

# Customizable Welcome and Introduction Page for New Galaxy Users

Alex Ostrovsky

# Current user initial experience

The screenshot displays the Galaxy web interface. At the top, a dark navigation bar contains the Galaxy logo, menu items (Analyze Data, Workflow, Visualize, Shared Data, Help, User), and a 'Using 0%' indicator. Below this is an orange warning banner: 'Your account has not been activated yet. Feel free to browse around and see what's available, but you won't be able to upload data or run jobs until you have verified your email address. Resend verification'. The main content area is divided into three sections. On the left is a 'Tools' sidebar with a search bar and a list of tool categories including 'Get Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'Datamash', 'GENOMIC FILE MANIPULATION', 'FASTA/FASTQ', 'FASTQ Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', 'Convert Formats', 'Lift-Over', 'COMMON GENOMICS TOOLS', 'Interactive tools', 'Operate on Genomic Intervals', 'Fetch Sequences/Alignments', 'GENOMICS ANALYSIS', and 'Assemblv'. The central section features a heading 'Galaxy is an open source, web-based platform for data intensive biomedical research...' followed by a portrait of James Taylor and a text block about a community video project. A 'How To Contribute' button is positioned below the text. A blue information banner at the bottom of the central section reads: 'Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the Galaxy SARS-CoV-2 portal at covid19.galaxyproject.org'. The right sidebar contains a 'History' section with a search bar and an 'Unnamed history' section that is currently empty. A blue information banner at the bottom of the right sidebar states: 'This history is empty. You can load your own data or get data from an external source'. At the bottom of the page, logos for PennState, Johns Hopkins University, Oregon Health & Science University, TACC, and CyVerse are displayed, along with text describing the Galaxy Team's affiliation and the infrastructure provided by CyVerse and the National Science Foundation.

**Galaxy** Analyze Data Workflow Visualize Shared Data Help User Using 0%

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**Tools** ☆

search tools ✕

Upload Data

Get Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Datamash

GENOMIC FILE MANIPULATION

FASTA/FASTQ

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**We are looking for contributions before April 30.**

[How To Contribute](#)

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**History** ↻ + ☰ ⚙

search datasets ? ✕

**Unnamed history**

(empty)

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**PennState** **JOHNS HOPKINS UNIVERSITY** **OREGON HEALTH & SCIENCE UNIVERSITY** **TACC** **CYVERSE**

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search tools

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## Get Data

## Collection Operations

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## Filter and Sort

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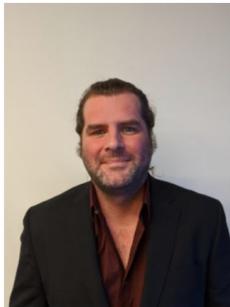
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# Priorities for new users

- Provide optional tutorial on how to use each part
- Differentiate specific server's capabilities/uses
- In-depth enough to get going, but not enough to get bored
  - More in-depth walkthroughs should go to Training
- Easily modifiable to update alongside new releases

# New User Welcome view: Topics

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes the Galaxy logo, a search bar for tools, and a menu with options: Analyze Data, Workflow, Visualize, Shared Data, Admin, Help, User, and a grid icon. The user's storage usage is shown as 'Using 8.6 MB'.

The main content area is titled 'Welcome to Galaxy' and contains the following text: 'Galaxy is web-based platform for reproducible computational analysis. Research in Galaxy is supported by 3 pillars: data, tools, and workflows. For an introduction to each, visit the below pages, or begin your analysis by setting a tool from the toolbar to the left.'

Below this text is the section 'Get to Know Galaxy', which features three topic cards:

- Data in Galaxy:** Represented by a database icon. Description: 'How to get datasets into Galaxy, and modify them once they're imported.' Includes a 'Learn more' button.
- Tools in Galaxy:** Represented by a briefcase icon. Description: 'Analysis in Galaxy using computational tools.' Includes a 'Learn more' button.
- Workflows in Galaxy:** Represented by a workflow diagram icon. Description: 'Running full analyses in Galaxy with workflows.' Includes a 'Learn more' button.

The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button. Below this is a list of categories: Get Data, Send Data, Collection Operations, Lift-Over, Text Manipulation, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, Operate on Genomic Intervals, Statistics, Graph/Display Data, Phenotype Association, and Interactive tools. The 'Interactive tools' section lists several tools with brief descriptions, including Samtools, Bowtie2, Filter BAM datasets, Filter FASTQ reads, and FastQC.

The right sidebar shows a 'History' section with a search bar and a message: 'Unnamed history (empty)'. A blue information box states: 'This history is empty. You can load your own data or get data from an external source'.

# New User Welcome view: Subtopics

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes the Galaxy logo, a search bar, and menu items: Analyze Data, Workflow, Visualize, Shared Data, Admin, Help, User, and a grid icon. The user's storage usage is shown as 'Using 8.6 MB'.

The left sidebar contains a 'Tools' section with a search bar and an 'Upload Data' button. Below this is a list of tool categories: Get Data, Send Data, Collection Operations, Lift-Over, Text Manipulation, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, Operate on Genomic Intervals, Statistics, Graph/Display Data, Phenotype Association, Interactive tools, and testing. Under 'testing', several tools are listed: Samtools fastx extract FASTA or FASTQ from alignment files, Bowtie2 - map reads against reference genome, Filter BAM datasets on a variety of attributes, Filter FASTQ reads by quality score and length, and FastQC Read Quality reports.

The main content area is titled 'Data in Galaxy' and features an introductory paragraph: 'Obtaining data in Galaxy is simple. You may upload from your machine, retrieve from a url, via ftp, or from any of several linked databases. Further, you may use shard data by accessing our 'shared data libraries' and 'shared histories'.' Below this are four subtopics, each with an icon, a description, and a 'Learn more' button:

- Importing via Data Uploader:** Represented by an upward arrow icon. Description: 'Loading in data from your machine or via URL.'
- Retrieving Data from Public Databases:** Represented by a cloud with a downward arrow icon. Description: 'Use data from major sources such as UCSC, SRA, or EMBL.'
- Obtaining Shared Data:** Represented by an icon of two people holding a screen. Description: 'Find and retrieve data shared between Galaxy users.'
- Data and Metadata in Galaxy:** Represented by an information 'i' icon. Description: 'Observing and modifying your data.'

A 'Return' button is located below the subtopics.

The right sidebar shows the 'History' section with a search bar and a notification: 'This history is empty. You can load your own data or get data from an external source'.

# New User Welcome view: Slides

The screenshot displays the Galaxy Data Uploader interface. At the top, the Galaxy logo and navigation menu are visible, including options like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Admin', 'Help', 'User', and a 'Using 8.6 MB' indicator. The main content area is titled 'Galaxy Data Uploader' and features a central text box with the message: 'Alternatively, the rule-based uploader can be used to upload many files at once, or data from a tabular file.' Below this, there are two tabs: 'Regular' and 'Rule-based', with the latter being selected. Under the 'Rule-based' tab, the text reads 'Tabular source data to extract collection files and metadata from'. There are two main sections for data input: 'Upload data as' with a 'Datasets' dropdown, and 'Load tabular data from' with a 'Pasted Table' dropdown. A large empty text area is provided for pasting data. At the bottom of this section are 'Reset', 'Build', and 'Close' buttons. On the left side, there is a 'Tools' sidebar with a search bar and a list of tool categories such as 'Get Data', 'Send Data', 'Collection Operations', 'Text Manipulation', etc. On the right side, there is a 'History' sidebar with a search bar and a message: 'This history is empty. You can load your own data or get data from an external source'.

# Default Welcome Includes:

- Data
  - Upload
  - Remote retrieval
  - Sharing
  - Modification
- Tools
  - Standard tool form
  - Visualizations
- Workflows
  - Extract
  - Import
  - Share

# How to customize

- New variable in galaxy.yml: `welcome_directory`
- Create new subdirectory in the static folder
- File “topics.json” used as prop for  
`client/src/components/NewUserWelcome/newUserWelcome.vue`
- Image files in subdirectories specified in the json file
- Can very easily clone and modify npm source repo as base for custom welcome

## Roadblocks:

- Dynamic imports
  - Webpack 5 required (<https://github.com/galaxyproject/galaxy/pull/11710>)

## Timeframe

- Deployable before GCC

## Request:

- Suggestions for additional standard content?

Questions/Comments?