'Create a model to recommend tools using deep learning', and 'FLUJOS DE TRABAJO' with a link to 'All workflows'. The main content area is titled 'FastQC Read Quality reports (Galaxy Version 0.73+galaxy0)'. It features sections for 'Raw read data from your current history' (listing '2: CA-CDPH-MC2335856_R1.fastq.gz'), 'Contaminant list' (listing 'No tabular dataset available.'), 'Adapter list' (listing 'No tabular dataset available.'), 'Submodule and Limit specifying file' (listing 'Nothing selected'), and configuration options like 'Disable grouping of bases for reads >50bp' (set to 'No') and 'Lower limit on the length of the sequence to be shown in the report' (with a text input field). The right sidebar shows the 'History' panel with an 'Unnamed history' containing two entries: '2: CA-CDPH-MC2335856_R1.fastq.gz' and '1: CA-CDPH-MC2335856_R2.fastq.gz', each with detailed file metadata and preview snippets.

4.2. Analysis

The screenshot shows the Galaxy Europe web interface. On the left, a sidebar titled 'Tools' lists various bioinformatics tools, including 'fastqc', 'Upload Data', 'Show Sections', and several deep learning models. Below this is a section for 'FLUJOS DE TRABAJO' (Workflows) with a link to 'All workflows'. The main content area is titled 'FastQC Read Quality reports (Galaxy Version 0.73+galaxy0)'. It contains sections for 'Raw read data from your current history' (listing a file '2: CA-CDPH-MC2335856_R1.fastq.gz'), 'Contaminant list' (empty), 'Adapter list' (empty), 'Submodule and Limit specifying file' (empty), and options for 'Disable grouping of bases for reads >50bp' (set to 'No') and 'Lower limit on the length of the sequence to be shown in the report' (set to '100'). At the top right, there's a 'History' panel showing an 'Unnamed history' with one entry: '2: CA-CDPH-MC2335856_R1.fastq.gz' (31.0 MB, fastqsanger.gz format). The bottom of the page has a footer with links to 'Using 0%' and other Galaxy resources.

4.2. Analysis

The screenshot shows the Galaxy Europe web interface. On the left, a sidebar lists various tools and sections. The main content area displays the documentation for the 'fastqc' tool, including its purpose, main functions, and inputs/outputs. A large 'Execute' button is prominently displayed. To the right, a vertical panel shows the user's history, listing an 'Unnamed history' entry and two specific tool runs (labeled 1 and 2) involving 'fastqc' and 'fastqsanger.gz' files.

Galaxy Europe

Flujo de Trabajo Visualizar ▾ Datos Compartidos ▾ Ayuda ▾ Usuario ▾

Using 0%

Tools

fastqc

Purpose

FastQC aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines. It provides a set of analyses which you can use to get a quick impression of whether your data has any problems of which you should be aware before doing any further analysis.

The main functions of FastQC are:

- Import of data from BAM, SAM or FastQ/FastQ.gz files (any variant),
- Providing a quick overview to tell you in which areas there may be problems
- Summary graphs and tables to quickly assess your data
- Export of results to an HTML based permanent report
- Offline operation to allow automated generation of reports without running the interactive application

FastQC

This is a Galaxy wrapper. It merely exposes the external package FastQC which is documented at FastQC Kindly acknowledge it as well as this tool if you use it. FastQC incorporates the Picard-tools libraries for SAM/BAM processing.

The contaminants file parameter was borrowed from the independently developed fastqcwrapper contributed to the Galaxy Community Tool Shed by J. Johnson. Adaption to version 0.11.2 by T. McGowan.

Inputs and outputs

FastQC is the best place to look for documentation - it's very good. A summary follows below for those in a tearing hurry.

This wrapper will accept a Galaxy fastq, fastq.gz, sam or bam as the input read file to check. It will also take an optional file containing a list of contaminants information, in the form of a tab-delimited file with 2 columns, name and sequence. As another option the tool takes a custom limits.txt file that allows setting the warning thresholds for the different modules and also specifies which modules to include in the output.

The tool produces a basic text and a HTML output file that contain all of the results, including the following:

History

buscar conjuntos de datos

Unnamed history

2 shown

61.61 MB

2: CA-CDPH-MC2335856_R

1.fastq.gz

31.0 MB

formato: **fastqsanger.gz**, base de datos: ?

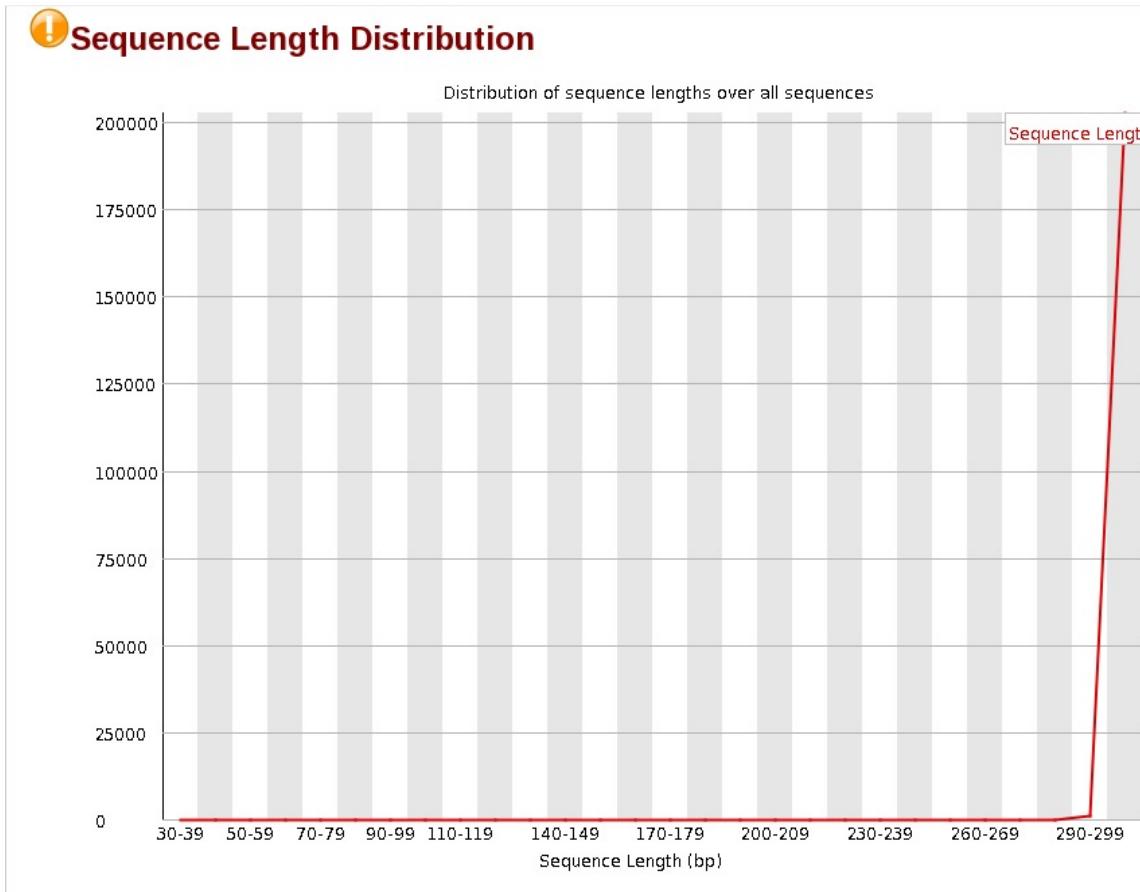
uploaded fastqsanger.gz file

1: CA-CDPH-MC2335856_R

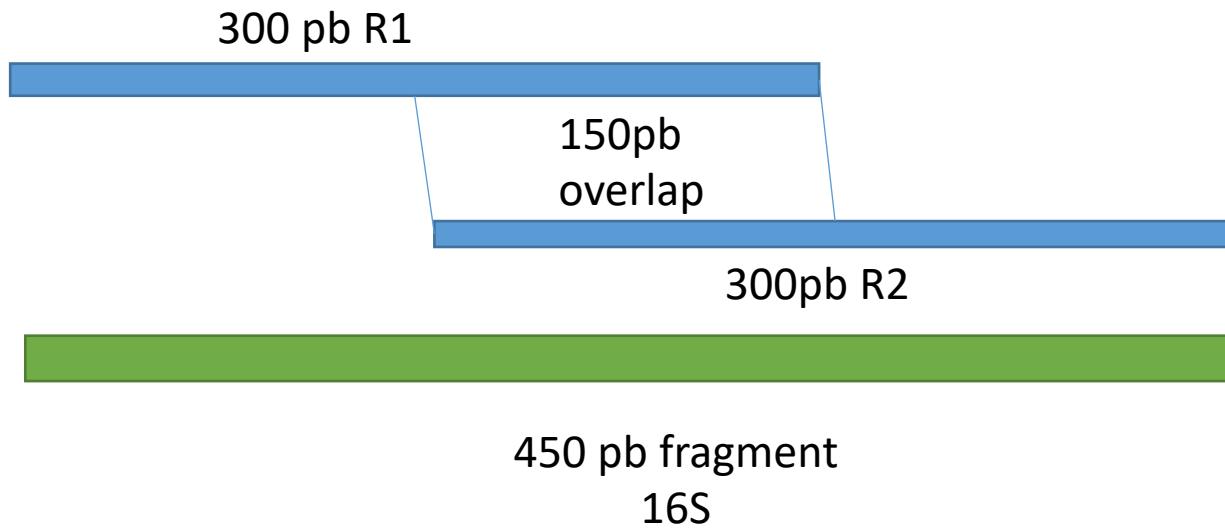
2.fastq.gz

4.2. Analysis

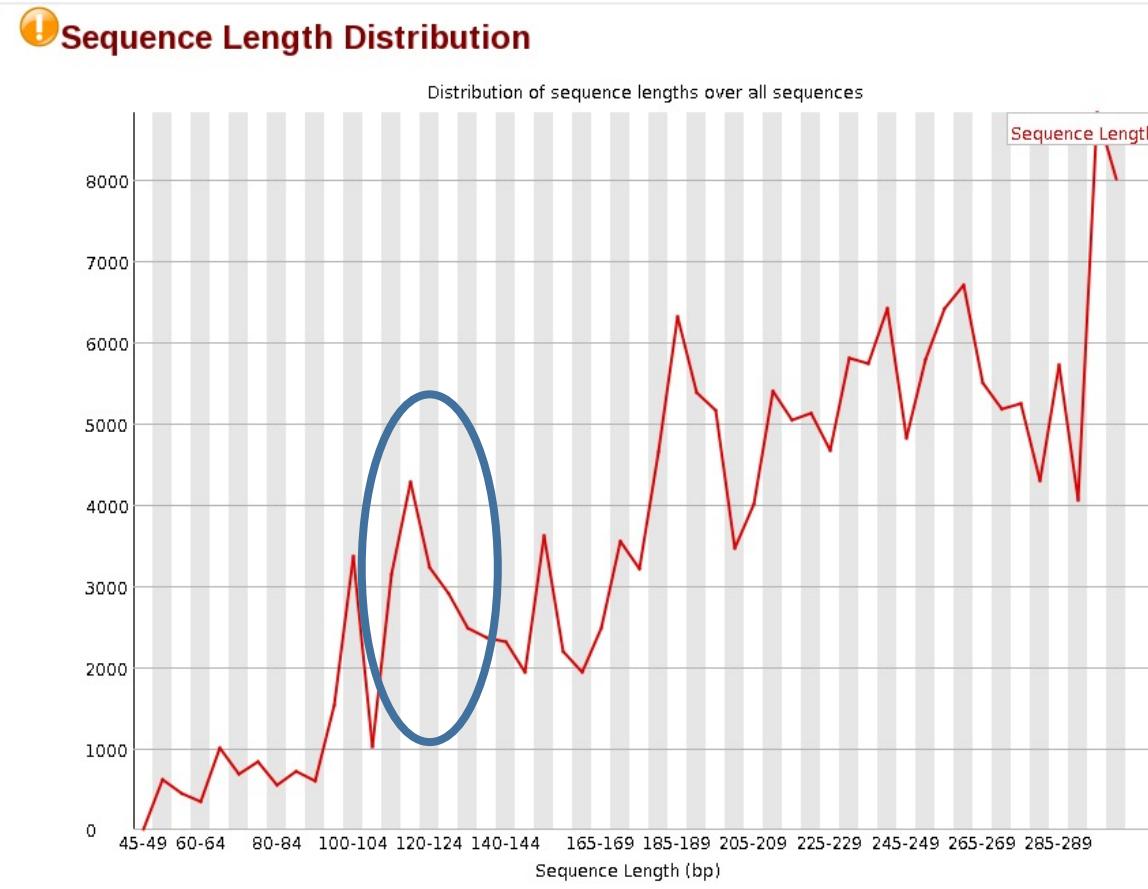
4.2. Analysis



4.2. Analysis



4.2. Analysis





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4.2. Analysis

100 pb R1



No overlap



100 pb R2



450 aprox. pb
fragment
V3-V4 16S
region

4.2. Analysis

4.2. Analysis

4.2. Analysis

4.2. Analysis

The screenshot shows the Galaxy Europe web interface. The top navigation bar includes links for Home, Flujo de Trabajo, Visualizar, Datos Compartidos, Ayuda, Usuario, and a user icon. A progress bar at the top right indicates "Using 0%".

Tools sidebar:

- search tools
- Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS (selected)

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

COVID-19 Research!

Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the [Galaxy SARS-CoV-2 portal](#). We mirror all **public SARS-CoV-2 data** from ENA in a [Galaxy data library](#) for your convenience. The Galaxy community has created [COVID-19 dedicated training materials](#). Please check our [recent activities](#) for more details.

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- Nov 8, 2021 - Nov 12, 2021 [ELIXIR BioHackathon Europe](#)
- Nov 16, 2021 - Nov 17, 2021 [5. NRZ-Authent Expertinnen- und Expertenworkshop](#)
- Nov 18, 2021 [Galaxy Paper Cuts](#)
- Nov 25, 2021 [Galaxy Metabolomics Community Call](#)

History

buscar conjuntos de datos

Unnamed history

6 shown

61.61 MB

6: FastQC on data 2: RawData

5: FastQC on data 2: Webpage

4: FastQC on data 1: RawData

3: FastQC on data 1: Webpage

2: CA-CDPH-MC233585_6_R1.fastq.gz
31.0 MB
formato: fastqsanger.gz,
base de datos: ?
uploaded fastqsanger.gz file

4.2. Analysis

Galaxy Europe

Using 0%

Flujo de Trabajo Visualizar ▾ Datos Compartidos ▾ Ayuda ▾ Usuario ▾

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

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History

buscar conjuntos de datos

Unnamed history

6 shown

68.28 MB

6: FastQC on data 2: Ra wData

5: FastQC on data 2: We bpage

4: FastQC on data 1: Ra wData

3: FastQC on data 1: We bpage

2: CA-CDPH-MC233585 6_R1.fastq.gz

31.0 MB formato: fastqsanger.gz, base de datos: ? uploaded fastqsanger.gz file

@AA01401:19:H7YTVDXXY:2:2101:3360:1016 1:N:0

4.2. Analysis



Understanding the tool form and running any standard tool

Standard Tools and the Tool Form



Easily view your data through graphs and other methods.

Data Visualization Tools

4.2. Analysis

Galaxy Europe

- [Flujo de Trabajo](#)
- [Visualizar](#) (selected)
- [Datos Compartidos](#)
- [Ayuda](#)
- [Usuario](#)
-
-

Using 0%

Tools

fastqc x

Upload Data

Show Sections

Create a model to recommend tools
using deep learning

FastQC Read Quality reports

Combine FASTA and QUAL into FASTQ

fastp - fast all-in-one preprocessing for FASTQ files

Map with PerM for SOLiD and Illumina

Manipulate FASTQ reads on various attributes

Create a model to recommend tools
using deep learning

FLUJOS DE TRABAJO

All workflows

Execute

Create Visualization

Entornos Interactivos

Purpose

FastQC aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines. It provides a set of analyses which you can use to get a quick impression of whether your data has any problems of which you should be aware before doing any further analysis.

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History

buscar conjuntos de datos ? x

Unnamed history

2 shown

61.61 MB ?

2: CA-CDPH-MC2335856_R ?
1.fastq.gz
31.0 MB
formato: **fastqsanger.gz**, base de datos: ?
uploaded fastqsanger.gz file

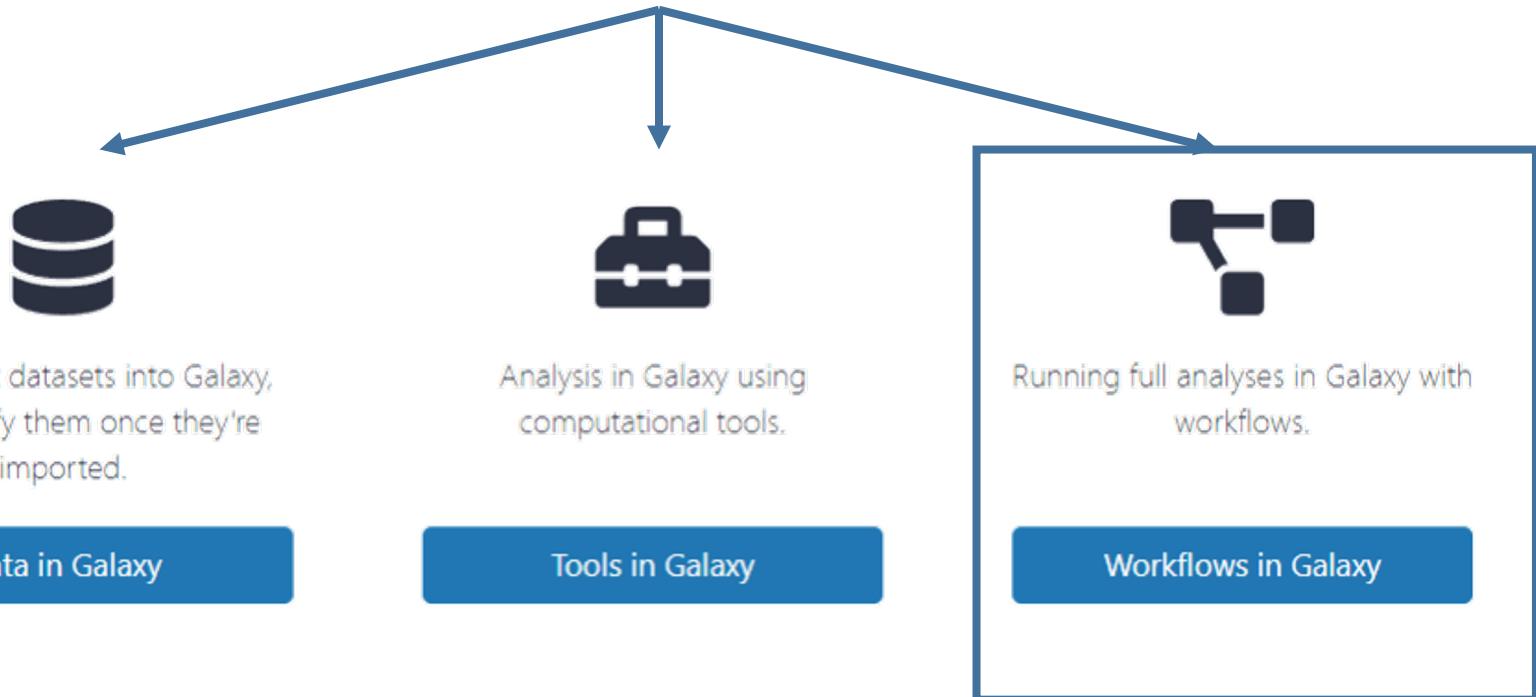
uploaded fastqsanger.gz file

2: CA-CDPH-MC2335856_R ?
1.fastq.gz
@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0:CC
NN
+ #####
@A01401:19:H7YTVDRXY:2:2101:6723:1016 1:N:0:CC
< >

4.2. Analysis

4. How to use Galaxy?

Galaxy





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4.3. Workflows



Generate Reproducible Workflows
from Your Analysis



Edit Workflows for New Data or
Analyses



Obtaining previously-run analyses
from yourself or others, and
recreating existing analyses.

Extract Workflows from
Analyses

Modify Workflows with the
Workflow Editor

Importing and Running
Workflows

4.3. Workflows

Galaxy Europe Using 0%

Flujo de Trabajo Visualizar ▾ Datos Compartidos ▾ Ayuda ▾ Usuario ▾  

Tools

search tools  

 Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

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Nov 18, 2021   [Galaxy Paper Cuts](#)

Nov 25, 2021   [Galaxy Metabolomics Community Call](#)

History

History Actions

Copy

Compartir o Publicar

Mostrar Estructura

Extraer Flujo de Trabajo

Set Permissions

Make Private

Reanudar Trabajos en Pausa

Acciones de Conjuntos de Datos

Copiar Conjuntos de Datos

Contraer Conjuntos de Datos Expandidos

Mostrar Conjuntos de Datos Ocultos

Eliminar Conjuntos de Datos Ocultos

Eliminar Definitivamente los Conjuntos de Datos Eliminados

Descargas

Exportar las Citas de la Herramienta

Exportar Historial a un Archivo

Beta Features

Use Beta History Panel

4.3. Workflows

The screenshot shows the Galaxy Europe web interface. The top navigation bar includes links for Home, Flujo de Trabajo (Workflow), Visualizar, Datos Compartidos, Ayuda, Usuario, and a gear icon for settings. A status bar at the top right indicates "Using 0%".

Tools sidebar:

- search tools
- Upload Data (button)

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Workflow name: Workflow constructed from history 'Unnamed history'

Create Workflow, **Check all**, **Uncheck all** buttons.

History panel:

buscar conjuntos de datos (? X)

Unnamed history

6 shown

68.28 MB

Details of history items:

- 6: FastQC on data 2: RawData
- 5: FastQC on data 2: Webpage
- 4: FastQC on data 1: RawData
- 3: FastQC on data 1: Webpage
- 2: CA-CDPH-MC2335855_R1.fastq.gz
- 1 CA-CDPH-MC2335856_R2.fastq.gz

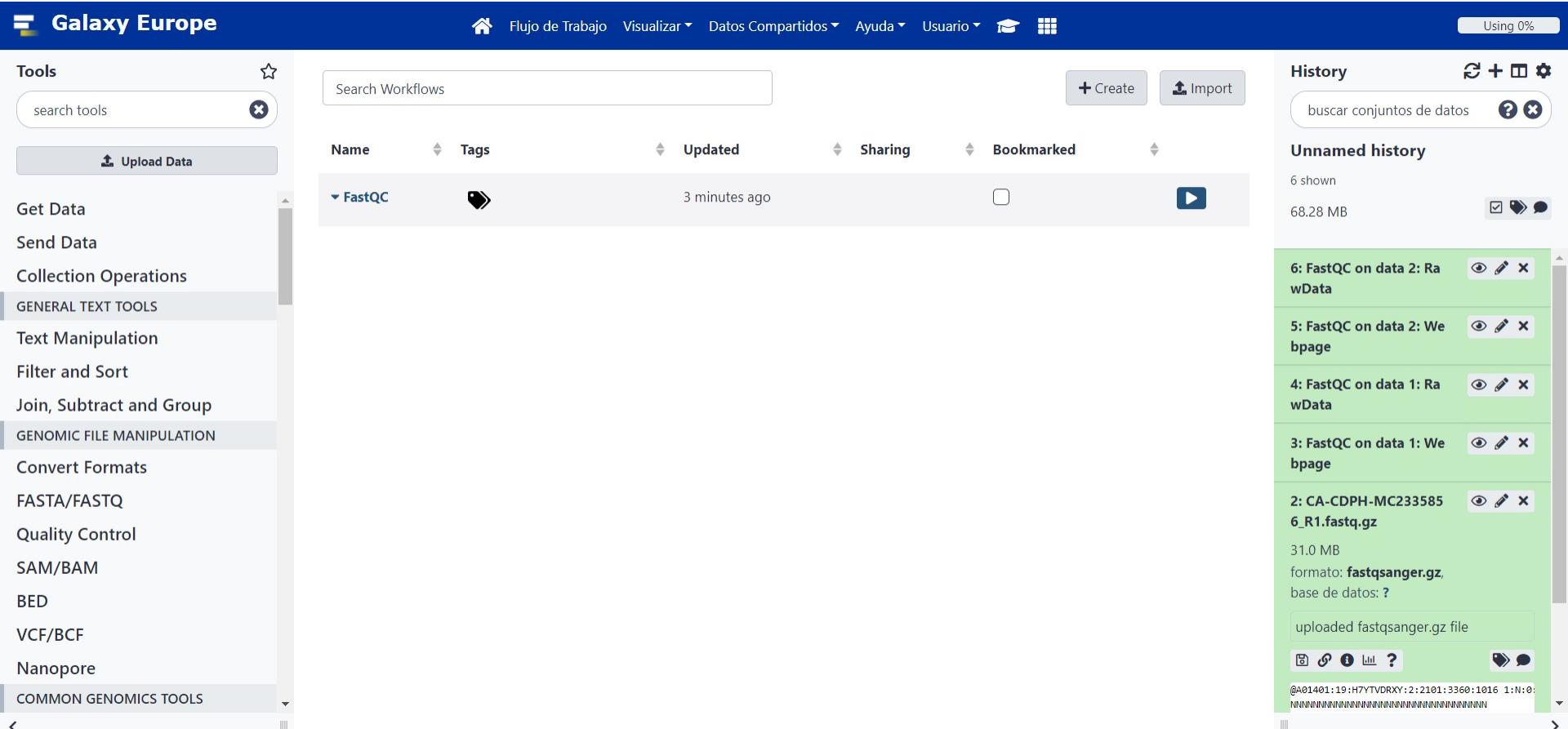
Tool configuration details:

- Upload File: This tool cannot be used in workflows
- FastQC: Include "FastQC" in workflow
- FastQC: Include "FastQC" in workflow

4.3. Workflows

The screenshot shows the Galaxy Europe web interface. At the top, there's a navigation bar with links for 'Flujo de Trabajo' (selected), 'Visualizar', 'Datos Compartidos', 'Ayuda', 'Usuario', and user profile icons. A status bar on the right indicates 'Using 0%'. The main area has a sidebar on the left titled 'Tools' with sections like 'Get Data', 'Send Data', 'Collection Operations', 'GENERAL TEXT TOOLS' (which is currently selected), 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'GENOMIC FILE MANIPULATION', 'Convert Formats', 'FASTA/FASTQ', 'Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', and 'COMMON GENOMICS TOOLS'. The central workspace displays a message: 'Workflow "FastQC" created from current history. You can [edit](#) or [run](#) the workflow.' To the right, a 'History' panel titled 'Unnamed history' shows six items: '6: FastQC on data 2: Ra wData', '5: FastQC on data 2: We bpage', '4: FastQC on data 1: Ra wData', '3: FastQC on data 1: We bpage', '2: CA-CDPH-MC233585 6_R1.fastq.gz', and an uploaded file 'fastqsanger.gz'. Each item has edit, run, and delete icons. Below the history is a preview of the fastqsanger.gz file content.

4.3. Workflows

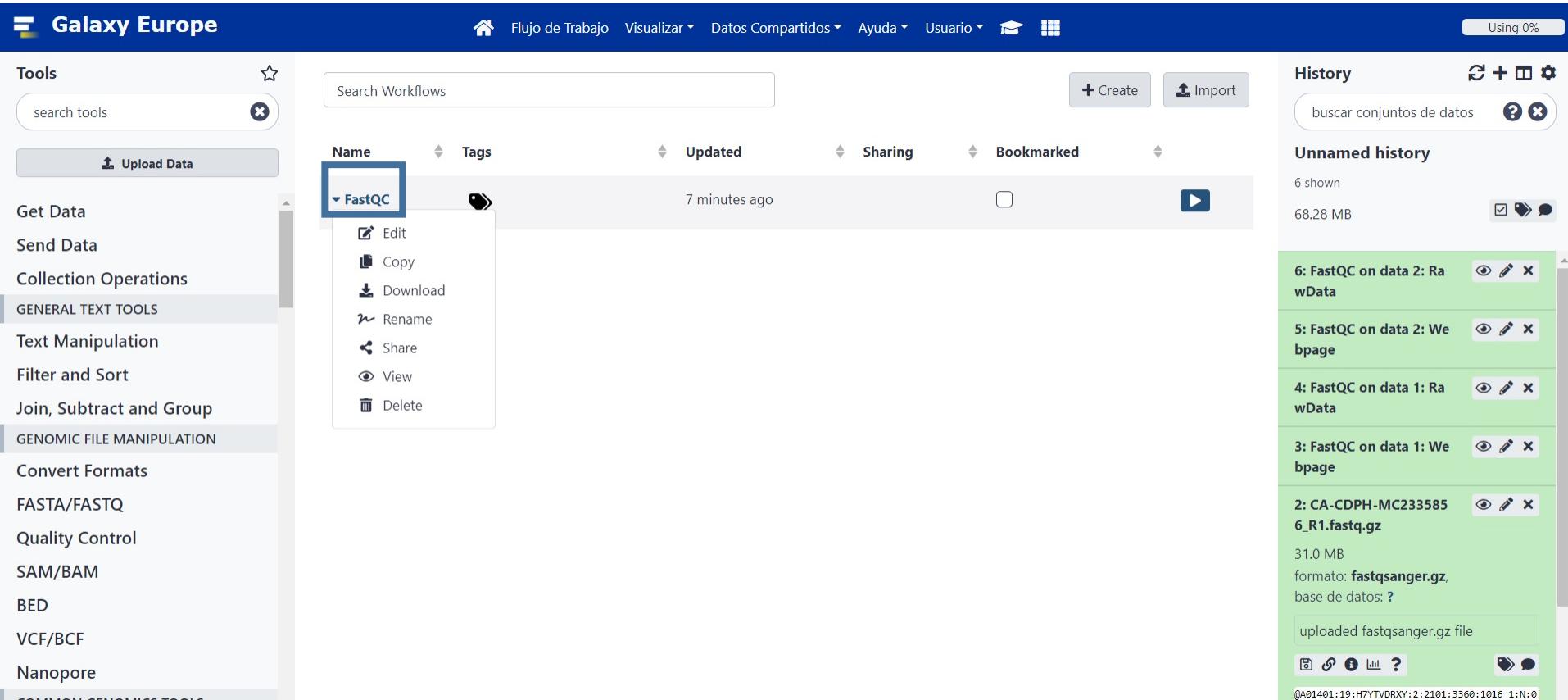


The screenshot shows the Galaxy Europe web interface. On the left, a sidebar lists various tool categories: Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS (which is currently selected), Text Manipulation, Filter and Sort, Join, Subtract and Group, GENOMIC FILE MANIPULATION, Convert Formats, FASTA/FASTQ, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, and COMMON GENOMICS TOOLS. The main workspace displays a workflow titled "FastQC" created 3 minutes ago. The history panel on the right shows a list of recent analyses, including:

- 6: FastQC on data 2: RawData
- 5: FastQC on data 2: Webpage
- 4: FastQC on data 1: RawData
- 3: FastQC on data 1: Webpage
- 2: CA-CDPH-MC233585_R1.fastq.gz

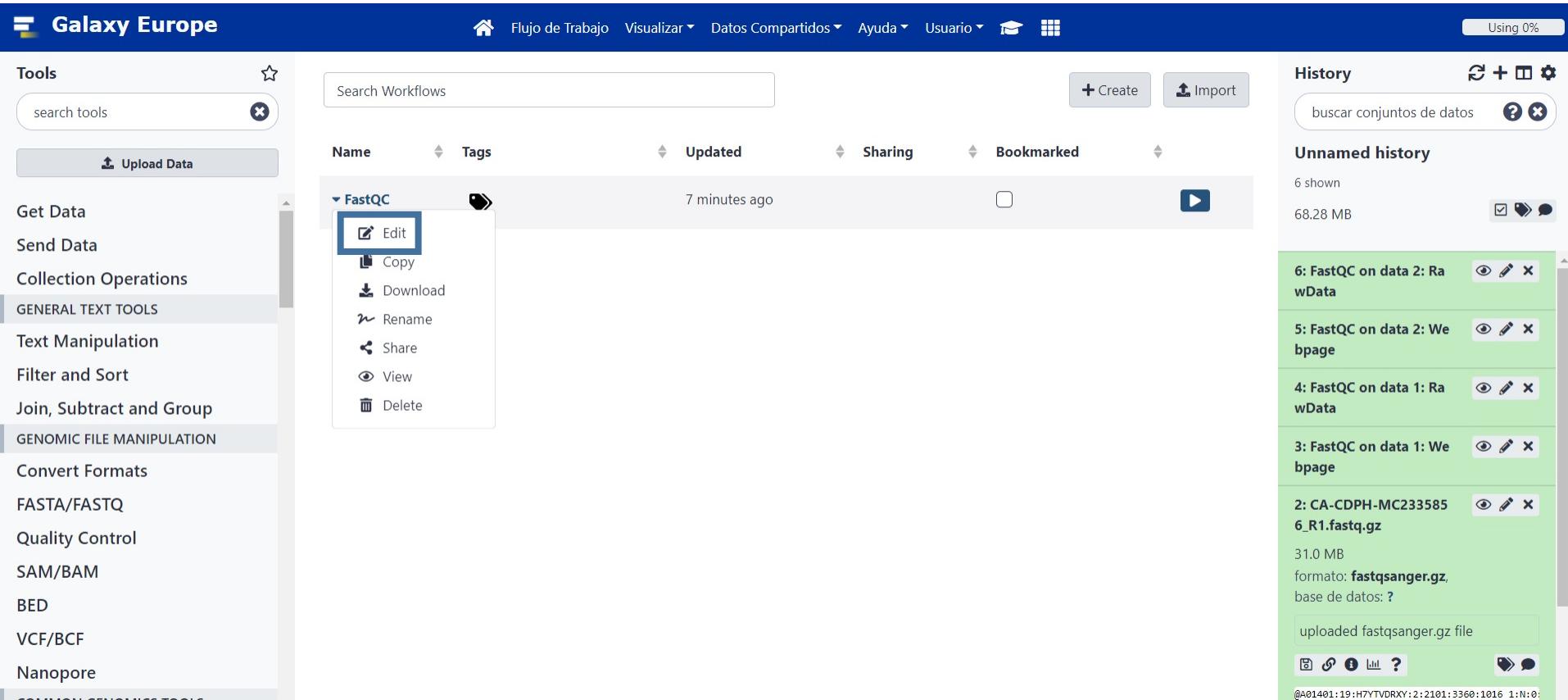
The history panel also includes a summary of the latest analysis: 31.0 MB, formato: fastqsanger.gz, base de datos: ?, uploaded fastqsanger.gz file.

4.3. Workflows



The screenshot shows the Galaxy Europe web interface. On the left, a sidebar lists various tool categories: Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS, Text Manipulation, Filter and Sort, Join, Subtract and Group, GENOMIC FILE MANIPULATION, Convert Formats, FASTA/FASTQ, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, and COMMON GENOMICS TOOLS. The 'GENERAL TEXT TOOLS' category is currently selected. In the main workspace, a workflow titled 'FastQC' is displayed. A context menu is open over this workflow, showing options: Edit, Copy, Download, Rename, Share, View, and Delete. The 'Edit' option is highlighted with a blue border. To the right of the workflow list is a 'History' panel titled 'Unnamed history'. It shows a list of six entries, each with a preview icon, edit/pencil icon, and delete/x icon. The entries are: 6: FastQC on data 2: Ra wData, 5: FastQC on data 2: We bpage, 4: FastQC on data 1: Ra wData, 3: FastQC on data 1: We bpage, 2: CA-CDPH-MC233585 6_R1.fastq.gz, and an uploaded fastqsanger.gz file. The bottom of the history panel shows a message: 'formato: fastqsanger.gz, base de datos: ?' and the identifier '@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0'.

4.3. Workflows



The screenshot shows the Galaxy Europe web interface. The top navigation bar includes links for 'Flujo de Trabajo', 'Visualizar', 'Datos Compartidos', 'Ayuda', 'Usuario', and a user icon. A blue header bar spans across the top. On the left, a sidebar lists various tool categories: 'Tools', 'Get Data', 'Send Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'GENOMIC FILE MANIPULATION', 'Convert Formats', 'FASTA/FASTQ', 'Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', and 'COMMON GENOMICS TOOLS'. The 'GENERAL TEXT TOOLS' category is currently selected. The main workspace displays a table of workflows. One workflow, 'FastQC', is highlighted and has a context menu open with options: 'Edit' (selected), 'Copy', 'Download', 'Rename', 'Share', 'View', and 'Delete'. The table columns are 'Name', 'Tags', 'Updated', 'Sharing', and 'Bookmarked'. The 'Updated' column shows '7 minutes ago'. To the right, the 'History' panel shows an 'Unnamed history' section with 6 items, each with a preview, edit, and delete icon. The first item is '6: FastQC on data 2: Ra wData'. At the bottom, there is a message about an uploaded file: 'uploaded fastqsanger.gz file'.

4.3. Workflows

Galaxy Europe

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario Using 0%

Tools

search tools

Inputs

Get Data

Send Data

Collection Operations

Expression Tools

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

FastQC

Raw read data from your current history

Contaminant list

FastQC

Raw read data from your current history

Contaminant list

Adapter list

Submodule and Limit specifying file

FastQC on input dataset(s): Webpage (html)

FastQC on input dataset(s): RawData (txt)

Name: FastQC

Version: 1: Nov 11th 2021, 2 steps

Annotation:

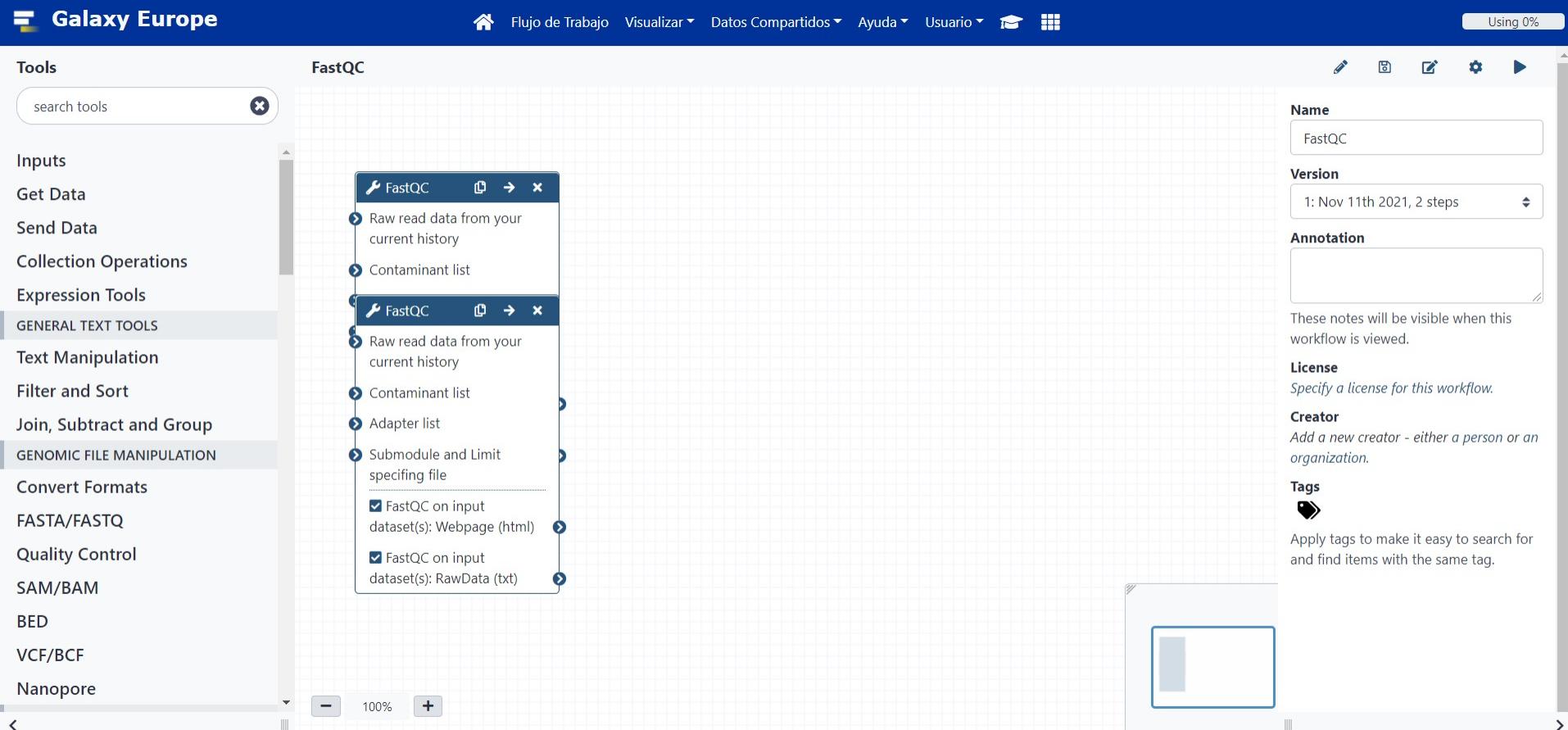
These notes will be visible when this workflow is viewed.

License: Specify a license for this workflow.

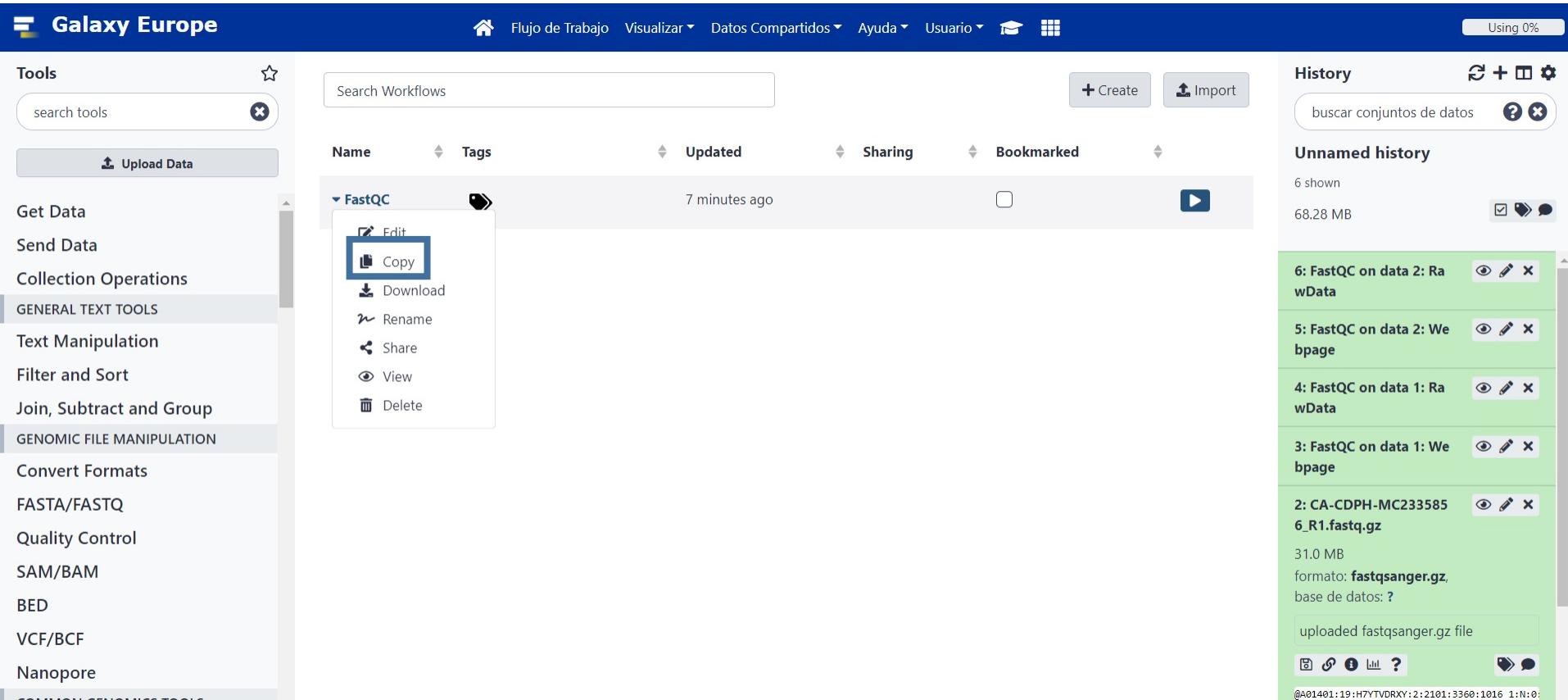
Creator: Add a new creator - either a person or an organization.

Tags:

Apply tags to make it easy to search for and find items with the same tag.



4.3. Workflows



The screenshot shows the Galaxy Europe interface. On the left, a sidebar lists various tool categories: Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS, Text Manipulation, Filter and Sort, Join, Subtract and Group, GENOMIC FILE MANIPULATION, Convert Formats, FASTA/FASTQ, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, and COMMON GENOMICS TOOLS. In the center, a main panel displays a workflow named "FastQC". A context menu is open over the workflow, showing options: Edit (highlighted), Copy, Download, Rename, Share, View, and Delete. Above the workflow list is a search bar labeled "Search Workflows" and buttons for "+ Create" and "Import". To the right, a "History" panel titled "Unnamed history" shows a list of previous runs, each with a preview icon, edit/pencil icon, and delete/x icon. The first run listed is "6: FastQC on data 2: Ra wData". At the bottom of the history panel, there is a message about an uploaded file: "uploaded fastqsanger.gz file" and a timestamp: "@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0".

4.3. Workflows

The screenshot shows the Galaxy Europe web interface. The top navigation bar includes links for Home, Flujo de Trabajo, Visualizar, Datos Compartidos, Ayuda, Usuario, and a user icon. A progress bar at the top right indicates "Using 0%".

The left sidebar contains a "Tools" section with a search bar and a "Upload Data" button. Below this are sections for "Get Data", "Send Data", "Collection Operations", and various tool categories under "GENERAL TEXT TOOLS" and "GENOMIC FILE MANIPULATION".

The main content area displays a success message: "Successfully copied workflow 'FastQC' to 'Copy of FastQC'." It features a search bar for "Search Workflows" and buttons for "+ Create" and "Import". A table lists two workflows:

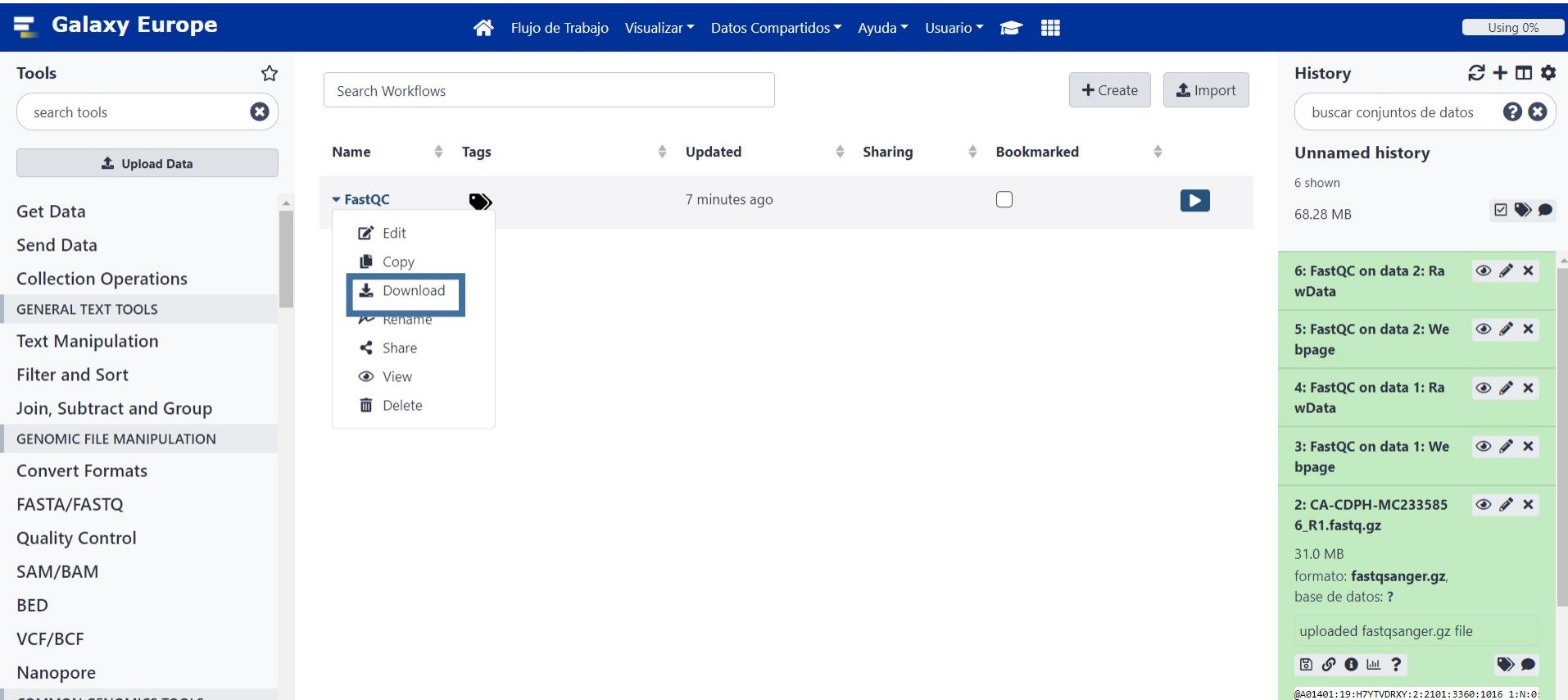
Name	Tags	Updated	Sharing	Bookmarked
Copy of FastQC	🔗	in a few seconds	<input type="checkbox"/>	▶
FastQC	🔗	3 minutes ago	<input type="checkbox"/>	▶

The right sidebar shows a "History" section titled "Unnamed history" with 6 items. Each item has a preview, edit, and delete icon. The items are:

- 6: FastQC on data 2: RawData
- 5: FastQC on data 2: Webpage
- 4: FastQC on data 1: RawData
- 3: FastQC on data 1: Webpage
- 2: CA-CDPH-MC233585_6_R1.fastq.gz
- 31.0 MB formato: fastqsanger.gz, base de datos: ? uploaded fastqsanger.gz file

At the bottom, there is a footer with a timestamp: "@01491:19:H7YTVDRXY:2:2101:3360:1016 1:N:0".

4.3. Workflows



Galaxy Europe

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario + Import

Using 0%

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Name Tags Updated Sharing Bookmarked

FastQC

7 minutes ago

Edit Copy Download Rename Share View Delete

History

buscar conjuntos de datos

Unnamed history

6 shown

68.28 MB

6: FastQC on data 2: Ra wData

5: FastQC on data 2: We bpage

4: FastQC on data 1: Ra wData

3: FastQC on data 1: We bpage

2: CA-CDPH-MC233585 6_R1.fastq.gz

uploaded fastqsanger.gz file

@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0

4.3. Workflows

Galaxy Europe Using 0%

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Name Tags Updated Sharing Bookmarked

FastQC

7 minutes ago

Edit Copy Download Rename Share View

Nombre: Galaxy-Workflow-FastQC.ga

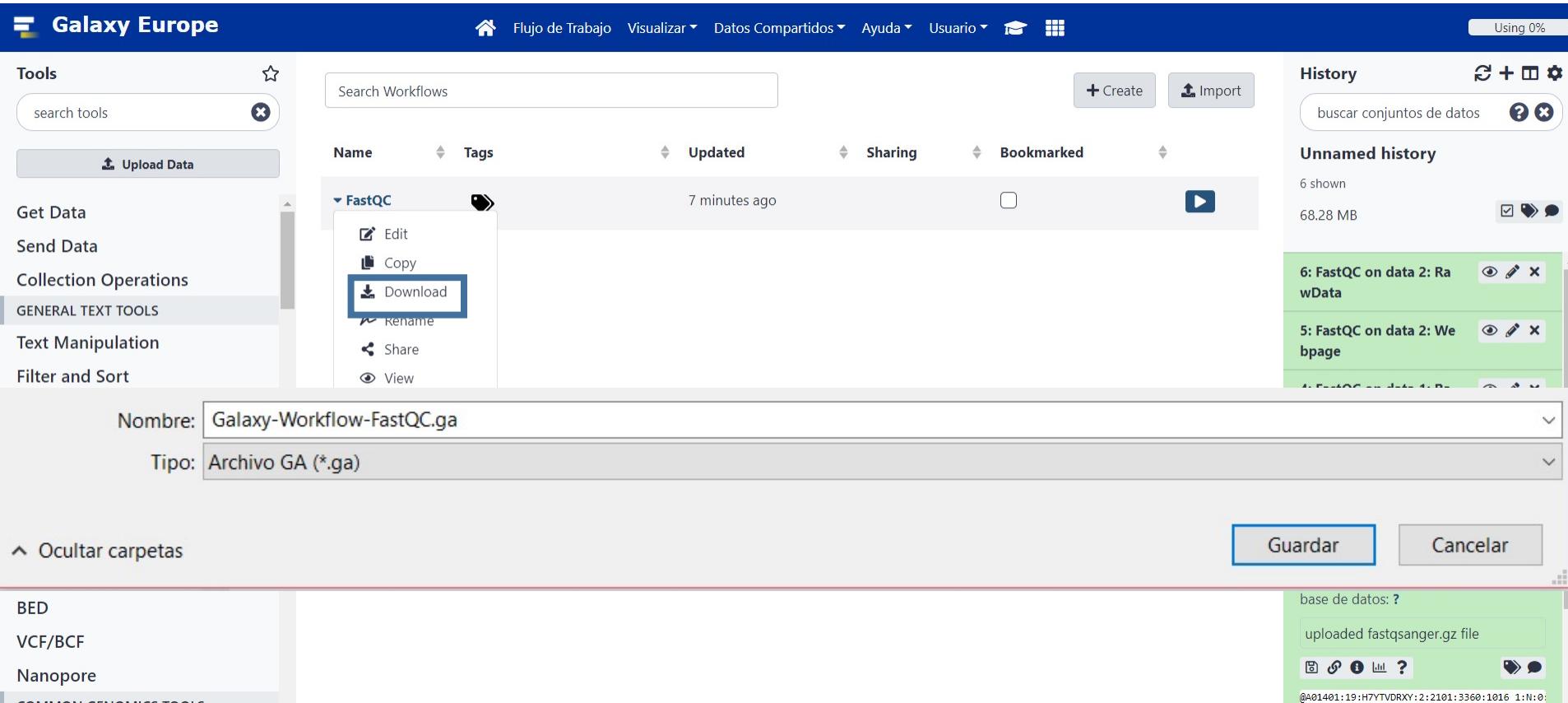
Tipo: Archivo GA (*.ga)

Ocultar carpetas

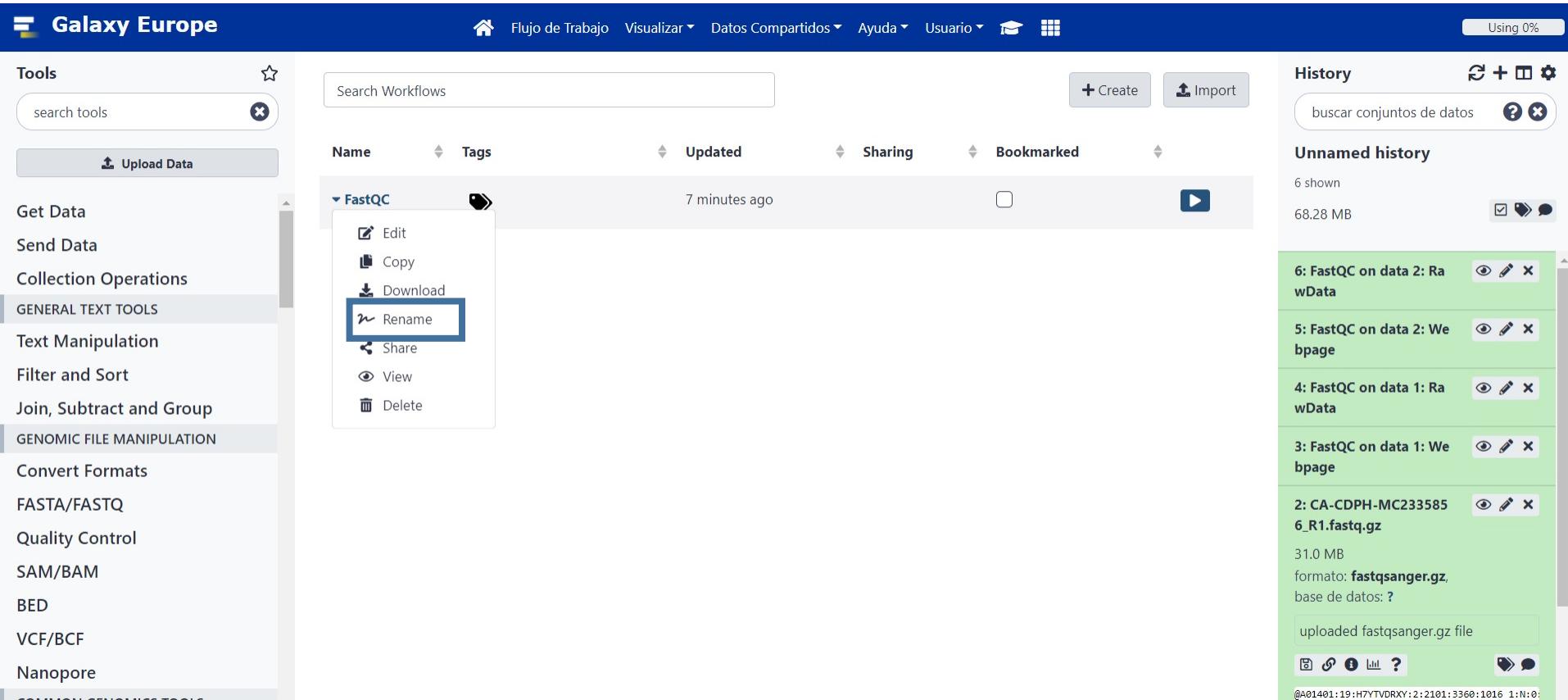
Guarda Cancelar

base de datos: ? uploaded fastqsanger.gz file

@A01401:19:H7YTVDRXY:2:2101:3360:1016 1:N:0



4.3. Workflows



The screenshot shows the Galaxy Europe interface. On the left, a sidebar lists various tool categories: Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS, Text Manipulation, Filter and Sort, Join, Subtract and Group, GENOMIC FILE MANIPULATION, Convert Formats, FASTA/FASTQ, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, and COMMON GENOMICS TOOLS. The 'GENERAL TEXT TOOLS' category is currently selected. In the main workspace, a workflow named 'FastQC' is displayed. A context menu is open over this workflow, showing options: Edit, Copy, Download, Rename (which is highlighted with a blue border), Share, View, and Delete. To the right of the workflow, there is a 'History' panel titled 'Unnamed history' which lists several previous runs of the 'FastQC' tool. The top navigation bar includes links for Flujo de Trabajo, Visualizar, Datos Compartidos, Ayuda, Usuario, and a sign-in icon.

Galaxy Europe

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario

Using 0%

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Search Workflows

+ Create Import

Name Tags Updated Sharing Bookmarked

FastQC

7 minutes ago

Edit Copy Download Rename Share View Delete

History

buscar conjuntos de datos

Unnamed history

6 shown

68.28 MB

6: FastQC on data 2: Ra wData

5: FastQC on data 2: We bpage

4: FastQC on data 1: Ra wData

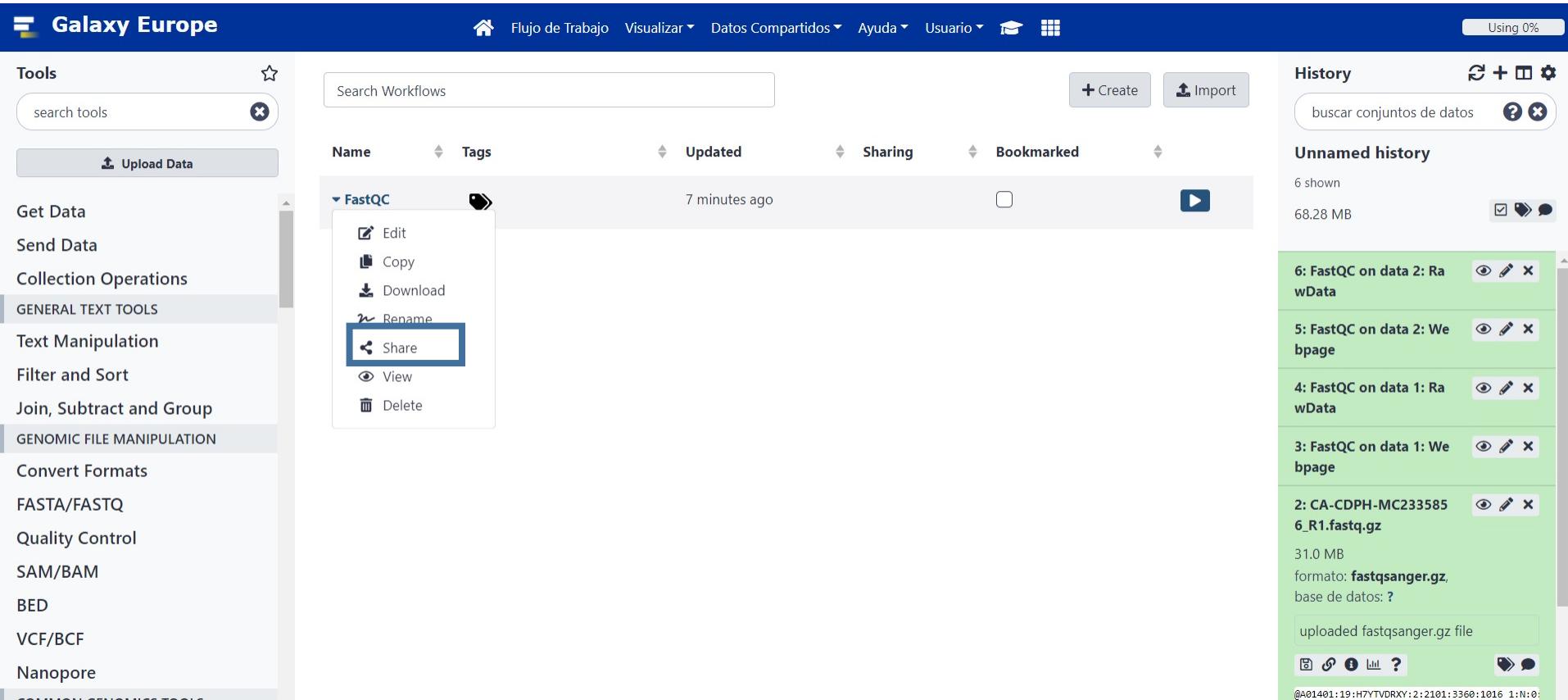
3: FastQC on data 1: We bpage

2: CA-CDPH-MC233585 6_R1.fastq.gz

uploaded fastqsanger.gz file

@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0

4.3. Workflows



The screenshot shows the Galaxy Europe interface. On the left, a sidebar lists various tool categories: Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS, Text Manipulation, Filter and Sort, Join, Subtract and Group, GENOMIC FILE MANIPULATION, Convert Formats, FASTA/FASTQ, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, and COMMON GENOMICS TOOLS. In the center, a workflow titled "FastQC" is displayed. A context menu for this workflow is open, with the "Share" option highlighted. The main workspace shows a search bar for workflows and buttons for "+ Create" and "Import". On the right, the "History" panel is visible, showing an "Unnamed history" section with a list of previous runs, their descriptions, and edit/delete icons.

Galaxy Europe

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario + Import

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Search Workflows

+ Create Import

Name Tags Updated Sharing Bookmarked

FastQC

7 minutes ago

Edit Copy Download Rename Share View Delete

History

buscar conjuntos de datos

Unnamed history

6 shown

68.28 MB

6: FastQC on data 2: Ra wData

5: FastQC on data 2: We bpage

4: FastQC on data 1: Ra wData

3: FastQC on data 1: We bpage

2: CA-CDPH-MC233585 6_R1.fastq.gz

uploaded fastqsanger.gz file

@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0

4.3. Workflows

Galaxy Europe Flujo de Trabajo Visualizar ▾ Datos Compartidos ▾ Ayuda ▾ Usuario ▾   Using 0%

[Go back to Workflows List](#)

Workflow 'FastQC'

Share

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

[Make Workflow Accessible via Link](#)

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

[Make Workflow Accessible and Publish](#)

Makes the workflow accessible via link (see above) and publishes the workflow to Galaxy's Published Workflows section, where it is publicly listed and searchable.

You have not shared this workflow with any users yet.

[Share with a user](#)

Export

[Download](#) workflow as a file so that it can be saved or imported into another Galaxy server.

This workflow must be accessible. Please use the option above to "Make Workflow Accessible and Publish" before receiving a URL for importing to another Galaxy.

[Create image](#) of workflow in SVG format

Export to the [www.myexperiment.org](#) site.

myExperiment username:



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de Salud
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4.3. Workflows

Galaxy Europe Using 0%

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Search Workflows

+ Create Import

Name	Tags	Updated	Sharing	Bookmarked
FastQC		7 minutes ago		

FastQC

- Edit
- Copy
- Download
- Rename
- Share
- View
- Delete

History

buscar conjuntos de datos

Unnamed history

6 shown

68.28 MB

6: FastQC on data 2: Ra wData

5: FastQC on data 2: We bpage

4: FastQC on data 1: Ra wData

3: FastQC on data 1: We bpage

2: CA-CDPH-MC233585 6_R1.fastq.gz

uploaded fastqsanger.gz file

@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0

4.3. Workflows

Galaxy Europe Using 0%

FastQC

Step	Annotation
Step 1: FastQC	<p>Raw read data from your current history <i>select at runtime</i></p> <p>Contaminant list <i>select at runtime</i></p> <p>Adapter list <i>select at runtime</i></p> <p>Submodule and Limit specifying file <i>select at runtime</i></p> <p>Disable grouping of bases for reads >50bp False</p> <p>Lower limit on the length of the sequence to be shown in the report Not available.</p> <p>Length of Kmer to look for 7</p>
Step 2: FastQC	<p>Raw read data from your current history</p>

About this Workflow

Author
svarona 

Related Workflows
All published workflows
Published workflows by svarona

Rating
Community 
(0 ratings, 0.0 average)

Tags
Yours: 
Community: none

Yours: 

4.3. Workflows

Galaxy Europe Using 0%

Tools

search tools

Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMIC FILE MANIPULATION

Convert Formats

FASTA/FASTQ

Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

COMMON GENOMICS TOOLS

Flujo de Trabajo Visualizar Datos Compartidos Ayuda Usuario + Import

Search Workflows

+ Create

Name Tags Updated Sharing Bookmarked

Copy of FastQC Edit Copy Download Rename Share View Delete

6 minutes ago

8 minutes ago

History

buscar conjuntos de datos

Unnamed history

6 shown

68.28 MB

6: FastQC on data 2: RawData

5: FastQC on data 2: Webpage

4: FastQC on data 1: RawData

3: FastQC on data 1: Webpage

2: CA-CDPH-MC233585_6_R1.fastq.gz

uploaded fastqsanger.gz file

@A01401:19:H7YTVDRX:2:2101:3360:1016 1:N:0

22/11/2021

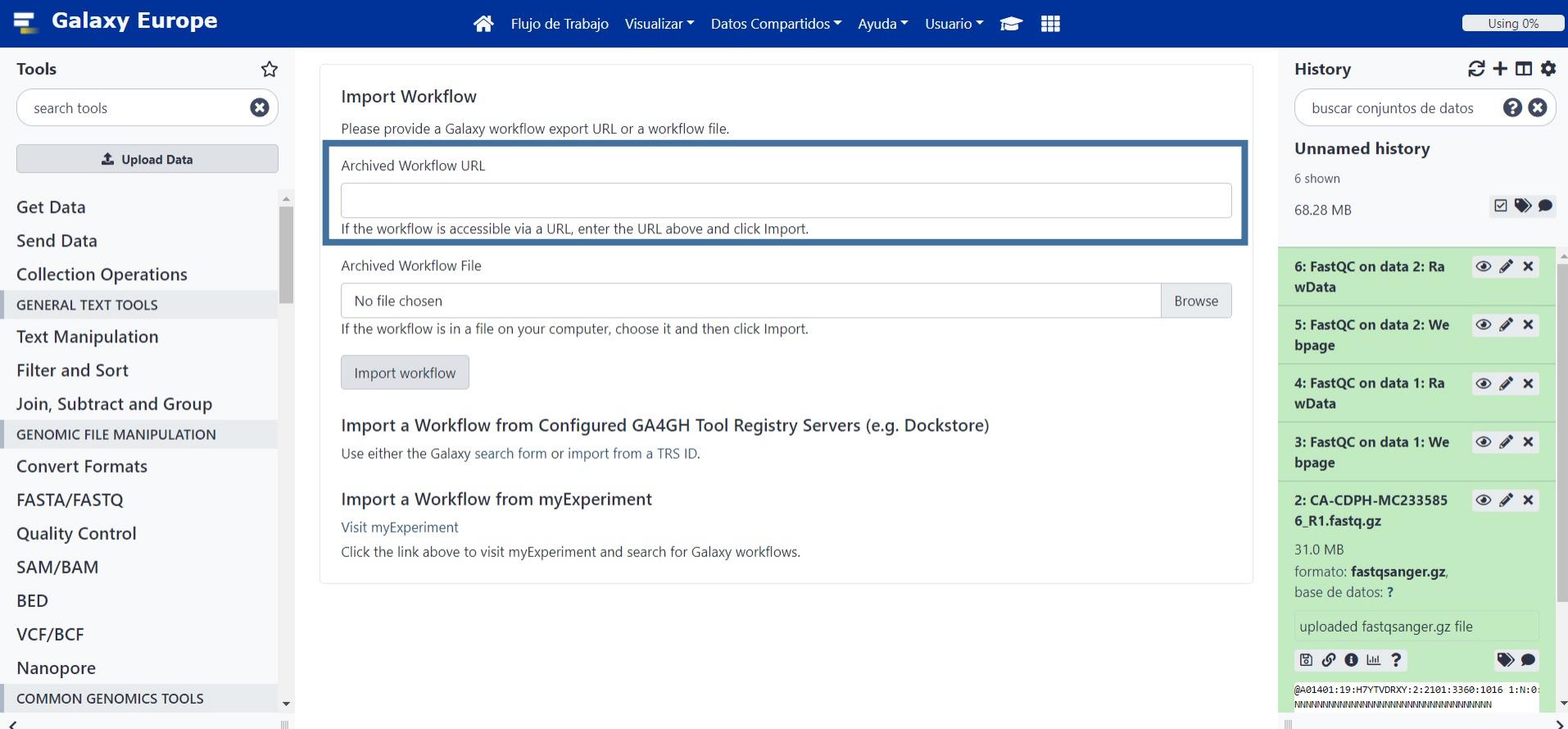
Análisis de Genomas Virales a través de la plataforma Galaxy

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4.3. Workflows

The screenshot shows the Galaxy Europe web interface. On the left, there's a sidebar with 'Tools' and 'History' sections. The 'Tools' section includes a search bar ('search tools'), an 'Upload Data' button, and a list of categories: 'Get Data', 'Send Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'GENOMIC FILE MANIPULATION', 'Convert Formats', 'FASTA/FASTQ', 'Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', and 'COMMON GENOMICS TOOLS'. The 'GENERAL TEXT TOOLS' category is currently selected. The 'History' section on the right shows an 'Unnamed history' with one entry: '6: FastQC on data 2: Ra wData'. The main area displays a workflow titled 'FastQC' with a status of '3 minutes ago'. At the top, there are buttons for '+ Create' and 'Import', with 'Import' being highlighted by a blue box. A search bar at the top says 'Search Workflows'.

4.3. Workflows



The screenshot shows the Galaxy Europe web interface. On the left, a sidebar lists various genomic tools categorized under 'GENERAL TEXT TOOLS' (Collection Operations, Text Manipulation, Filter and Sort, Join, Subtract and Group), 'GENOMIC FILE MANIPULATION' (Convert Formats, FASTA/FASTQ, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore), and 'COMMON GENOMICS TOOLS'. The main content area is titled 'Import Workflow' and instructs users to provide a Galaxy workflow export URL or a workflow file. It includes fields for 'Archived Workflow URL' (with a placeholder for a URL) and 'Archived Workflow File' (with a 'Browse' button). Below these are sections for importing from 'Configured GA4GH Tool Registry Servers' (Dockstore) and 'myExperiment'. On the right, a 'History' panel shows a list of recent workflows: '6: FastQC on data 2: Ra wData', '5: FastQC on data 2: We bpage', '4: FastQC on data 1: Ra wData', '3: FastQC on data 1: We bpage', '2: CA-CDPH-MC233585 6_R1.fastq.gz', and a newly uploaded 'fastqsanger.gz' file.

4.3. Workflows



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¿Questions?