

次世代シーケンサーデータの解析手法 第12回Galaxy: ヒストリーとワークフロー ウェブ資料

寺田朋子、大田達郎*、清水謙多郎、門田 幸二*

W1: ウェブブラウザに注意

①Internet Explorer (IE)でGalaxyを実行すると不具合に遭遇しやすいので注意が必要。推奨ウェブブラウザは、②ChromeまたはFirefox

https://biostar.usegalaxy.org/p/10665/

Best Browser for Galaxy?

View Posts Home Log In

Question: Best Browser for Galaxy?

dritter • 0 wrote:

What is the best browser to use for Galaxy?

I have a classroom of students, and Galaxy always has issues on Internet Explorer (does not render the eyeball to view data). Sometimes it has issues on Firefox too (after click the eyeball to view data, the data is not displayed at all).

It would be nice to know a browser (and version if needed) that is very well tested for galaxy, so I could have all students on that browser and version, and stop spending time fixing individual issues for students to use galaxy!

Thank you,

Deb

browser • 463 views

ADD COMMENT • link • Not following • modified 2.9 years ago by Martin Čech ♦♦ 4.3k • written 2.9 years ago by dritter • 0

Martin Čech ♦♦ 4.3k wrote:

Short answer: I would recommend latest Chrome and Firefox.

There are not many Galaxy developers that use IE so some glitches may be present. However if some icon is not visible at all that is an unexpected bug and we will fix it. I will look into the IE bug later today.

I was not able to reproduce the bug you reported for Firefox, can you give me some more details please? On what system and version of FF, and what were you doing would be a good start.

Traffic: 68 users visited in the last hour

W1: ウェブブラウザに注意

というわけで、今回はウェブブラウザChromeを用いて説明します

The screenshot shows a web browser window with the following content:

- Browser tab: Best Browser for Galaxy? x
- Address bar: Secure | https://biostar.usegalaxy.org/p/10665/
- Navigation buttons: View Posts, Home, Log In
- Question title: Question: Best Browser for Galaxy?
- Author: dritter • 0 wrote:
- Text: What is the best browser to use for Galaxy?
- Text: I have a classroom of students, and Galaxy always has issues on Internet Explorer (does not render the eyeball to view data). Sometimes it has issues on Firefox too (after click the eyeball to view data, the data is not displayed at all).
- Text: It would be nice to know a browser (and version if needed) that is very well tested for galaxy, so I could have all students on that browser and version, and stop spending time fixing individual issues for students to use galaxy!
- Text: Thank you,
- Text: Deb
- Tags: browser • 463 views
- Buttons: ADD COMMENT, link, Not following
- Metadata: modified 2.9 years ago by Martin Čech ♦♦ 4.3k • written 2.9 years ago by dritter • 0
- Answer author: Martin Čech ♦♦ 4.3k wrote:
- Text: Short answer: I would recommend latest Chrome and Firefox.
- Text: There are not many Galaxy developers that use IE so some glitches may be present. However if some icon is not visible at all that is an unexpected bug and we will fix it. I will look into the IE bug later today.
- Text: I was not able to reproduce the bug you reported for Firefox, can you give me some more details please? On what system and version of FF, and what were you doing would be a good start.
- Footer: Traffic: 68 users visited in the last hour

①の見栄えが少し異なるが、第11回W13-4と同じ状態

W2: 前回の最後と同じ状態

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start [here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." Below this is a "Try Galaxy on the Cloud" banner with the text "Now you can have a personal Galaxy within the infinite Universe".

The left sidebar contains a "Tools" section with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, and NGS: RNA Structure.

The right sidebar shows the "History" section with a search bar and a list of datasets. A red box highlights the following items:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

A red arrow with the number 1 points to the top of the red box.

W2: 前回の最後と同じ状態

① Galaxyにユーザ登録済みの今回のメインユーザ(kadota_registered)がログイン中であることがわかる

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The user is logged in as 'kadota@iu.a.u-tokyo.ac.jp'. A dropdown menu is open, showing options like 'Preferences', 'Custom Builds', 'Logout', 'Saved Histories', 'Saved Datasets', and 'Saved Pages'. A red circle with the number 1 points to the user name in the dropdown. The main content area displays a welcome message for Galaxy. A central text box contains the following text:

Looking to learn?
New comprehensive tutorials on:
Diploid variant calling
Reference based RNAseq
Processing multiple samples
Introduction to NGS technologies
Galaxy 101, parts 1 & 2

The right sidebar shows a list of jobs with their names and icons for viewing, editing, and deleting. The jobs listed are:

- 6: FastQC on data 5: W ebpape
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: R awData
- 3: FastQC on data 2: W ebpape
- 2: DRR024501sub_1.fastq

W3-1: 第11回の作業のおさら

①Illumina MiSeqを用いて得られた30万リードからなるgzip圧縮FASTQファイル(DRR024501sub_1.fastq.gz)のアップロード

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed." Below this is a "Try Galaxy on the Cloud" banner with the text "Now you can have a personal Galaxy within the infinite Universe".

The left sidebar contains a "Tools" section with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, and NGS: RNA Structure.

The right sidebar shows the "History" panel with a search bar and a list of datasets. The dataset "2: DRR024501sub_1.fastq" is highlighted with a red box, and a red arrow points to it from the right. The other datasets in the history are:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage

W3-2: 第11回の作業のおさらい

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." Below this is a "Try Galaxy on the Cloud" banner with the text "Now you can have a personal Galaxy within the infinite Universe".

The left sidebar contains a "Tools" panel with a search bar and various tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, and NGS: RNA Structure.

The right sidebar shows the "History" panel, which lists a series of jobs. Job 4, "FastQC on data 2: RawData", is highlighted with a red box and a red arrow pointing to it with the number 2. The other jobs listed are:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W3-3: 第11回の作業のおさらい

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start [here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." Below this is a "Try Galaxy on the Cloud" banner with the text "Now you can have a personal Galaxy within the infinite Universe".

The left sidebar contains a "Tools" panel with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, and NGS: RNA Structure.

The right sidebar contains a "History" panel with a search bar and a list of jobs. The jobs are:

- 7: FastQC on data 5: R awData
- 6: FastQC on data 5: W ebpage
- 5: Trimmomatic on DR R024501sub_1.fastq** (highlighted with a red box and a red arrow labeled '3')
- 4: FastQC on data 2: R awData
- 3: FastQC on data 2: W ebpage
- 2: DRR024501sub_1.f astq

W3-4: 第11回の作業のおさらい

④ Trimmomatic実行後のファイルに対して、再度FastQCを実行

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed." Below this is a "Try Galaxy on the Cloud" banner with the text "Now you can have a personal Galaxy within the infinite Universe".

The left sidebar contains a "Tools" section with a search bar and various tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, and NGS: RNA Structure.

The right sidebar shows the "History" section with a search bar and a list of jobs. A red box highlights job 6: "FastQC on data 5: W ebpage". A red arrow with the number 4 points to this job. The history list includes:

- 7: FastQC on data 5: R awData
- 6: FastQC on data 5: W ebpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: R awData
- 3: FastQC on data 2: W ebpage
- 2: DRR024501sub_1.fastq

W4-1 : History options

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start [here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)."

The History panel on the right shows a list of datasets:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

A red arrow with the number 1 points to the gear icon (History options) in the top right of the History panel.

Looking to learn?
New comprehensive tutorials on:
Diploid variant calling
Reference based RNAseq
Processing multiple samples
Introduction to NGS technologies
Galaxy 101, parts 1 & 2

W4-2: Share or Publish

The screenshot shows the Galaxy web interface. The main content area displays a tutorial titled "Running Your Own Understanding how Galaxy works" with the subtitle "An in-depth tutorial". On the right side, a history list is visible, and a context menu is open over it. The menu items include "HISTORY LISTS", "CURRENT HISTORY", "DATASET ACTIONS", "DOWNLOADS", and "OTHER ACTIONS". The "Share or Publish" option is highlighted with a red arrow and a circled "1".

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).

Running Your Own Understanding how Galaxy works

An in-depth tutorial

- HISTORY LISTS
 - Saved Histories
 - Histories Shared with Me
- CURRENT HISTORY
 - Create New
 - Copy History
 - Share or Publish**
 - Show Structure
 - Extract Workflow
 - Delete
 - Delete Permanently
- DATASET ACTIONS
 - Copy Datasets
 - Dataset Security
 - Resume Paused Jobs
 - Collapse Expanded Datasets
 - Unhide Hidden Datasets
 - Delete Hidden Datasets
 - Purge Deleted Datasets
- DOWNLOADS
 - Export Tool Citations
 - Export History to File
- OTHER ACTIONS

W4-2: Share or Publish

①中央のパネルがこんな感じになります

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 0%'. A red arrow with the number 1 points to the 'Using 0%' indicator. The central panel is titled 'Share or Publish History 'Unnamed history'' and contains the following content:

Share or Publish History 'Unnamed history'

Make History Accessible via Link and Publish It

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

- Generates a web link that you can share with other people so that they can view and import the history.
- Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Share History with Individual Users

You have not shared this history with any users.

[Back to Histories List](#)

The right-hand panel is titled 'History' and shows a list of datasets:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W4-3: 共有手段は3つ

①はリンク先のURLを知っているヒト達で共有、②はGalaxy mainのPublished Historiesというサイト上で公開、③は特定のユーザーのみと共有するというもの。制限が緩い順に②、①、③の順番となる。

The screenshot shows the Galaxy web interface. The main content area is titled "Share or Publish History 'Unnamed history'". It contains three sections:

- Make History Accessible via Link and Publish It**: This section explains that the history is currently restricted. It offers two options: "Make History Accessible via Link" (labeled ①) and "Make History Accessible and Publish" (labeled ②). The second option also publishes the history to the "Published Histories" section.
- Share History with Individual Users**: This section states that the history has not been shared with any users and offers a "Share with a user" button (labeled ③).
- Share or Publish History**: This is the main heading for the page.

The right sidebar shows a list of history items:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W4-4: Published Histories

The screenshot shows the Galaxy web interface at <https://usegalaxy.org>. The main content area displays the title "Share or Publish History 'Unnamed history'" and a sub-heading "Make History Accessible via Link and Publish It". Below this, there are two buttons: "Make History Accessible via Link" and "Make History Accessible and Publish". A red arrow with the number "1" points to the "Make History Accessible and Publish" button. The right sidebar shows a "History" panel with a list of datasets, including "7: FastQC on data 5: RawData", "6: FastQC on data 5: Webpage", "5: Trimmomatic on DR R024501sub_1.fastq", "4: FastQC on data 2: RawData", "3: FastQC on data 2: Webpage", and "2: DRR024501sub_1.fastq".

W4-4: Published Histories

①このUnnamed historyは、②とは独立のもので、③のバーを少し右に移動させると…

The screenshot shows the Galaxy web interface. The main content area is titled "Published Histories" and contains a search bar and a table of history entries. The table has two columns: "Name" and "Annotation". The first entry is "Unnamed history". A red arrow labeled "1" points to this entry. The right-hand panel is titled "History" and shows a list of datasets. The first entry is "Unnamed history" with a size of 348.45 MB. A red arrow labeled "2" points to this entry. A red arrow labeled "3" points to the scrollbar of the main list.

Name	Annotation
Unnamed history	
Spiro files	
MSc Blood Sciences - RNA-Seq	
Galaxy 101-Run Workflow	
DataWexIllumina	
Galaksio use case: Mouse ChIP-seq data	
myhist	
Gastric Cancer	
Cancer de colon	
Cancer higado	
Genomics RNA-seq practical 01/2018	

History
search datasets
Unnamed history 6 shown, 1 deleted
348.45 MB
7: FastQC on data 5: RawData
6: FastQC on data 5: W ebpage
5: Trimmomatic on DR R024501sub_1.fastq
4: FastQC on data 2: RawData
3: FastQC on data 2: W ebpage
2: DRR024501sub_1.fastq

W4-4: Published H

①このあたりまで移動させると、②公開した履歴の所有者(owner)情報がわかります。さきほど一番上にあったUnnamed historyの所有者はPublic name(第11回のW4-3)がuditaさんという方。私(Public nameがagribio_t_t_desu)ではないことがわかる

Galaxy | Histories

Secure | https://usegalaxy.org/histories/list_published

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

Tools search tools

Annotation	Owner	Community Rating	Con
	udita	☆☆☆☆☆	
	paul-fourounjian	☆☆☆☆☆	
	drdtonge	☆☆☆☆☆	
	vpecci	☆☆☆☆☆	
	sjnewhouse	☆☆☆☆☆	ngs
	tomkl	☆☆☆☆☆	
	anuprulez	☆☆☆☆☆	
	curro-pr	☆☆☆☆☆	
	curro-pruiz	☆☆☆☆☆	
	curro-pruiz	☆☆☆☆☆	
	prevorovsky	☆☆☆☆☆	

History search datasets

Unnamed history 6 shown, 1 deleted 348.45 MB

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W4-4: Published Histories

①バーを右端まで移動させたところ。②Last Updated情報がわかる。このことから、今このスライドを見ているあなたが同じURLにアクセスしても、同じものは見られないことがわかる

The screenshot shows the Galaxy web interface with the following components:

- Browser:** Galaxy | Histories, Secure | https://usegalaxy.org/histories/list_published
- Navigation:** Analyze Data, Workflow, Shared Data, Visualization, Help, User, Using 0%
- Tools Panel (Left):** search tools, Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, NGS: RNA Structure
- History List (Table):**

Community Rating	Community Tags	Last Updated!
★★★★★		~53 minutes ago
★★★★★		~11 hours ago
★★★★★		~3 days ago
★★★★★		~4 days ago
★★★★★	ngs fastq testdata exome illumina	~5 days ago
★★★★★		~6 days ago
★★★★★		~6 days ago
★★★★★		Jan 21, 2018
★★★★★		Jan 21, 2018
★★★★★		Jan 21, 2018
★★★★★		Jan 16, 2018
- History Detail Panel (Right):** Unnamed history, 6 shown, 1 deleted, 348.45 MB. List of history items:
 - 7: FastQC on data 5: RawData
 - 6: FastQC on data 5: Webpage
 - 5: Trimmomatic on DR R024501sub_1.fastq
 - 4: FastQC on data 2: RawData
 - 3: FastQC on data 2: Webpage
 - 2: DRR024501sub_1.fastq

W4-5: 公開されたものを概観

①再度一番左側に移動させて、uditaさんが作成した② Unnamed historyを眺める

The screenshot shows the Galaxy web interface. The main content area is titled "Published Histories" and contains a search bar and a list of history entries. The entries are:

Name	Annotation
Unnamed history	
Spiro files	
MSc Blood Sciences - RNA-Seq	
Galaxy 101-Run Workflow	
DataWexIllumina	
Galaksio use case: Mouse ChIP-seq data	
myhist	
Gastric Cancer	
Cancer de colon	
Cancer higado	
Genomics RNA-seq practical 01/2018	

The right sidebar shows a "History" panel with a search bar and a list of datasets. The datasets are:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W4-5: 公開されたものを概観

眺めたところで、何のことかなんて大抵わかりません(爆)。
①諦めて元のページに戻る

The screenshot shows the Galaxy web interface. The browser address bar indicates the URL: <https://usegalaxy.org/u/udita/h/unnamed-history>. A red arrow with the number '1' points to the back button in the browser. The main content area displays a list of datasets under the heading 'Unnamed history' (5.97 GB). The datasets are listed in a table with columns for 'Dataset' and 'Annotation'. The 'Dataset' column contains links to various analysis jobs, and the 'Annotation' column is currently empty. The right sidebar shows metadata for the history, including the author 'udita', related histories, and a rating section.

Dataset	Annotation
519: ANNOVAR Annotate VCF on data 475	
518: ANNOVAR Annotate VCF on data 472	
517: ANNOVAR Annotate VCF on data 170	
516: ANNOVAR Annotate VCF on data 514	
514: FreeBayes on data 513 (variants)	
513: RmDup on data 474	
476: VCFfilter: on data 475	
475: FreeBayes on data 474 (variants)	
474: CleanSam on data 473: cleaned BAM dataset	
473: ReorderSam on data 453: Reordered BAM	

W4-5:元のページへ

The screenshot shows the Galaxy web interface. The browser address bar is at the top, with a red arrow pointing to the back button, labeled with a circled '1'. The URL is https://usegalaxy.org/histories/list_published. The main content area is titled 'Published Histories' and contains a search bar and a list of history entries. On the right, a 'History' panel shows details for a selected history, including its name, size, and a list of steps.

Name	Annotation
Unnamed history	
Spiro files	
MSc Blood Sciences - RNA-Seq	
Galaxy 101-Run Workflow	
DataWexIllumina	
Galaksio use case: Mouse ChIP-seq data	
myhist	
Gastric Cancer	
Cancer de colon	
Cancer higado	
Genomics RNA-seq practical 01/2018	

History
Unnamed history 6 shown, 1 deleted 348.45 MB
7: FastQC on data 5: RawData
6: FastQC on data 5: Webpage
5: Trimmomatic on DR R024501sub_1.fastq
4: FastQC on data 2: RawData
3: FastQC on data 2: Webpage
2: DRR024501sub_1.fastq

W5-1 : Unnamed history

デフォルトのヒストリー名である①
Unnamed historyとなっているが、それ
は②の部分が **Unnamed history** だから

The screenshot shows the Galaxy web interface. The main content area is titled "Share or Publish History 'Unnamed history'". Below the title, there are two main sections: "Make History Accessible via Link and Publish It" and "Share History with Individual Users".

The "Make History Accessible via Link and Publish It" section contains two buttons: "Make History Accessible via Link" and "Make History Accessible and Publish". The "Make History Accessible and Publish" button is highlighted with a red arrow labeled ①.

The "Share History with Individual Users" section contains a "Share with a user" button.

On the right side of the interface, there is a "History" panel. It shows a search bar for datasets and a list of history items. The top item is "Unnamed history", which is highlighted with a red arrow labeled ②. Below it, there are several other history items, each with a name, size, and icons for viewing, editing, and deleting.

The "History" panel items are:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W5-2: rename

①赤枠内にポインタを移動させると、Click to rename historyと表示される

The screenshot shows the Galaxy web interface. The main content area displays the title "Share or Publish History 'Unnamed history'" and a sub-section "Make History Accessible via Link and Publish It". Below this, there are two buttons: "Make History Accessible via Link" and "Make History Accessible and Publish". The "Make History Accessible and Publish" button is highlighted. The right sidebar shows a "History" panel with a list of datasets. The top entry, "Unnamed history", is highlighted with a red box and a red arrow pointing to it. A tooltip "Click to rename history" is visible over the red box. Below it are several other history entries, each with a name, size, and icons for viewing, editing, and deleting.

Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

search tools

Get Data

Send Data

Lift-Over

Collection Operations

Text Manipulation

Datamash

Convert Formats

Filter and Sort

Join, Subtract and Group

Fetch Alignments/Sequences

NGS: QC and manipulation

NGS: DeepTools

NGS: Mapping

NGS: RNA Analysis

NGS: SAMtools

NGS: BamTools

NGS: Picard

NGS: VCF Manipulation

NGS: Peak Calling

NGS: Variant Analysis

NGS: RNA Structure

Share or Publish History 'Unnamed history'

Make History Accessible via Link and Publish It

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

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

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

Share History with Individual Users

You have not shared this history with any users.

[Back to Histories List](#)

History

search datasets

Unnamed history Click to rename history

6 shown, 1 deleted

348.45 MB

7: [FastQC on data 5: RawData](#)

6: [FastQC on data 5: Webpage](#)

5: [Trimmomatic on DR R024501sub_1.fastq](#)

4: [FastQC on data 2: RawData](#)

3: [FastQC on data 2: Webpage](#)

2: [DRR024501sub_1.fastq](#)

W5-2: rename

①確かにクリックすると、この部分の記述内容を変更できることがわかる

The screenshot shows the Galaxy web interface. The main content area displays the 'Share or Publish History' page for an 'Unnamed history'. The page includes sections for 'Make History Accessible via Link and Publish It' and 'Share History with Individual Users'. On the right side, the 'History' panel lists several datasets, with the top entry 'Unnamed history' highlighted in a red box. A red arrow with the number '1' points to this entry, and a tooltip indicates 'Click to rename history'. The left sidebar contains a list of tools categorized by function, such as 'Get Data', 'Send Data', and 'Text Manipulation'.

W5-2: rename

① inudoshi_desu と名前を変更 (rename) して...

The screenshot shows the Galaxy web interface. The main content area displays the 'Share or Publish History' page for an 'Unnamed history'. The 'History' panel on the right lists several datasets, with the top one 'inudoshi_desu' highlighted in red. A tooltip 'Click to rename history' is visible over the highlighted name. A red arrow with the number '1' points to the highlighted name.

Tools

- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis
- NGS: RNA Structure

Share or Publish History 'Unnamed history'

Make History Accessible via Link and Publish It

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

-
-

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

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

Share History with Individual Users

You have not shared this history with any users.

[Back to Histories List](#)

History

search datasets

inudoshi_desu Click to rename history

6 shown, 1 deleted

348.45 MB

- 7: [FastQC on data 5: RawData](#)
- 6: [FastQC on data 5: Webpage](#)
- 5: [Trimmomatic on DR R024501sub_1.fastq](#)
- 4: [FastQC on data 2: RawData](#)
- 3: [FastQC on data 2: Webpage](#)
- 2: [DRR024501sub_1.fastq](#)

W5-2: rename

①リターンキーを押したところ。②中央パネルはUnnamed historyのままとなっているので

The screenshot shows the Galaxy web interface. The browser address bar is <https://usegalaxy.org>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The left sidebar contains tool categories such as 'Get Data', 'Send Data', 'Text Manipulation', and 'NGS: QC and manipulation'. The main content area is titled 'Share or Publish History 'Unnamed history'' and contains sections for 'Make History Accessible via Link and Publish It' and 'Share History with Individual Users'. The right sidebar shows a 'History' panel with a search bar and a list of datasets. The top dataset is 'inudoshi_desu', which is highlighted with a red box. A tooltip 'Click to rename history' is displayed over the dataset name. A red arrow labeled '1' points to the 'inudoshi_desu' entry, and another red arrow labeled '2' points to the main content area.

W5-3: Share or Publish

The screenshot shows the Galaxy web interface at <https://usegalaxy.org>. The main content area displays the page title "Share or Publish History 'Unnamed history'" and instructions on how to make the history accessible via link or publish it. A dropdown menu is open on the right side, showing various history and dataset actions. A red arrow labeled "1" points to the history menu icon in the top right corner, and another red arrow labeled "2" points to the "Share or Publish" option in the dropdown menu.

Tools

- search tools
- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis
- NGS: RNA Structure

Share or Publish History 'Unnamed history'

Make History Accessible via Link and Publish It

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

- [Make History Accessible via Link](#)
- [Make History Accessible and Publish](#)

Share History with Individual Users

You have not shared this history with any users.

[Share with a user](#)

[Back to Histories List](#)

HISTORY LIST

- 7: F awl
- 6: F ebp
- 5: T R02
- 4: F awl
- 3: F ebp
- 2: D asto

HISTORY ACTIONS

- Share or Publish
- Show Structure
- Extract Workflow
- Delete
- Delete Permanently

DATASET ACTIONS

- Copy Datasets
- Dataset Security
- Resume Paused Jobs
- Collapse Expanded Datasets
- Unhide Hidden Datasets
- Delete Hidden Datasets
- Purge Deleted Datasets

DOWNLOADS

- Export Tool Citations
- Export History to File

OTHER ACTIONS

無事①inudoshi_desuが②
のところに反映されました

W5-3: Share or Publish

The screenshot shows the Galaxy web interface. The browser address bar is <https://usegalaxy.org>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 0%'. The left sidebar lists tool categories such as 'Get Data', 'Send Data', 'Text Manipulation', etc. The main content area is titled 'Share or Publish History 'inudoshi_desu'' and contains instructions on how to share or publish the history. Two red arrows are overlaid on the image: arrow 1 points to the 'inudoshi_desu' dataset name in the History panel on the right, and arrow 2 points to the 'Share or Publish History' title. The History panel on the right shows a list of datasets, including '7: FastQC on data 5: RawData', '6: FastQC on data 5: Webpage', '5: Trimmomatic on DR R024501sub_1.fastq', '4: FastQC on data 2: RawData', '3: FastQC on data 2: Webpage', and '2: DRR024501sub_1.fastq'.

W5-4: URL情報を取得

①ヒストリーinudoshi_desu
の②リンク先情報を取得

The screenshot shows the Galaxy web interface. The main content area is titled "Share or Publish History 'inudoshi_desu'". It contains the following sections:

- Make History Accessible via Link and Publish It**
 - This history is currently restricted so that only you and the users listed below can access it. You can:
 - Make History Accessible via Link** (indicated by a red arrow with the number 2): Generates a web link that you can share with other people so that they can view and import the history.
 - Make History Accessible and Publish**: Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.
- Share History with Individual Users**
 - You have not shared this history with any users.
 - [Share with a user](#)
- [Back to Histories List](#)

The right sidebar shows the "History" panel with a search bar and a list of datasets:

- Search datasets: inudoshi_desu (6 shown, 1 deleted) (indicated by a red arrow with the number 1)
- 348.45 MB
- 7: [FastQC on data 5: RawData](#)
- 6: [FastQC on data 5: Webpage](#)
- 5: [Trimmomatic on DR R024501sub_1.fastq](#)
- 4: [FastQC on data 2: RawData](#)
- 3: [FastQC on data 2: Webpage](#)
- 2: [DRR024501sub_1.fastq](#)

W6-1: URL情報を取得

Galaxy | Histories

Secure | https://usegalaxy.org/histories/list_published

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

Share or Publish History 'inudoshi_desu'

Make History Accessible via Link and Publish It

This history is currently **accessible via link**.
Anyone can view and import this history by visiting the following URL:

https://usegalaxy.org/u/aqribio_t_t_desu/h/inudoshidesu

You can:

- Disable Access to History Link**
Disables history's link so that it is not accessible.
- Publish History**
Publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Share History with Individual Users

You have not shared this history with any users.

History

search datasets

inudoshi_desu
6 shown, 1 deleted
348.45 MB

- 7: FastQC on data 5: RawData**
- 6: FastQC on data 5: Webpage**
- 5: Trimmomatic on DR R024501sub_1.fastq**
- 4: FastQC on data 2: RawData**
- 3: FastQC on data 2: Webpage**
- 2: DRR024501sub_1.fastq**

W6-1: URL情報を取

①が第11回のW4-3で作成した自分のPublic name (agribio_t_t_desu)。②の部分③ヒストリー名からアンダースコア(_)を取っ払ったものなのでわかりやすい

The screenshot shows the Galaxy web interface. The main content area is titled "Share or Publish History 'inudoshi_desu'". It contains the following text and elements:

- Make History Accessible via Link and Publish It**
- This history is currently **accessible via link**.
- Anyone can view and import this history by visiting the following URL:
`https://usegalaxy.org/u/agribio_t_t_desu/h/inudoshidesu`
- You can:
 - Disable Access to History Link**: Disables history's link so that it is not accessible.
 - Publish History**: Publishes the history to Galaxy's **Published Histories** section, where it is publicly listed and searchable.
- Share History with Individual Users**: You have not shared this history with any users.

The right sidebar shows a list of history items:

- inudoshi_desu (6 shown, 1 deleted)
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W6-1: URL情報を取得

④の部分をクリックして②の文字列を任意に変更することもできる(がここではやらない)

Galaxy | Histories

Secure | https://usegalaxy.org/histories/list_published

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

Share or Publish History 'inudoshi_desu'

Make History Accessible via Link and Publish It

This history is currently **accessible via link**. Anyone can view and import this history by visiting the following URL:

https://usegalaxy.org/u/aqribio_t_t_desu/h/inudoshidesu

You can:

- Disables history's link so that it is not accessible.
- Publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Share History with Individual Users

You have not shared this history with any users.

History

search datasets

- inudoshi_desu** 6 shown, 1 deleted 348.45 MB
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W6-2: URL情報を送信

①kadota_unregisteredさんに、②ヒストリーinudoshi_desuのURL情報を、③メール送信

The screenshot shows the Outlook 'Compose' window. The 'To' field contains 'kojikadota@gmail.com' (callout ①). The 'Subject' field contains 'ヒストリーinudoshi_desuのURL' (callout ②). The 'Body' text contains 'kadota_unregistered さま' (underlined), '表題の件につきまして URL 情報を以下に示します。', and the URL 'https://usegalaxy.org/u/agribio_t_t_desu/h/inudoshidesu' (callout ②). The 'Send' button is highlighted with a callout ③.

W6-3:メール受信



W6-4: リンク先にアクセス

こんな感じになります。確かにこのヒストリーの所有者は①agribio_t_t_desuさん(kadota_registeredのPublic name)です

Galaxy | Accessible History x

Secure | https://usegalaxy.org/u/agribio_t_t_desu/h/inudoshidesu


Galaxy Analyze Data Workflow Shared Data Visualization Help Login or Register Using 0 bytes

Accessible History | inudoshi_desu Import history About this History


inudoshi_desu
348.45 MB

search datasets

Dataset	Annotation
7: FastQC on data 5: RawData	
6: FastQC on data 5: Webpage	
5: Trimmomatic on DRR024501sub_1.fastq	
4: FastQC on data 2: RawData	
3: FastQC on data 2: Webpage	
2: DRR024501sub_1.fastq	

Author
agribio_t_t_desu 

Related Histories
[All published histories](#)
[Published histories by agribio_t_t_desu](#)

Rating
Community 
(0 ratings, 0.0 average)

Tags
Community: none

W6-5: ログインしていないよ

確かにGalaxy mainにログインしていない未登録ユーザ(kadota_unregistered)であることがわかる

The screenshot shows the Galaxy web interface. The browser address bar displays the URL `https://usegalaxy.org/u/agribio_t_t_desu/h/inudoshidesu`. The top navigation bar includes the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Help, and Login or Register. A red arrow with the number '1' points to the 'Login or Register' button. Below the navigation bar, the user's profile 'inudoshi_desu' is shown with a storage usage of 348.45 MB. A search bar for datasets is present. A table lists datasets with columns for Dataset and Annotation. The right sidebar displays the user's profile information, including the author name 'agribio_t_t_desu', a red diamond pattern profile picture, 'Related Histories' links, a 'Rating' section with five empty stars, and 'Tags'.

Dataset	Annotation
7: FastQC on data 5: RawData	
6: FastQC on data 5: Webpage	
5: Trimmomatic on DRR024501sub_1.fastq	
4: FastQC on data 2: RawData	
3: FastQC on data 2: Webpage	
2: DRR024501sub_1.fastq	

W6-6: おさらい

①目玉マークはデータを中央パネル上に表示(第11回W6-2)だったのでやってみる。①をクリック

The screenshot shows the Galaxy web interface. The browser address bar displays the URL https://usegalaxy.org/u/agribio_t_t_desu/h/inudoshidesu. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'Login or Register', and 'Using 0%'. The page title is 'Accessible History | inudoshi_desu'. The main content area shows a list of datasets for 'inudoshi_desu' (348.45 MB). The datasets are listed in a table with columns for 'Dataset' and 'Annotation'. A search bar for datasets is present. A red arrow with the number 1 points to the eye icon of the dataset '6: FastQC on data 5: Webpage'. The right sidebar contains information about the history, including the author 'agribio_t_t_desu', related histories, a rating of 0 stars, and no tags.

Dataset	Annotation
7: FastQC on data 5: RawData	
6: FastQC on data 5: Webpage	
5: Trimmomatic on DRR024501sub_1.fastq	
4: FastQC on data 2: RawData	
3: FastQC on data 2: Webpage	
2: DRR024501sub_1.fastq	

W6-7: FastQC

①新規タブが開いて、FastQCのhtmlレポートが見られる。これは第11回W13-6で見ているものと同じ(はず)。念のため②Basic Statisticsも見てみる。今はkadota_registeredからもらった解析結果を、何もやってないkadota_unregisteredさんが見させてもらっている状況です。ちゃんと共有できていることを示し、何をどの程度までできるのかを示そうとしています

Trimmomatic_on_DRR024501sub_1.fastq FastQC Report

FastQC Report
Wed 31 May 2017
Trimmomatic_on_DRR024501sub_1.fastq

Summary

- [Basic Statistics](#)
- [Per base sequence quality](#)
- [Per tile sequence quality](#)
- [Per sequence quality scores](#)
- [Per base sequence content](#)
- [Per sequence GC content](#)
- [Per base N content](#)
- [Sequence Length Distribution](#)
- [Sequence Duplication Levels](#)
- [Overrepresented sequences](#)
- [Adapter Content](#)

W6-7: FastQC

①若干見栄えが異なるが、第11回W13-6と同じ数値。②ページを上部にスクロールさせれば1つ前のスライドと同じところにいけます

Basic Statistics

Measure	Value
Filename	Trimmomatic_on_DRR024501sub_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	297724
Sequences flagged as poor quality	0
Sequence length	2-251
%GC	38

Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

W6-8: 見るだけじゃ...

①ページ上部に移動後。このようなhtmlファイル程度であれば、②画面上で右クリックして、③Save as ...などとやって結果ファイルをダウンロードしてもよいが、ここではやらない

The screenshot shows a web browser window with the URL <https://usegalaxy.org/datasets/bbd44e69cb8906b586ac342a5e72e07d/display/?preview=True#M0>. The page title is "Trimmomatic_on_DRR024501sub_1.fastq FastQC Report". The page content includes a "Summary" section with a list of items, each with a status icon (green checkmark, red X, or orange exclamation mark) and a link to the corresponding report section. A context menu is open over the "Save as..." option, which is highlighted. Red arrows with numbers 1, 2, and 3 point to the scroll bar, the context menu, and the "Save as..." option, respectively.

Trimmomatic_on_DRR024501sub_1.fastq FastQC Report

FastQC Report
Wed 31 May 2017
Trimmomatic_on_DRR024501sub_1.fastq

Summary

- [Basic Statistics](#)
- [Per base sequence quality](#)
- [Per tile sequence quality](#)
- [Per sequence quality scores](#)
- [Per base sequence content](#)
- [Per sequence GC content](#)
- [Per base N content](#)
- [Sequence Length Distribution](#)
- [Sequence Duplication Levels](#)
- [Overrepresented sequences](#)
- [Adapter Content](#)

W7-1: インポート

今は「閲覧のみ」みたいな状況です。共有元のkadota_registeredさんが何でもできるように、kadota_unregisteredさんも自在に編集したいので、共有された履歴を取り込む(importする)作業を行います。①Import history

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'History', 'Login or Register', and 'Using 0%'. The main content area is titled 'Accessible History | inudoshi_desu'. Below this, there is a search bar for datasets and a table of datasets. The table has two columns: 'Dataset' and 'Annotation'. The datasets listed are:

Dataset	Annotation
7: FastQC on data 5: RawData	
6: FastQC on data 5: Webpage	
5: Trimmomatic on DRR024501sub_1.fastq	View data
4: FastQC on data 2: RawData	
3: FastQC on data 2: Webpage	
2: DRR024501sub_1.fastq	

On the right side of the interface, there is a sidebar with the following information:

- Author:** agrbio_t_t_desu
- Related Histories:** [All published histories](#), [Published histories by agrbio_t_t_desu](#)
- Rating:** Community (0 ratings, 0.0 average)
- Tags:** Community: none

A red arrow with the number '1' points to the 'Import history' button in the top navigation bar. A tooltip above the arrow says 'Make a copy of this history and switch to it'.

W7-1: インポート

今は、kadota_unregisterdさんの画面。Galaxy mainに登録していないので①an anonymous userなのです。それゆえ、Galaxy mainにログインまたは登録せずにinudoshi_desuというkadota_registeredさんが行った解析結果の履歴を取り込むと、それ以前にkadota_unregisterdさんが何か作業を行った履歴があったとしても消えてしまいますよ、という警告です。通常は、Galaxy mainにログインもしていないヒトが何か解析をやってなくなったら困るような履歴はないはずなので、ここでは無視して②Import

Galaxy | Accessible History | <https://usegalaxy.org/datasets>

Secure | https://usegalaxy.org/u/agribio_t_t_desu/h/inudoshi_desu

Galaxy Analyze Data Workflow Shared Data

Accessible History | inudoshi_desu | 348.45 MB

search datasets

Dataset

- 7: FastQC on data 5
- 6: FastQC on data 5
- 5: Trimmomatic on
- 4: FastQC on data 2
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

Importing history "inudoshi_desu"

① As an anonymous user, unless you login or register, you will lose your current history after importing this history. You can [login here](#) or [register here](#).

Enter a title for the new history:

imported: inudoshi_desu

Cancel Import

②

W7-2: インポート完了

kadota_unregisteredさんが、①ログインせずに
ヒストリーinudoshi_desuをインポートした直後の
状態。②ログインしていなくてもこれだけの容
量のデータを使わせてくれるのね。この後は、
③ツール選択パネルから独立に解析可能

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'Login or Register', and 'Using 6%'. The left sidebar contains a 'Tools' panel with a search bar and various tool categories like 'Get Data', 'Send Data', 'Text Manipulation', etc. The main content area displays a welcome message and a 'Public Galaxy Servers and still counting' banner. The right sidebar shows a 'History' panel with a search bar and a list of workflow steps, including 'imported: inudoshi_desu' (348.45 MB) and several 'FastQC' and 'Trimmomatic' steps.

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).

080+
Public Galaxy Servers
and *still* counting

History

search datasets

imported: inudoshi_desu
6 shown
348.45 MB

7: FastQC on data 5: R awData

6: FastQC on data 5: W ebpage

5: Trimmomatic on DR R024501sub 1.fastq

4: FastQC on data 2: R awData

3: FastQC on data 2: W ebpage

2: DRR024501sub 1.fastq

W7-3: ログインしてないので...

①タブ、または②ブラウザを閉じると全て消える

The screenshot shows the Galaxy web interface. The main content area displays a message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." Below this message is a logo for "080+" and the text "Public Galaxy Servers and still counting".

The left sidebar contains a "Tools" section with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, and NGS: RNA Structure.

The right sidebar contains a "History" section with a search bar and a list of datasets: imported: inudoshi_desu (6 shown, 348.45 MB), 7: FastQC on data 5: R awData, 6: FastQC on data 5: W ebpage, 5: Trimmomatic on DR R024501sub_1.fastq, 4: FastQC on data 2: R awData, 3: FastQC on data 2: W ebpage, and 2: DRR024501sub_1.fastq.

Red arrows point to the browser tab (labeled ①) and the browser window (labeled ②).

W8-1: 利用例

Trimmomatic①前と②後のFastQC結果を眺めておいて、当時はデフォルト設定で実行したが、オプションを変更した方がいいのではと(例えばkadota_unregisteredさんが)思いついたとする。それを実行に移すべく、③からFastQCを探す。第11回のW9-2では、すぐにFastQCが表示されたが、今回みたら表示されなかったなので、④下にスクロールしてTrimmomaticを探す

The screenshot shows the Galaxy web interface. On the left is the 'Tools' panel with a search bar and various tool categories. A red arrow labeled '3' points to the 'NGS: QC and manipulation' category. In the center, a message reads 'Galaxy is an open source, web-based platform for data intensive biomedical research...' and 'Try Galaxy on the Cloud'. On the right is the 'History' panel showing a list of jobs. A red arrow labeled '1' points to the job '3: FastQC on data 2: W ebpage', and another red arrow labeled '2' points to the job '6: FastQC on data 5: W ebpage'. A red arrow labeled '4' points to the search bar in the Tools panel.

W8-2: Trimmomatic発見

①今回はこのあたりで、② Trimmomaticを発見。クリック

The screenshot shows the Galaxy web interface. The main content area displays a tutorial titled "Running Your Own Understanding how Galaxy works" with a sub-heading "An in-depth tutorial". The left sidebar contains a search results list for "search tools". A red arrow labeled "1" points to the "Trim Galore! Quality and adapter trimmer of reads" entry. A second red arrow labeled "2" points to the "Trimmomatic flexible read trimming tool for Illumina NGS data" entry. The right sidebar shows a "History" panel with a list of datasets, including "7: FastQC on data 5: RawData", "6: FastQC on data 5: Webpage", "5: Trimmomatic on DRR024501sub_1.fastq", "4: FastQC on data 2: RawData", "3: FastQC on data 2: Webpage", and "2: DRR024501sub_1.fastq".

W8-3: 中央パネル

①第1候補の入カファイルは最新のものになるので、②と同じものが見えています。つまりデフォルト設定で実行したTrimmomaticの出カファイル

The screenshot displays the Galaxy web interface for the 'Trimmomatic flexible read trimming' tool. The tool configuration is as follows:

- Single-end or paired-end reads?**: Single-end
- Input FASTQ file**: 5: Trimmomatic on DRR024501sub_1.fa... (indicated by red arrow ①)
- Perform initial ILLUMINACLIP step?**: No
- Trimmomatic Operation**:
 - 1: Trimmomatic Operation**
 - Select Trimmomatic operation to perform**: Sliding window trimming (SLIDINGWINDOW)
 - Number of bases to average across**: 4
 - Average quality required**: 20
- Execute**: [Execute]

The **History** panel on the right shows a list of datasets:

- 7: FastQC on data 5: R awData
- 6: FastQC on data 5: W ebpage
- 5: Trimmomatic on DRR024501sub_1.fastq (indicated by red arrow ②)
- 4: FastQC on data 2: R awData
- 3: FastQC on data 2: W ebpage
- 2: DRR024501sub_1.fastq

W8-4: 入力を変更

①の入カファイルは同じにしてデフォルト設定との違いを見たいので、前回と同じ②を入力とすべく...

The screenshot displays the Galaxy web interface for the 'Trimmomatic flexible read trimming' tool. The tool configuration is as follows:

- Single-end or paired-end reads?**: Single-end
- Input FASTQ file**: 5: Trimmomatic on DRR024501sub_1.fa... (marked with ①)
- Perform initial ILLUMINA**: Yes
- Trimmomatic Operation**: 1: Trimmomatic Operation
 - Select Trimmomatic operation to perform**: Sliding window trimming (SLIDINGWINDOW)
 - Number of bases to average across**: 4
 - Average quality required**: 20
- Execute**: [Execute]

The **History** panel on the right shows the following jobs:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W8-4: 入力を変更

The screenshot displays the Galaxy web interface for the Trimmomatic flexible read trimming tool. The tool configuration is as follows:

- Tool:** Trimmomatic flexible read trimming (Galaxy Version 0.36.3)
- Single-end or paired-end reads?:** Single-end
- Input FASTQ file:** 5: Trimmomatic on DRR024501sub_1.fa...
- Perform initial Illumina quality check:** Yes
- Trimmomatic Operation:** 1: Trimmomatic Operation
- Select Trimmomatic operation to perform:** Sliding window trimming (SLIDINGWINDOW)
- Number of bases to average across:** 4
- Average quality required:** 20

A red arrow with the number '1' points to the 'Input FASTQ file' dropdown menu, which is open and showing a list of files. The file '2: DRR024501sub_1.fastq' is highlighted in blue.

The 'History' panel on the right shows a list of jobs:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W8-4: 入力を変更

①こんな感じにすれば、②をTrimmomaticの入力ファイルに変更できたことになる

The screenshot displays the Galaxy web interface for the Trimmomatic flexible read trimming tool. The tool configuration is as follows:

- Trimmomatic flexible read trimming** (Galaxy Version 0.36.3)
- Single-end or paired-end reads?**: Single-end
- Input FASTQ file**: 2: DRR024501sub_1.fastq (indicated by red arrow ①)
- Perform initial ILLUMINACLIP step?**: No
- Trimmomatic Operation**: 1: Trimmomatic Operation
- Select Trimmomatic operation to perform**: Sliding window trimming (SLIDINGWINDOW)
- Number of bases to average across**: 4 (indicated by red arrow ②)
- Average quality required**: 20
- Execute** button is visible.

The **History** panel on the right shows a list of jobs:

- 7: FastQC on data 5: R awData
- 6: FastQC on data 5: W ebpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: R awData
- 3: FastQC on data 2: W ebpage
- 2: DRR024501sub_1.fastq (highlighted in green)

W8-5: オプション変更・実行

ここでは①平均クオリティスコアの閾値を20から30に上げて、②実行

The screenshot shows the Galaxy web interface for the 'Trimmomatic flexible read trimming' tool. The tool is configured for 'Single-end' reads, using the input file '2: DRR024501sub_1.fastq'. The 'Perform initial ILLUMINACLIP step?' is set to 'No'. Under 'Trimmomatic Operation', the 'Select Trimmomatic operation to perform' is 'Sliding window trimming (SLIDINGWINDOW)'. The 'Number of bases to average across' is set to 4. The 'Average quality required' field is highlighted with a red arrow and a circled '1', and its value is '30'. Below this field is an 'Insert Trimmomatic Operation' button. At the bottom of the configuration panel, the 'Execute' button is highlighted with a red arrow and a circled '2'. The right sidebar shows a 'History' panel with a list of previous jobs, including '7: FastQC on data 5: R awData', '6: FastQC on data 5: W ebpage', '5: Trimmomatic on DRR024501sub_1.fastq', '4: FastQC on data 2: R awData', '3: FastQC on data 2: W ebpage', and '2: DRR024501sub_1.fastq'.

W8-6: 実行待ち

① Trimmomatic実行命令の受付完了(ジョブ投げ完了)。② 灰色は実行待ち状態(第11回W9-9)

The screenshot shows the Galaxy web interface. A green notification box at the top center contains a checkmark and the text: "1 job has been successfully added to the queue - resulting in the following datasets: 8: Trimmomatic on DRR024501sub_1.fastq". Below this, it says: "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." A red arrow labeled "1" points to the notification box. On the right side, the "History" pane shows a list of jobs. The top job, "8: Trimmomatic on DRR024501sub_1.fastq", is highlighted in grey, indicating it is in a waiting state. A red arrow labeled "2" points to this job entry. The "Tools" pane on the left is visible, and the browser address bar shows the URL: "https://usegalaxy.org/?tool_id=toolshed.g2.bx.psu.edu%2Frepos%2Fpjbbriggs%2Ftrimmomatic%2F0...".

W8-7: 実行完了

①緑色に変わったので実行が無事完了

The screenshot shows the Galaxy web interface. A central green notification box contains a checkmark icon and the text: "1 job has been successfully added to the queue - resulting in the following datasets: 8: Trimmomatic on DRR024501sub_1.fastq". Below this, it provides instructions on how to check the status of the job in the History pane. The History pane on the right shows a list of datasets, with the top entry "8: Trimmomatic on DRR024501sub_1.fastq" highlighted in green. A red arrow with the number "1" points to this green entry. The left sidebar shows a search for tools, with "Trimmomatic" selected. The top navigation bar includes "Galaxy", "Analyze Data", "Workflow", "Shared Data", "Visualization", "Help", "Login or Register", and "Using 9%".

W8-8: 違いがわからない

①が平均クオリティスコアの閾値を30に変更して実行した結果。②がデフォルトの20の結果だが、2つの名前が同じなのでぱっと見ではわからないので

The screenshot shows the Galaxy web interface. On the left is a 'Tools' sidebar with a search bar and various tool options. The main area displays a green notification box with a checkmark icon, stating: '1 job has been successfully added to the queue - resulting in the following datasets: 8: Trimmomatic on DRR024501sub_1.fastq'. Below this, it provides instructions on how to check the status of queued jobs. On the right, the 'History' panel shows a list of jobs. Job 8, '8: Trimmomatic on DRR024501sub_1.fastq', is highlighted with a red box and a red arrow labeled '1'. Job 5, '5: Trimmomatic on DRR024501sub_1.fastq', is also highlighted with a red box and a red arrow labeled '2'. Other jobs in the history include FastQC on data 5: RawData, FastQC on data 5: Webpage, FastQC on data 2: RawData, and FastQC on data 2: Webpage. Job 2 is 'DRR024501sub_1.fastq'.

W8-9: 名前を変更

①後からやったほうを閾値30に変更したことを明示させよう。②で編集する

The screenshot displays the Galaxy web interface for editing dataset attributes. The main panel, titled "Edit dataset attributes", shows the current dataset name as "Trimmomatic on DRR024501sub_1.fastq". A red arrow labeled "1" points to this name field. The "Info" section contains technical details about the Trimmomatic process. The "Annotation" section is empty. The "Database/Build" dropdown is set to "unspecified (?)".

On the right, the "History" panel lists recent datasets. The top entry, "8: Trimmomatic on DR R024501sub_1.fastq", is highlighted in green. A red arrow labeled "2" points to the edit icon (pencil) next to this entry. Below it, other datasets like "7: FastQC on data 5: R awData" and "6: FastQC on data 5: W ebpage" are listed.

W8-10: オプションの数値

ちょっと話がそれますが、この部分を見ることで、①Trimmomatic実行時に平均クオリティスコアを30に変更して実行しているのだということがわかります

The screenshot shows the Galaxy web interface. The main content area is titled "Edit dataset attributes" and displays the following information:

- Name:** Trimmomatic on DRR024501sub_1.fastq
- Info:**

```
repirmam/job001/018/520/18520502/_job_tmp -Xmx7g -Xms256m  
TrimmomaticSE: Started with arguments:  
-threads 1 -phred33 fastq_in.fastqsanger fastq_out.fastqsanger  
SLIDINGWINDOW:4:30  
Input Reads: 300000 Su
```

 A red arrow with the number 1 points to the "SLIDINGWINDOW:4:30" line.
- Annotation:** (Empty text area)
- Database/Build:** unspecified (?)

The right sidebar shows the "History" section with a list of jobs:

- 8: Trimmomatic on DR R024501sub_1.fastq
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DR R024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

とりあえず①Q30を追加した名前にして、②Save

W8-11: 名前の変更(本番)

The screenshot shows the Galaxy web interface for editing dataset attributes. The main content area is titled "Edit dataset attributes" and has tabs for "Attributes", "Convert", "Datatypes", and "Permissions". The "Attributes" tab is active, showing a form with the following sections:

- Edit attributes:** Includes "Auto-detect" and "Save" buttons.
- Name:** A text input field containing "Trimmomatic on DRR024501sub_1.fastq Q30".
- Info:** A text area containing technical details: "Xms256m", "TrimmomaticSE: Started with arguments: -threads 1 -phred33 fastq_in.fastqsanger fastq_out.fastqsanger SLIDINGWINDOW:4:30", and "Input Reads: 300000 Su".
- Annotation:** An empty text area for adding notes.
- Database/Build:** A dropdown menu currently set to "unspecified (?)".

On the right side, there is a "History" panel showing a list of datasets. The top entry is "imported: inudoshi_desu" (7 shown). Below it are several other datasets, each with a name, a size, and icons for viewing, editing, and deleting. The dataset "8: Trimmomatic on DR R024501sub_1.fastq" is highlighted in green, indicating it is the current dataset being edited.

W8-12: 名前の変更(完了)

①無事変更が反映された。こんな感じで研究グループ内のヒトにわかるように、任意に変更可能です

The screenshot displays the Galaxy web interface for editing dataset attributes. The main panel, titled "Edit dataset attributes", shows a green notification bar indicating "Attributes updated." Below this, there are tabs for "Attributes", "Convert", "Datatypes", and "Permissions". The "Edit attributes" section includes a "Name" field containing "Trimmomatic on DRR024501sub_1.fastq Q30", an "Info" field with system logs, and an "Annotation" field. The "Database/Build" dropdown is set to "unspecified (?)". On the right, the "History" panel lists recent operations, with the top entry "8: Trimmomatic on DR R024501sub_1.fastq Q30" highlighted in green and marked with a red arrow and the number 1.

W9-1 : FastQC

①のTrimmomatic実行結果ファイルを入力として、②FastQCを、③実行

The screenshot displays the Galaxy web interface for running FastQC. The main panel shows the configuration for 'FastQC Read Quality reports (Galaxy) Version 0.69'. The 'Short read data from your current history' section is set to '8: Trimmomatic on DRR024501sub_1.fastq...'. The 'Contaminant list' is set to 'Nothing selected'. The 'Submodule and Limit specifying file' is also set to 'Nothing selected'. The 'Execute' button is highlighted with a red arrow and the number 3. The 'History' panel on the right shows a list of jobs, with '8: Trimmomatic on DR R024501sub_1.fastq Q 30' highlighted in green and marked with a red arrow and the number 1. The 'Tools' panel on the left shows 'FastQC Read Quality reports' highlighted with a red arrow and the number 2.

W9-2: 実行待ち

Galaxy

Analyze Data Workflow Shared Data Visualization Help Login or Register Using 9%

Tools

search tools

FASTQ Groomer convert between various FASTQ quality formats

Filter FASTQ reads by quality score and length

Combine FASTA and QUAL into FASTQ

Trim Galore! Quality and adapter trimmer of reads

FastQC Read Quality reports

multiqc aggregate results from bioinformatics analyses into a single report

Trimmomatic flexible read trimming tool for Illumina NGS data

Select high quality segments

Build base quality distribution

Draw quality score boxplot

Quality format converter (ASCII-Numeric)

History

search datasets

imported: inudoshi_desu
9 shown
474.38 MB

10: FastQC on data 8: RawData

9: FastQC on data 8: Webpage

8: Trimmomatic on DRR024501sub_1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub_1.fastq

4: FastQC on data 2: RawData

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

9: FastQC on data 8: Webpage

10: FastQC on data 8: RawData

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



①

W9-3: 実行完了

The screenshot shows the Galaxy web interface. A green notification box in the center states: "1 job has been successfully added to the queue - resulting in the following datasets: 9: FastQC on data 8: Webpage, 10: FastQC on data 8: RawData". Below this, it provides instructions on how to check the status of queued jobs. On the right, the History panel lists several datasets, with the two most recent ones, "10: FastQC on data 8: RawData" and "9: FastQC on data 8: Webpage", highlighted in green and enclosed in a red box. A red arrow with the number "1" points to this red box. The left sidebar contains a list of tools, and the top navigation bar includes options like "Analyze Data", "Workflow", and "Shared Data".

Galaxy
Analyze Data Workflow Shared Data Visualization Help Login or Register Using 9%

Tools
various attributes
search tools
FASTQ Groomer convert
between various FASTQ
quality formats
Filter FASTQ reads by quality
score and length
Combine FASTA and QUAL into
FASTQ
Trim Galore! Quality and
adapter trimmer of reads
FastQC Read Quality reports
multiqc aggregate results
from bioinformatics analyses
into a single report
Trimmomatic flexible read
trimming tool for Illumina
NGS data
Select high quality segments
Build base quality distribution
Draw quality score boxplot
Quality format converter
(ASCII-Numeric)

History
search datasets
imported: inudoshi_desu
9 shown
475.66 MB
10: FastQC on data 8: RawData
9: FastQC on data 8: Webpage
8: Trimmomatic on
DRR024501sub 1.f
astq Q30
7: FastQC on data 5:
RawData
6: FastQC on data 5:
Webpage
5: Trimmomatic on
DRR024501sub 1.f
astq
4: FastQC on data 2:
RawData
3: FastQC on data 2:

1

W9-4: 保存

FastQC実行結果のhtmlファイルをダウンロードすべく、①をクリック

The screenshot shows the Galaxy web interface. A central green notification box contains the following text:

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

- 9: FastQC on data 8: Webpage
- 10: FastQC on data 8: RawData

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.

A red arrow with the number 1 points to the download icon (a floppy disk) in the History pane for the job "9: FastQC on data 8: Webpage".

The History pane on the right shows the following jobs:

- 10: FastQC on data 8: RawData (475.66 MB)
- 9: FastQC on data 8: Webpage (267.5 KB, format: html, database: ?)
- 8: Trimmomatic on DRR024501sub 1.f astq Q30
- 7: FastQC on data 5: ...

W9-4: 保存

The screenshot shows the Galaxy web interface. A green notification box in the center states: "1 job has been successfully added to the queue - resulting in the following datasets: 9: FastQC on data 8: Webpage, 10: FastQC on data 8: RawData. 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." The History pane on the right shows a list of datasets, with the entry "10: FastQC on data 8: RawData" highlighted in green. A red arrow with the number "1" points to the "Download" button below this entry. The URL in the address bar is "https://usegalaxy.org/?tool_id=toolshed.g2.bx.psu.edu%2Frepos%2Fdevteam%2Ffastqc%2Ffastqc%2F0.69&version=...".

W9-5: 保存完了

私の環境では赤枠のようになりました。①を左クリックでデスクトップ上に保存されます

The screenshot shows the Galaxy web interface. A central green notification box contains the following text:

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

- 9: FastQC on data 8: Webpage
- 10: FastQC on data 8: RawData

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.

On the right, the History pane shows the following jobs:

- 10: FastQC on data 8: RawData (267.5 KB, format: html, database: ?)
- 9: FastQC on data 8: Webpage (267.5 KB, format: html, database: ?)
- 8: Trimmomatic on ...

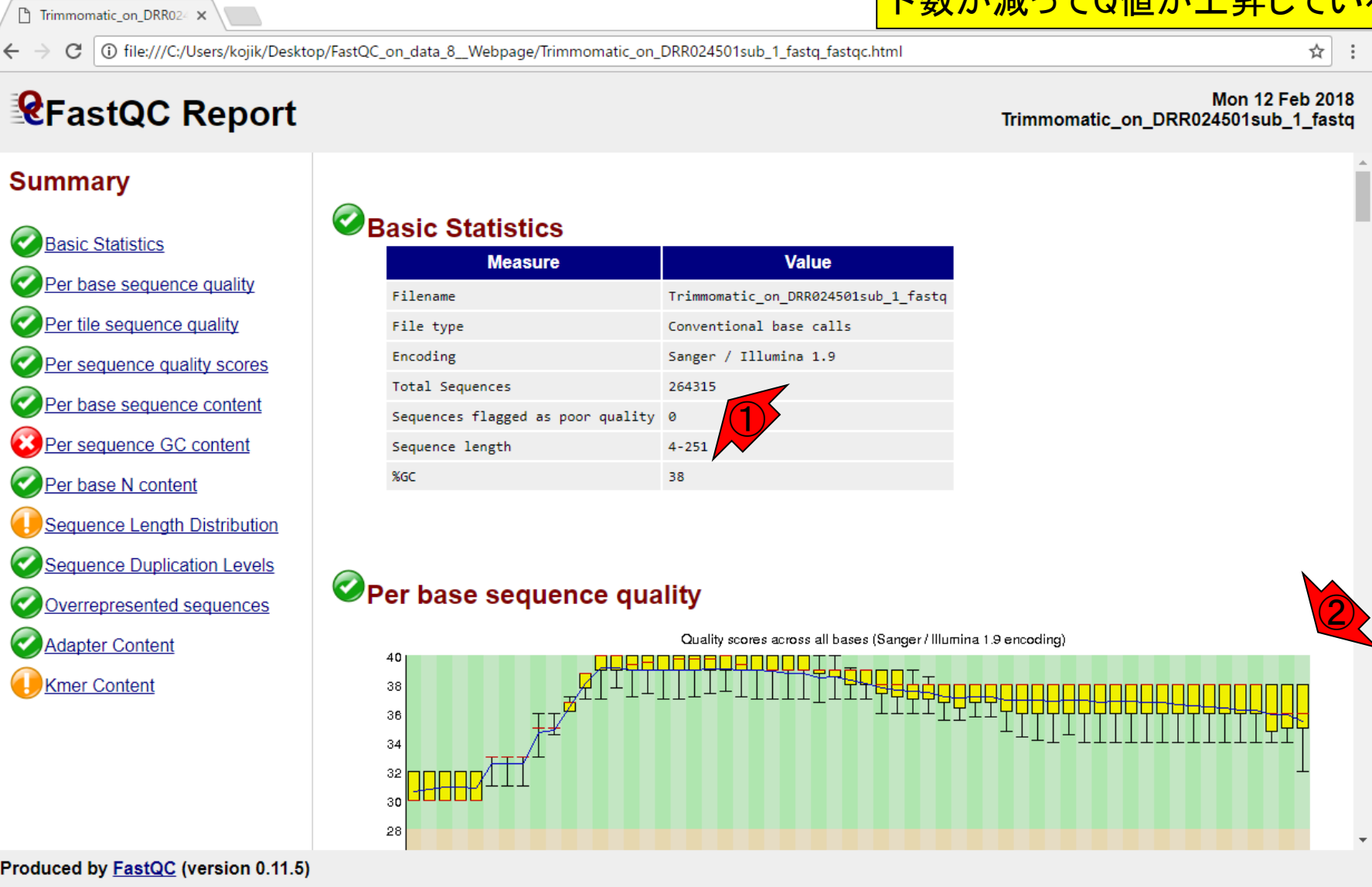
At the bottom, a red arrow labeled '①' points to a download notification for 'FastQC_on_data_8_....zip' in the browser's notification area.

W9-6: FastQC結果を眺める

The screenshot shows the Galaxy web interface with a green notification box stating: "1 job has been successfully added to the queue - resulting in the following datasets: 9: FastQC on data 8: Webpage, 10: FastQC on data 8: Raw...". Below this, instructions are provided: "You can check the status of queue data by refreshing the History panel...". A file explorer window is overlaid on the interface, showing the directory "FastQC_on_data_8_Webpage" with files like "Trimmomatic_on_DRR024501sub_1_fastq...", "FastQC_on_data_8_Webpage.html.html", and "rgFastQCcasgvs.log". A red arrow labeled "1" points to the HTML file. The Galaxy interface also shows a "Tools" sidebar on the left and a "History" panel on the right.

W9-6: FastQC結果を眺

①リード数は264315。②クオリティスコア(Q値)分布も確かに30以上のものばかり。デフォルトのFastQC実行結果(W6-7)よりもリード数が減ってQ値が上昇しているのが妥当



W10-1: 未ログインは機能限定

①ログインせずに、②History options、③Share or Publishをやろうとしても(W5-3)...

The screenshot shows the Galaxy web interface. At the top, there is a navigation bar with 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'Login or Register', and 'Using 9%'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (1)'. The main content area features a green success message: '1 job has been successfully added to the queue - resulting in the following datasets: 9: FastQC on data 8: Webpage, 10: FastQC on data 8: RawData. 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.' On the left, a 'Tools' sidebar lists various bioinformatics tools. On the right, the 'History' panel shows a list of datasets: 'imported: inudoshi_desu' (475.66 MB) and '10: FastQC on data 8: RawData' (267.5 KB). A 'History options' dropdown menu is open, showing 'HTML file' and 'HTML file' options. A red arrow labeled '1' points to the 'Login or Register' link, and another red arrow labeled '2' points to the 'History options' dropdown.

①Share or Publish
がありません(爆)

W10-1: 未ログインは機能限定

The screenshot shows the Galaxy web interface. At the top, there's a navigation bar with 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'Login or Register', and 'Using 9%'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. The main content area is divided into three panes. The left pane is 'Tools' with a search box and a list of tools like 'Trim Galore!', 'FastQC', 'multiqc', etc. The middle pane shows a green notification box with a checkmark: '1 job has been successfully added to the queue - resulting in the following datasets: 9: FastQC on data 8: Webpage, 10: FastQC on data 8: RawData. 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.' The right pane is 'History' showing a list of jobs. A context menu is open over the '10: FastQC on data 8: RawData' job, listing actions like 'CURRENT HISTORY', 'Show Structure', 'Delete', 'Delete Permanently', 'DATASET ACTIONS', 'Resume Paused Jobs', 'Unhide Hidden Datasets', 'Delete Hidden Datasets', 'Purge Deleted Datasets', 'Export Tool Citations', and 'Export History to File'. A red arrow with the number '1' points to this menu.

W11-1: ログイン

The screenshot shows the Galaxy web interface. At the top, there is a navigation bar with the Galaxy logo and menu items: Analyze Data, Workflow, Shared Data, Visualization, Help, and Login or Register. A dropdown menu is open under 'Login or Register', showing 'Login' and 'Register' options. Red arrows with circled numbers 1 and 2 point to the 'Login' option and the dropdown menu respectively. Below the navigation bar, a notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any bugs to the bug icon on error (red)'. In the center, a green notification box with a checkmark icon says: '1 job has been successfully added to the queue - resulting in the following datasets:'. It lists two datasets: '9: FastQC on data 8: Webpage' and '10: FastQC on data 8: RawData'. Below this, it provides instructions: '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.' On the right side, the 'History' pane shows a list of datasets. The top dataset is 'imported: inudoshi_desu' (475.66 MB). Below it are '10: FastQC on data 8: RawData' (267.5 KB) and '9: FastQC on data 8: Webpage' (267.5 KB). The bottom dataset is '8: Trimmomatic on DRR024501sub 1.f'. The left sidebar contains a 'Tools' section with various bioinformatics tools listed, such as 'Trim Galore!', 'FastQC', 'multiqc', 'Trimmomatic', 'Select high quality segments', 'Build base quality distribution', 'Draw quality score boxplot', 'Quality format converter', 'Filter by quality', 'Remove sequencing artifacts', 'Barcode Splitter', and 'Clip adapter sequences'. The browser address bar shows the URL: 'https://usegalaxy.org/?tool_id=toolshed.g2.bx.psu.edu%2Frepos%2Fdevteam%2Ffastqc%2F0.69&version=...'. The bottom status bar shows the URL: 'https://usegalaxy.org/user/login'.

W11-1:ログイン

The screenshot shows the Galaxy web interface. At the top, there is a navigation bar with 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'Login or Register', and a 'Using 9%' indicator. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. The main content area is divided into three sections: 'Tools' on the left, 'Login' in the center, and 'History' on the right. The 'Login' section is highlighted in yellow and contains a form with the following fields: 'Username / Email Address:' with the value 'kadota@iu.a.u-tokyo.ac.jp', 'Password:' with masked characters '.....', and a 'Login' button. A red arrow with the number '1' points to the 'Login' button. Below the 'Login' form is an 'OpenID Login' section with an 'OpenID URL:' field and a dropdown menu for 'GenomeSpace'. The 'History' panel on the right shows a list of datasets, including 'imported: inudoshi_desu' (475.66 MB) and '10: FastQC on data 8: RawData' (267.5 KB).

W11-2: ログイン直後

kadota_registeredさんのログイン直後の状態。こんな感じになります。これはkadota_unregisteredのW9-4までの結果と同じ。最新のkadota_registeredのヒストリーは、本来W6-1のような感じになっているべきと思うかもしれないが、そうではない

The screenshot shows the Galaxy web interface. The main content area displays the 'FastQC Read Quality reports (Galaxy Version 0.69)' tool interface. It includes sections for 'Short read data from your current history' (selected: 8: Trimmomatic on DRR024501sub_1.fastq...), 'Contaminant list' (selected: Nothing selected), and 'Submodule and Limit specifying file' (selected: Nothing selected). There is an 'Execute' button at the bottom of the tool interface. Below the tool interface, the 'Purpose' section explains that FastQC aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines.

The right-hand side of the interface shows the 'History' panel, which lists recent jobs. The top job is 'imported: inudoshi_desu' (9 shown, 475.66 MB). Below it are two jobs related to FastQC: '10: FastQC on data 8: RawData' (267.5 KB, format: html, database: ?) and '8: Trimmomatic on DRR024501sub_1.f'.

The left-hand side of the interface shows the 'Tools' panel with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, and NGS: Peak Calling.

W11-3: 以前のヒストリー

では以前のW6-1で見えていたヒストリーはどうなったのか?それは①のView all historiesを見ればわかる

The screenshot shows the Galaxy web interface. The main content area displays the configuration for the 'FastQC Read Quality reports' tool (Version 0.69). The tool is configured to process '8: Trimmomatic on DRR024501sub_1.fastq...'. The 'Contaminant list' and 'Submodule and Limit specifying file' are both set to 'Nothing selected'. The 'Execute' button is visible at the bottom of the tool configuration.

The right-hand panel shows the 'History' section. It contains a search bar for datasets and a list of recent jobs. The top job is 'imported: inudoshi_desu' (9 shown, 475.66 MB). Below it are two jobs related to FastQC: '10: FastQC on data 8: RawData' (267.5 KB) and '9: FastQC on data 8: Webpage' (267.5 KB). The '9: FastQC on data 8: Webpage' job is expanded, showing its output: 'Picked up _JAVA_OPTIONS: -Djava.io.tmpdir=/galaxy-repl/main/jobdir/018/363/183634 -Xmx7g -Xms256m'. Below this is the job '8: Trimmomatic on DRR024501sub_1.f...'. A red arrow points to the 'View all histories' button in the top right corner of the History panel.

At the bottom of the screenshot, the URL 'https://usegalaxy.org/history/view_multiple' is visible, and the text 'functions of FastQC are:' is partially shown.

W11-4: Histories

こんな感じになります。今は kadota_registered の環境です

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to

imported: inudoshi_desu
9 shown
475.66 MB

search datasets

Drag datasets here to copy them to the current history

10: FastQC on data 8: RawData

9: FastQC on data 8: Webpage
267.5 KB
format: **html**, database: ?

```
Picked up _JAVA_OPTIONS: -Djava.io.tmpdir=/galaxy-repl/main/jobdir/018/363/18363476/_job_tr -Xmx7g -Xms256m
```

HTML file

inudoshi_desu
6 shown, 1 deleted
348.45 MB

search datasets

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub 1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub 1.fastq

W11-4: Histories

The screenshot shows the Galaxy web interface with two history panels. The left panel, titled 'imported: inudoshi_desu', shows 9 datasets with a size of 475.66 MB. The right panel, titled 'inudoshi_desu', shows 6 datasets with a size of 348.45 MB. The right panel is highlighted with a red box, and a red arrow labeled '1' points to it. The right panel contains the following history items:

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W11-4: Histories

左側の①がW9-4までのヒストリーです。これはログインしていないkadota_unregisteredさんがやっていたヒストリーです。同じweb画面上でkadota_registeredさんがログインすると、そのヒストリーが取り込まれることがわかります

The screenshot shows the Galaxy web interface. The browser address bar is `https://usegalaxy.org/history/view_multiple`. The navigation bar includes "Galaxy", "Analyze Data", "Workflow", "Shared Data", "Visualization", "Help", "User", and "Using 0%". A notification banner states: "Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)".

The main content area is titled "Current History" and contains two panels. The left panel, outlined in red, shows a search bar with "search histories" and a red box with a circled "1" pointing to it. Below the search bar, it displays "imported: inudoshi_desu" with "9 shown" and "475.66 MB". A "search datasets" input field is present. Below this, it says "Drag datasets here to copy them to the current history". A list of history items is shown, including "10: FastQC on data 8: RawData ta", "9: FastQC on data 8: Webpage e", and a code block for Java options: `Picked up _JAVA_OPTIONS: -Djava.io.tmpdir=/galaxy-repl/main/jobdir/018/363/18363476/_job_tr -Xmx7g -Xms256m`. The right panel shows "inudoshi_desu" with "6 shown, 1 deleted" and "348.45 MB". It also has a "search datasets" input field and a list of history items: "7: FastQC on data 5: RawData", "6: FastQC on data 5: Webpage", "5: Trimmomatic on DRR024501sub 1.fastq", "4: FastQC on data 2: RawData", "3: FastQC on data 2: Webpage", and "2: DRR024501sub 1.fastq".

W11-4: Histories

こうなるのが嫌なら、ログイン前にW10-1の①ウェブブラウザまたは②タブを終了するなりしておけばよい(この画面はもうそうなっているので手遅れw)

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to

imported: inudoshi_desu
9 shown
475.66 MB

search datasets

Drag datasets here to copy them to the current history

10: FastQC on data 8: RawData

9: FastQC on data 8: Webpage
267.5 KB
format: **html**, database: ?

```
Picked up _JAVA_OPTIONS: -Djava.io.tmpdir=/galaxy-repl/main/jobdir/018/363/18363476/_job_tr-  
-Xmx7g -Xms256m
```

HTML file

inudoshi_desu
6 shown, 1 deleted
348.45 MB

search datasets

- 7: FastQC on data 5: RawData**
- 6: FastQC on data 5: Webpage**
- 5: Trimmomatic on DRR024501sub_1.fastq**
- 4: FastQC on data 2: RawData**
- 3: FastQC on data 2: Webpage**
- 2: DRR024501sub_1.fastq**

W11-5: ブラウザの再起動

①このように既に取り込まれている状態で、②を押してブラウザを再起動しても同じことになる

The screenshot shows a web browser window displaying the Galaxy interface. The address bar shows the URL https://usegalaxy.org/history/view_multiple. The page title is "Galaxy | Histories". The main content area is titled "Current History" and contains a list of datasets. A red box highlights the left-hand panel of the "Current History" section, which includes a search bar, a "search datasets" button, and a list of datasets. A red arrow labeled "1" points to the search bar. Another red arrow labeled "2" points to the refresh button in the browser's address bar.

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History

imported: inudoshi_desu
9 shown
475.66 MB

search datasets

Drag datasets here to copy them to the current history

10: FastQC on data 8: RawData
9: FastQC on data 8: Webpage
267.5 KB
format: **html**, database: ?
Picked up _JAVA_OPTIONS: -Djava.io.tmpdir=/galaxy-repl/main/jobdir/018/363/18363476/_job_t...-Xmx7g -Xms256m

HTML file

inudoshi_desu
6 shown, 1 deleted
348.45 MB

search datasets

7: FastQC on data 5: RawData
6: FastQC on data 5: Webpage
5: Trimmomatic on DRR024501sub 1.fastq
4: FastQC on data 2: RawData
3: FastQC on data 2: Webpage
2: DRR024501sub 1.fastq

W11-6: 再起動後の状態

一旦ブラウザを閉じて、再度Galaxy mainにログインした直後の状態。①
右側のヒストリーパネルが再起動前と同じであることがわかる

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)."

Below the welcome message is a "Want help? Get answers." banner for Biostars, with the text "GALAXY EXPLAINED" and a logo.

The right-hand side of the interface features a "History" panel. This panel is highlighted with a red border and a red arrow labeled "1". It contains a search bar for "search datasets" and a list of recent jobs:

- imported: inudoshi_desu (9 shown, 475.66 MB)
- 10: FastQC on data 8: RawData
- 9: FastQC on data 8: Webpage
- 8: Trimmomatic on DRR024501sub 1.f astq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub 1.f astq
- 4: FastQC on data 2:

The left-hand side of the interface shows a "Tools" panel with a search bar and a list of tool categories such as "Get Data", "Send Data", "Lift-Over", "Collection Operations", "Text Manipulation", "Datamash", "Convert Formats", "Filter and Sort", "Join, Subtract and Group", "Fetch Alignments/Sequences", "NGS: QC and manipulation", "NGS: DeepTools", "NGS: Mapping", "NGS: RNA Analysis", "NGS: SAMtools", "NGS: BamTools", "NGS: Picard", "NGS: VCF Manipulation", and "NGS: Peak Calling".

①確かにkadota_registered
さんです。ただの確認

W11-6: 再起動後の状態

The screenshot shows the Galaxy web interface. The browser address bar is `https://usegalaxy.org`. The user is logged in as `kadota@iu.a.u-tokyo.ac.jp`. The main content area features a banner for "Public Galaxy Servers and still counting" with a "080+" logo. The left sidebar contains a "Tools" section with a search bar and various tool categories. The right-hand panel displays a list of jobs, including "10: FastQC on data 8: RawData", "9: FastQC on data 8: Webpage", "8: Trimmomatic on DRR024501sub_1.f astq Q30", "7: FastQC on data 5: RawData", "6: FastQC on data 5: Webpage", "5: Trimmomatic on DRR024501sub_1.f astq", and "4: FastQC on data 2:". A red arrow points to the user's name in the top right corner.

W12-1 : Histories

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." Below this is a "Try Galaxy on the Cloud" banner.

The History panel on the right shows a list of datasets and jobs. The top job is "imported: inudoshi_desu" (9 shown, 475.66 MB). Below it are several "FastQC on data" jobs and "Trimmomatic" jobs. A red arrow points to the "View all histories" button in the History panel header.

The left sidebar contains a "Tools" section with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, and NGS: Peak Calling.

The browser address bar shows "https://usegalaxy.org". The status bar at the bottom of the browser shows "Using 0%".

W12-1: Histories

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to

imported: inudoshi_desu
9 shown
475.66 MB

search datasets

Drag datasets here to copy them to the current history

- 10: FastQC on data 8: RawData
- 9: FastQC on data 8: Webpage
- 8: Trimmomatic on DRR024501sub_1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData

inudoshi_desu
6 shown, 1 deleted
348.45 MB

search datasets

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W12-2: ヒストリーの削除

①を押すと、3つの選択肢が現れる。② Deleteはゴミ箱に入れると同じ。③Purgeはゴミ箱に入れて空にする。見るだけ

The screenshot shows the Galaxy web interface with a search bar and a list of history items. A context menu is open over the first item, showing 'Copy', 'Delete', and 'Purge' options. Red arrows point to these options and the 'Switch to' dropdown. The 'Delete' option is highlighted in yellow in the original image.

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to

imported: inudoshi_d Copy
9 shown Delete
475.66 MB Purge

search datasets

Drag datasets here to copy them to the current history

10: FastQC on data 8: RawData
9: FastQC on data 8: Webpage
8: Trimmomatic on DRR024501sub_1.fastq Q30
7: FastQC on data 5: RawData
6: FastQC on data 5: Webpage
5: Trimmomatic on DRR024501sub_1.fastq
4: FastQC on data 2: RawData

inudoshi_desu
6 shown, 1 deleted
348.45 MB

search datasets

7: FastQC on data 5: RawData
6: FastQC on data 5: Webpage
5: Trimmomatic on DRR024501sub_1.fastq
4: FastQC on data 2: RawData
3: FastQC on data 2: Webpage
2: DRR024501sub_1.fastq

W12-3: ヒストリーの切替

①を押すと、ここで見えている左右のヒストリーが切り替わります

The screenshot shows the Galaxy web interface. The browser address bar displays https://usegalaxy.org/history/view_multiple. The Galaxy navigation bar includes links for Analyze Data, Workflow, Shared Data, Visualization, Help, and User, along with a 'Using 0%' indicator. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. Below the notification, there are search bars for 'search histories' and 'search all datasets', and a 'Create new' button. The main content area is divided into two panels. The left panel, titled 'Current History', shows a list of datasets including 'imported: inudoshi_desu' (475.66 MB) and several 'FastQC on data' and 'Trimmomatic on DRR024501sub 1.fastq' entries. The right panel, titled 'Switch to', shows a list of datasets including 'inudoshi_desu' (348.45 MB) and several 'FastQC on data' and 'Trimmomatic on DRR024501sub 1.fastq' entries. A red arrow points to the 'Switch to' dropdown menu, which is labeled with a circled '1'.

W12-3: ヒストリーの切替

切替後の状態。①もう1回押すとまた切り替わる(がやらない)

The screenshot shows the Galaxy web interface with two history panels. The left panel is titled 'Current History' and shows a history for 'inudoshi_desu' with 6 items. The right panel is titled 'imported: inudoshi_desu' and shows a history with 9 items. A red arrow points to the 'Switch to' button between the panels, which has a circled '1' next to it. The interface includes a search bar, a navigation menu, and a notification banner at the top.

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to ①

inudoshi_desu
6 shown, 1 deleted
348.45 MB

search datasets

Drag datasets here to copy them to the current history

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub 1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub 1.fastq

imported: inudoshi_desu
9 shown
475.66 MB

search datasets

- 10: FastQC on data 8: RawData
- 9: FastQC on data 8: Webpage
- 8: Trimmomatic on DRR024501sub 1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub 1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub 1.fastq

W12-4: ヒストリーの反映

① Doneを押せば、赤枠内のCurrent Historyが反映されます(がここではやらない)

The screenshot shows the Galaxy web interface with two history panels. The left panel, titled "inudoshi_desu", is highlighted with a red border and contains a list of workflow steps: 2: DRR024501sub 1.fastq, 3: FastQC on data 2: Webpage, 4: FastQC on data 2: RawData, 5: Trimmomatic on DRR024501 sub 1.fastq, 6: FastQC on data 5: Webpage, and 7: FastQC on data 5: RawData. The right panel, titled "imported: inudoshi_desu", shows a similar list of steps: 2: DRR024501sub 1.fastq, 3: FastQC on data 2: Webpage, 4: FastQC on data 2: RawData, 5: Trimmomatic on DRR024501sub 1.fastq, 6: FastQC on data 5: Webpage, 7: FastQC on data 5: RawData, 8: Trimmomatic on DRR024501sub 1.fastq Q30, 9: FastQC on data 8: Webpage, and 10: FastQC on data 8: RawData. A red arrow points to the "Done" button in the top left of the interface.

W12-5: ヒストリーの新規作成

The screenshot shows the Galaxy web interface. The browser address bar displays https://usegalaxy.org/history/view_multiple. The Galaxy logo and navigation menu are visible at the top. A notification banner indicates a recent upgrade to version 18.01. Below the notification, there are search bars for 'search histories' and 'search all datasets'. A red arrow with the number '1' points to the 'Create new' button located in the top right corner of the interface.

Current History

inudoshi_desu
6 shown, 1 deleted
348.45 MB

imported: inudoshi_desu
9 shown
475.66 MB

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501 sub 1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub 1.fastq

10: FastQC on data 8: RawData

9: FastQC on data 8: Webpage

8: Trimmomatic on DRR024501sub 1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub 1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub 1.fastq

赤枠のように新規の履歴を作成することができます。①Done

W12-5: ヒストリーの新規作成

The screenshot shows the Galaxy web interface. The browser address bar is https://usegalaxy.org/history/view_multiple. The navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 0%'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. Below the navigation bar, there are search bars for 'search histories' and 'search all datasets'. The 'Current History' section is divided into three panels. The left panel, titled 'Unnamed history', is highlighted with a red border and contains the text '(empty)', a search bar, and a message 'This history is empty'. A red arrow points to the 'Done' button in the search bar. The middle panel, titled 'imported: inudoshi_desu', shows 9 datasets. The right panel, titled 'inudoshi_desu', shows 6 datasets, with 1 deleted. Each dataset entry includes a name, a small icon, and a delete button.

W12-6: 反映完了

①こんな感じで、新たな解析を行っていくこともできます

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', and 'NGS: Peak Calling'. The main content area features a text block: 'Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).' Below this is a logo for '080+' and the text 'Public Galaxy Servers and still counting'. The right sidebar shows a 'History' panel with a search bar, the title 'Unnamed history', and the status '(empty)'. A message box in the history panel reads: 'This history is empty. You can [load your own data](#) or [get data from an external source](#)'. A red arrow with the number '1' points to the history panel.

W12-7: Histories

The screenshot shows the Galaxy web interface. The main content area displays a welcome message and a list of tool categories on the left. The History panel on the right shows an empty history with a message: "This history is empty. You can load your own data or get data from an external source". A red arrow points to the "View all histories" button (a square icon with a red circle containing the number 1) in the History panel's header.

W12-7: Histories

①をカレントヒストリーに変更
したい場合は、②Switch to

The screenshot shows the Galaxy web interface with the following components:

- Browser:** Galaxy | Histories, URL: https://usegalaxy.org/history/view_multiple
- Navigation:** Analyze Data, Workflow, Shared Data, Visualization, Help, User, Using 0%
- Message:** Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01).
- Search:** Done, search histories, search all datasets, Create new
- Current History:** Unnamed history (empty)
- imported: inudoshi_desu:** 9 shown, 475.66 MB. List of jobs: 10: FastQC on data 8: RawData, 9: FastQC on data 8: Webpage, 8: Trimmomatic on DRR024501 sub 1.fastq Q30, 7: FastQC on data 5: RawData, 6: FastQC on data 5: Webpage, 5: Trimmomatic on DRR024501 sub 1.fastq, 4: FastQC on data 2: RawData, 3: FastQC on data 2: Webpage.
- inudoshi_desu:** 6 shown, 1 deleted, 348.45 MB. List of jobs: 7: FastQC on data 5: RawData, 6: FastQC on data 5: Webpage, 5: Trimmomatic on DRR024501 sub 1.fastq, 4: FastQC on data 2: RawData, 3: FastQC on data 2: Webpage, 2: DRR024501 sub 1.fastq.

Red arrows indicate the 'Switch to' button (②) and the 'inudoshi_desu' panel (①).

W12-7: Histories

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to

inudoshi_desu
6 shown, 1 deleted
348.45 MB
search datasets
Drag datasets here to copy them to the current history

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

Unnamed history Switch to

(empty)
search datasets
This history is empty

imported: inudoshi_desu
9 shown
475.66 MB
search datasets

- 10: FastQC on data 8: RawData
- 9: FastQC on data 8: Webpage
- 8: Trimmomatic on DRR024501 sub_1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage

W13-1: データのコピー

ここに、① Drag datasets here to copy them to the current historyと書いてあります。この部分に他のヒストリー内のデータをコピーすることができます

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History Switch to Switch to

inudoshi_desu
6 shown, 1 deleted
348.45 MB
search datasets
Drag datasets here to copy them to the current history

- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

Unnamed history
(empty)
search datasets
This history is empty

imported: inudoshi_desu
9 shown
475.66 MB
search datasets

- 10: FastQC on data 8: RawData
- 9: FastQC on data 8: Webpage
- 8: Trimmomatic on DRR024501 sub_1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage

W13-2: コピー前

例えば、①Trimmomatic実行後のFASTQファイルを赤矢印のような感じでドラッグ&ドロップすると…

The screenshot shows the Galaxy web interface with three history panels. The 'Current History' panel on the left contains a list of datasets, with a red dashed box around the text 'Drag datasets here to copy them to the current history'. The 'Unnamed history' panel in the center is empty. The 'imported: inudoshi_desu' panel on the right contains a list of datasets, with a red box around the entry '8: Trimmomatic on DRR024501 sub_1.fastq Q30' and a red arrow pointing to it with the number '1'.

History Panel	Dataset Name	Dataset ID
Current History (inudoshi_desu)	7: FastQC on data 5: RawData	7
	6: FastQC on data 5: Webpage	6
	5: Trimmomatic on DRR024501 sub_1.fastq	5
	4: FastQC on data 2: RawData	4
	3: FastQC on data 2: Webpage	3
	2: DRR024501sub_1.fastq	2
Unnamed history	(empty)	
imported: inudoshi_desu	10: FastQC on data 8: RawData	10
	9: FastQC on data 8: Webpage	9
	8: Trimmomatic on DRR024501 sub_1.fastq Q30	8
	7: FastQC on data 5: RawData	7
	6: FastQC on data 5: Webpage	6
	5: Trimmomatic on DRR024501 sub_1.fastq	5
	4: FastQC on data 2: RawData	4
	3: FastQC on data 2: Webpage	3

W13-3:コピー後

こんな感じでコピーすることができて、Trimmomaticをやったことにすることができる。
①ファイルサイズも増加していることがわかる

The screenshot displays the Galaxy web interface with three history panels. The left panel, titled 'inudoshi_desu', shows a list of jobs with a file size of 474.38 MB. A red arrow with the number '1' points to the file size. The middle panel, titled 'Unnamed history', is empty. The right panel, titled 'imported: inudoshi_desu', shows a list of jobs with a file size of 475.66 MB. The job list in the right panel is a duplicate of the left panel, but the top job, '8: Trimmomatic on DRR024501 sub_1.fastq Q30', is highlighted in green, indicating it is the current job. The interface includes a search bar, a 'Create new' button, and a notification about a Galaxy upgrade.

W13-4: 新規ヒストリーに切替え

The screenshot displays the Galaxy web interface. At the top, there is a navigation bar with 'Galaxy' and various menu items like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. Below this is a search bar with 'search histories' and 'search all datasets' options. The main content area is divided into three panels. The left panel, titled 'Current History', shows a list of workflows for user 'inudoshi_desu'. The middle panel, titled 'Unnamed history', is currently empty. The right panel, titled 'imported: inudoshi_desu', shows a list of workflows. A red arrow points to the 'Switch to' dropdown menu, which is currently set to 'Unnamed history'. A red circle with the number '1' is placed over the dropdown menu.

W13-5: コピー前

The screenshot shows the Galaxy web interface with three history panels. The 'Current History' panel on the left is empty and contains a text box that says 'Drag datasets here to copy them to the current history'. A red dashed box highlights this text box, and a red arrow points from it to the dataset '2: DRR024501sub_1.fastq' in the middle panel. This dataset is highlighted with a red box and a red arrow with the number '1' inside. The middle panel is titled 'inudoshi_desu' and contains a list of datasets. The right panel is titled 'imported: inudoshi_desu' and contains a list of datasets.

History Panel	Dataset Name	Dataset ID
Current History	(empty)	
inudoshi_desu	8: Trimmomatic on DRR024501sub_1.fastq Q30	8
inudoshi_desu	7: FastQC on data 5: RawData	7
inudoshi_desu	6: FastQC on data 5: Webpage	6
inudoshi_desu	5: Trimmomatic on DRR024501sub_1.fastq	5
inudoshi_desu	4: FastQC on data 2: RawData	4
inudoshi_desu	3: FastQC on data 2: Webpage	3
inudoshi_desu	2: DRR024501sub_1.fastq	2
imported: inudoshi_desu	10: FastQC on data 8: RawData	10
imported: inudoshi_desu	9: FastQC on data 8: Webpage	9
imported: inudoshi_desu	8: Trimmomatic on DRR024501sub_1.fastq Q30	8
imported: inudoshi_desu	7: FastQC on data 5: RawData	7
imported: inudoshi_desu	6: FastQC on data 5: Webpage	6
imported: inudoshi_desu	5: Trimmomatic on DRR024501sub_1.fastq	5
imported: inudoshi_desu	4: FastQC on data 2: RawData	4
imported: inudoshi_desu	3: FastQC on data 2: Webpage	3

W13-6:コピー中

ドラッグ&ドロップ中は、
こんな感じになるはず

The screenshot shows the Galaxy web interface with three history panels. The left panel is 'Unnamed history' and is empty. The middle panel is 'inudoshi_desu' and contains a list of workflow steps. The right panel is 'imported: inudoshi_desu' and also contains a list of workflow steps. A red arrow points from a dataset in the 'Current History' panel to a dataset in the 'inudoshi_desu' history panel, indicating a drag-and-drop operation.

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done search histories search all datasets Create new

Current History

Switch to

Switch to

Unnamed history

(empty)

search datasets

Drag datasets here to copy them to the current history

2: DRR024501sub 1.fastq

This history is empty

inudoshi_desu

7 shown, 1 deleted

474.38 MB

search datasets

8: Trimmomatic on DRR024501sub 1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub 1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub 1.fastq

imported: inudoshi_desu

9 shown

475.66 MB

search datasets

10: FastQC on data 8: RawData

9: FastQC on data 8: Webpage

8: Trimmomatic on DRR024501sub 1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub 1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

W13-7:コピー後

こんな感じになります。こうすることで、ファイルのアップロード作業を省略することができる。① Doneを押せば、②を入力として解析を始められる(がここではまだ①Doneしない)

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done ① search histories search all datasets Create new

Current History

Switch to Switch to

Unnamed history
1 shown
186.06 MB
search datasets
1: DRR024501sub_1.fastq ②

inudoshi_desu
7 shown, 1 deleted
474.38 MB
search datasets
8: Trimmomatic on DRR024501sub_1.fastq Q30
7: FastQC on data 5: RawData
6: FastQC on data 5: Webpage
5: Trimmomatic on DRR024501sub_1.fastq
4: FastQC on data 2: RawData
3: FastQC on data 2: Webpage
2: DRR024501sub_1.fastq

imported: inudoshi_desu
9 shown
475.66 MB
search datasets
10: FastQC on data 8: RawData
9: FastQC on data 8: Webpage
8: Trimmomatic on DRR024501sub_1.fastq Q30
7: FastQC on data 5: RawData
6: FastQC on data 5: Webpage
5: Trimmomatic on DRR024501sub_1.fastq
4: FastQC on data 2: RawData
3: FastQC on data 2: Webpage

W14-1 : inudoshi_desu

①ヒストリーinudoshi_desu
を利用すべく、②Switch to

The screenshot shows the Galaxy web interface with three history panels. The central panel, titled 'inudoshi_desu' (indicated by a red arrow labeled '1'), is selected. Above this panel, a red arrow labeled '2' points to the 'Switch to' button. The interface includes a search bar for datasets, a 'Create new' button, and a list of workflow steps for each history. The 'inudoshi_desu' history contains 7 steps, while the 'imported: inudoshi_desu' history contains 9 steps. The 'Current History' panel on the left shows 'Unnamed history' with 1 step.

W14-1 : inudoshi_desu

Galaxy | Histories

Secure | https://usegalaxy.org/history/view_multiple

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Done **①** Search histories search all datasets Create new

Current History Switch to Switch to

inudoshi_desu
7 shown, 1 deleted
474.38 MB

search datasets

Drag datasets here to copy them to the current history

- 8: Trimmomatic on DRR024501 sub 1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub 1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub 1.fastq

Unnamed history
1 shown
186.06 MB

search datasets

- 1: DRR024501sub 1.fastq

imported: inudoshi_desu
9 shown
475.66 MB

search datasets

- 10: FastQC on data 8: RawData
- 9: FastQC on data 8: Webpage
- 8: Trimmomatic on DRR024501 sub 1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501 sub 1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage

W14-2: inudoshi_desu

①無事inudoshi_desuが現在のHistoryに表示されています。②下にスクロール

The screenshot shows the Galaxy web interface. The main content area displays a tutorial titled "Running Your Own Understanding how Galaxy works". On the right, the "History" panel is open, showing a search for "inudoshi_desu" with 7 results. A red arrow labeled "1" points to the search bar. Another red arrow labeled "2" points to the scroll bar on the right side of the History panel, indicating that the user should scroll down to see more jobs.

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).

Running Your Own Understanding how Galaxy works

An in-depth tutorial

History

search datasets

inudoshi_desu
7 shown, 1 deleted
474.38 MB

- 8: Trimmomatic on DRR024501sub 1.f astq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub 1.f astq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub

W14-2: inudoshi_desu

①下にスクロール後。②これがIllumina MiSeqを用いて得られた30万リードからなるpaired-endデータのforward側ファイル

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." Below this is a "Try Galaxy on the Cloud" banner with the text "Now you can have a personal Galaxy within the infinite Universe".

The left sidebar contains a "Tools" section with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, and NGS: Peak Calling.

The right sidebar shows the "History" panel with a search bar and a list of datasets. The datasets are listed in descending order of size. The dataset "2: DRR024501sub_1.fastq" is highlighted with a red box and a red arrow labeled "2". The dataset "5: Trimmomatic on DRR024501sub_1.fastq" is also highlighted with a red box and a red arrow labeled "1".

Dataset Name	Size	Actions
7: FastQC on data 5: RawData	474.38 MB	View, Edit, Delete
6: FastQC on data 5: Webpage		View, Edit, Delete
5: Trimmomatic on DRR024501sub_1.fastq		View, Edit, Delete
4: FastQC on data 2: RawData		View, Edit, Delete
3: FastQC on data 2: Webpage		View, Edit, Delete
2: DRR024501sub_1.fastq		View, Edit, Delete

W14-3: ワークフローを抽出

The screenshot shows the Galaxy web interface. At the top, there is a navigation bar with 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on en'. On the right side of the notification, a red arrow with the number '1' points to a gear icon labeled 'History options'.

The main content area is divided into three sections:

- Tools:** A sidebar on the left with a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, and NGS: Peak Calling.
- Center:** A text block describing Galaxy as an open source, web-based platform for data intensive biomedical research. Below the text is a graphic with the text 'Try Galaxy on the Cloud' and 'Now you can have a personal Galaxy within the infinite Universe'.
- History:** A panel on the right showing a list of datasets and workflows. The top entry is 'inudoshi_desu' with 7 shown and 1 deleted. Below it are several workflow entries, each with a green background and icons for viewing, editing, and deleting:
 - 7: FastQC on data 5: RawData
 - 6: FastQC on data 5: Webpage
 - 5: Trimmomatic on DRR024501sub 1.f astq
 - 4: FastQC on data 2: RawData
 - 3: FastQC on data 2: Webpage
 - 2: DRR024501sub 1.fastq

The browser address bar at the bottom shows the URL: https://usegalaxy.org/root/history_options.

W14-3: ワークフローを抽出

①History options、②Extract Workflow(ワークフローを抽出)

The screenshot shows the Galaxy web interface. The browser address bar displays <https://usegalaxy.org>. The navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner at the top states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on en'. The left sidebar contains a 'Tools' section with a search bar and various tool categories like 'Get Data', 'Send Data', 'Lift-Over', etc. The main content area features a 'Try Galaxy on the Cloud' banner. On the right, the 'History' panel is open, showing a list of history items. A red arrow labeled '1' points to the history menu icon, and another red arrow labeled '2' points to the 'Extract Workflow' option in the dropdown menu.

W14-4: ワークフローを編集1

こんな画面になります。
①でワークフロー名を任意に変更できます

The screenshot shows the Galaxy web interface. The main content area displays a list of tools that were run to create datasets in the current history. The workflow name is set to "Workflow constructed from history 'inudoshi_desu'". A red arrow with the number 1 points to this text field. Below the workflow name are buttons for "Create Workflow", "Check all", and "Uncheck all".

Workflow name
Workflow constructed from history 'inudoshi_desu'

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

Tool	History items created
Upload File <i>This tool cannot be used in workflows</i>	2 DRR024501sub_1.fastq <input checked="" type="checkbox"/> Treat as input dataset DRR024501sub_1.fastq
FastQC <input checked="" type="checkbox"/> Include "FastQC" in workflow	3 FastQC on data 2: Webpage 4 FastQC on data 2: Raw Data
Trimmomatic	5 Trimmomatic on DRR0

The right sidebar shows the "History" panel with a search bar and a list of datasets. The top dataset is "inudoshi_desu" (7 shown, 1 deleted, 474.38 MB). Below it are several FastQC and Trimmomatic jobs on various data files.

W14-5: ワークフローを編集2

①ここが入力データ部分。とりあえずそのまま

The screenshot shows the Galaxy web interface. The main content area displays a list of tools used in the current history. A red box highlights the 'Upload File' tool, which is marked as 'This tool cannot be used in workflows'. The 'History' panel on the right shows a list of datasets, with the top one highlighted in green.

Tools

search tools

Get Data

Send Data

Lift-Over

Collection Operations

Text Manipulation

Datamash

Convert Formats

Filter and Sort

Join, Subtract and Group

Fetch Alignments/Sequences

NGS: QC and manipulation

NGS: DeepTools

NGS: Mapping

NGS: RNA Analysis

NGS: SAMtools

NGS: BamTools

NGS: Picard

NGS: VCF Manipulation

NGS: Peak Calling

The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

Workflow name

Workflow constructed from history 'inudoshi_desu'

Create Workflow Check all Uncheck all

Tool	History items created
Upload File <i>This tool cannot be used in workflows</i>	2 DRR024501sub_1.fastq <input checked="" type="checkbox"/> Treat as input dataset DRR024501sub_1.fastq
FastQC <input checked="" type="checkbox"/> Include "FastQC" in workflow	3 FastQC on data 2: Webpage 4 FastQC on data 2: Raw Data
Trimmomatic	5 Trimmomatic on DRR0

History

search datasets

inudoshi_desu
7 shown, 1 deleted
474.38 MB

DRR024501sub_1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub_1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub_1.fastq

①FastQC実行部分
。②下にスクロール

W14-6: ワークフローを編集3

The screenshot shows the Galaxy web interface for editing a workflow. The 'Tools' panel on the left lists various tools, with 'FastQC' selected and highlighted by a red box labeled '1'. The 'History' panel on the right shows a list of datasets, with 'DRR024501sub_1.fastq Q30' highlighted by a red arrow labeled '2'. The main panel shows the workflow construction options, including 'Workflow name', 'Create Workflow', 'Check all', and 'Uncheck all' buttons. Below these are columns for 'Tool' and 'History items created'. The 'FastQC' tool is listed with the option 'Include "FastQC" in workflow' checked. The 'History items created' column shows the following items:

Tool	History items created
Upload File	2 DRR024501sub_1.fastq Treat as input dataset DRR024501sub_1.fastq
FastQC	3 FastQC on data 2: Webpage 4 FastQC on data 2: Raw Data
Trimmomatic	5 Trimmomatic on DRR0

W14-7: ワークフローを編集4

一番下までスクロールした状態。①と②と④が同じ入力データ。③のみが②の実行結果を入力としている(ただのおさらい)。④についてはW8を参照

The screenshot displays the Galaxy web interface with a workflow editor. The workflow consists of four steps, each highlighted with a red box and a red arrow pointing to its tool configuration:

- Step 1:** Tool: FastQC. Input: DRR024501sub_1.fastq. Configuration: Treat as input dataset, Include "FastQC" in workflow. Output: 3 FastQC on data 2: Webpage.
- Step 2:** Tool: Trimmomatic. Input: DRR024501sub_1.fastq. Configuration: Include "Trimmomatic" in workflow. Output: 5 Trimmomatic on DRR024501sub_1.fastq.
- Step 3:** Tool: FastQC. Input: 5 Trimmomatic on DRR024501sub_1.fastq. Configuration: Include "FastQC" in workflow. Output: 6 FastQC on data 5: Webpage.
- Step 4:** Tool: Trimmomatic. Input: 6 FastQC on data 5: Webpage. Configuration: Include "Trimmomatic" in workflow. Output: 8 Trimmomatic on DRR024501sub_1.fastq Q30.

The History panel on the right shows the execution history of these steps, with the most recent step at the top. The history items are: 7: FastQC on data 5: RawData, 6: FastQC on data 5: Webpage, 5: Trimmomatic on DRR024501sub_1.fastq, 4: FastQC on data 2: RawData, 3: FastQC on data 2: Webpage, and 2: DRR024501sub_1.fastq.

W14-8: 自由に選択可能

①～④は、デフォルトでチェックが入っている。ワークフローは解析手順なので、⑤入力ファイルが含まれないのは当然

The screenshot displays the Galaxy web interface for configuring a workflow. The 'Tools' sidebar on the left lists various categories such as 'Get Data', 'Send Data', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', and 'NGS: Peak Calling'. The central workflow editor shows four tool configurations, each with a checkbox to 'Include [tool name] in workflow'. A red box highlights the 'Treat as input dataset' checkbox for the file 'DRR024501sub_1.fastq'. The 'History' panel on the right shows a sequence of steps: 2: DRR024501sub_1.fastq, 3: FastQC on data 2: Webpage, 4: FastQC on data 2: RawData, 5: Trimmomatic on DRR024501sub_1.fastq, 6: FastQC on data 5: Webpage, 7: FastQC on data 5: RawData, and 8: Trimmomatic on DRR024501sub_1.fastq Q30.

W14-8: 自由に選択可能

とりあえずここでは、①4ステップ目の平均クオリティスコアの閾値を30にしてTrimmomaticを実行する箇所を含めないようにして…、②上にスクロール

The screenshot shows the Galaxy web interface with the following elements:

- Tools Panel (Left):** Lists various tools including FastQC and Trimmomatic. A red arrow labeled '1' points to the Trimmomatic tool.
- Workflow Editor (Center):** Shows a sequence of steps. A red box highlights the 'Treat as input dataset' checkbox for the first step, '3 FastQC on data 2: Webpage'. Other steps include '4 FastQC on data 2: Raw Data', '5 Trimmomatic on DRR024501sub_1.fastq', '6 FastQC on data 5: Webpage', '7 FastQC on data 5: Raw Data', and '8 Trimmomatic on DRR024501sub_1.fastq Q30'. A red arrow labeled '2' points to the 'FastQC' step (step 4).
- History Panel (Right):** Shows a list of datasets and steps. The top dataset is 'inudoshi_desu'. Below it are several steps, including '7: FastQC on data 5: RawData', '6: FastQC on data 5: Webpage', '5: Trimmomatic on DRR024501sub_1.fastq', '4: FastQC on data 2: RawData', '3: FastQC on data 2: Webpage', and '2: DRR024501sub_1.fastq'.

W14-8: 自由に選択可能

①上にスクロール後。②入力ファイルを変更するので、このチェックも外す
(チェックの有無は大勢に影響しない)

The screenshot displays the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. The main content area is divided into three panels:

- Tools Panel (Left):** Contains a search bar and a list of tool categories: Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, and NGS: Peak Calling.
- Workflow Configuration Panel (Center):** Shows the workflow name 'Workflow constructed from history 'inudoshi_desu''. It includes buttons for 'Create Workflow', 'Check all', and 'Uncheck all'. Below is a table of tool selections:

Tool	History items created
Upload File <i>This tool cannot be used in workflows</i>	2 DRR024501sub_1.fastq <input checked="" type="checkbox"/> Treat as input dataset DRR024501sub_1.fastq
FastQC <input checked="" type="checkbox"/> Include "FastQC" in workflow	3 FastQC on data 2: Webpage 4 FastQC on data 2: Raw Data
Trimmomatic	5 Trimmomatic on DRR0

The 'History' panel (Right) shows a list of datasets and their associated tools:

- inudoshi_desu (7 shown, 1 deleted, 474.38 MB)
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W14-9: ワークフローの作成

①チェックを外して、②Create Workflowすると、③の名前のワークフローができる

The screenshot displays the Galaxy web interface for creating a workflow. The 'Tools' panel on the left lists various tools. The main area shows a list of 'History items created' with checkboxes to include or exclude them from the workflow. The 'Workflow name' field is set to 'Workflow constructed from history 'inudoshi_desu''. The 'History' panel on the right shows the sequence of tools used to create the datasets.

Workflow name: Workflow constructed from history 'inudoshi_desu'

Tools: Upload File, FastQC, Trimmomatic

History items created:

- 2 DRR024501sub_1.fastq (checkbox checked)
- 3 FastQC on data 2: Webpage (checkbox checked)
- 4 FastQC on data 2: Raw Data (checkbox checked)
- 5 Trimmomatic on DRR0 (checkbox checked)

History:

- inudoshi_desu (7 shown, 1 deleted)
- 474.38 MB
- DRR024501sub_1.fastq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.fastq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W14-10: 作成完了

こんな感じになります。中央パネルに、「現在のヒストリーをベースとしてワークフローを作成した。①編集したり②実行できる。」と書いてあることがわかる。見るだけ

The screenshot shows the Galaxy web interface. At the top, there is a navigation bar with 'Galaxy' logo and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. Below the navigation bar, there are three main panels. On the left is the 'Tools' panel with a search bar and a list of tool categories like 'Get Data', 'Send Data', etc. In the center is a light blue notification box with an information icon and the text: 'Workflow "Workflow constructed from history 'inudoshi_desu"' created from current history. You can edit or run the workflow.' Two red arrows with circled numbers point to the 'edit' and 'run' links. On the right is the 'History' panel with a search bar and a list of workflow steps, including '7: FastQC on data 5: RawData', '6: FastQC on data 5: Webpage', '5: Trimmomatic on DRR024501sub 1.f astq', '4: FastQC on data 2: RawData', '3: FastQC on data 2: Webpage', and '2: DRR024501sub 1.fastq'. The bottom status bar shows 'Waiting for usegalaxy.org...'

W15-1: ワークフロー概観

①Workflowでは、自分が作成したワークフローを眺めることができる。①をクリック

The screenshot displays the Galaxy web interface. The browser address bar shows <https://usegalaxy.org>. The navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner at the top states: 'Galaxy has recently been upgraded to a pre-release (18.01). Please report any issues you encounter using the bug icon on error (red)'. A red arrow points to the 'Workflow' tab. A central blue information box contains the text: 'Workflow "Workflow constructed from history 'inudoshi_desu"' created from current history. You can [edit](#) or [run](#) the workflow.' The left sidebar lists tool categories such as 'Get Data', 'Send Data', 'Text Manipulation', and 'NGS: QC and manipulation'. The right sidebar, titled 'History', shows a list of workflow steps for 'inudoshi_desu' (7 shown, 1 deleted, 474.38 MB). The steps are: 2: DRR024501sub 1.fastq, 3: FastQC on data 2: Webpage, 4: FastQC on data 2: RawData, 5: Trimmomatic on DRR024501sub 1.f astq, 6: FastQC on data 5: Webpage, 7: FastQC on data 5: RawData, and DRR024501sub 1.f astq Q30. The URL at the bottom is <https://usegalaxy.org/workflows/list>.

W15-2: Your workflows

①自分のワークフローは、今のところ
②さきほど作成したもののみ。ワークフ
ロー名がW14-9で最後に確認したもの
と同じで安心。③このワークフローは、
FastQC → Trimmomatic → FastQCの
3 stepから構成されているので妥当

The screenshot shows the Galaxy Workflows interface. On the left is a sidebar with tool categories. The main area is titled "Your workflows" and contains a table of workflows. A red arrow labeled "1" points to the "Your workflows" header. A red arrow labeled "2" points to the sidebar. A red arrow labeled "3" points to the "3" in the "# of Steps" column of the workflow table. The history panel on the right shows a list of datasets with their respective workflow steps highlighted in green.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input type="checkbox"/>

History panel content:

- inudoshi_desu (7 shown, 1 deleted)
- 474.38 MB
- DRR024501sub_1.f astq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.f astq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_1.fastq

W15-3: Show in tools panel

① Show in tools panelにチェックを入れると、②左側のToolsパネル上に、③このワークフローが表示されるようになる

The screenshot shows the Galaxy web interface. The 'Tools' sidebar on the left is highlighted with a red arrow labeled '2'. The 'Your workflows' section in the center contains a table with workflow information. A red arrow labeled '1' points to the 'Show in tools panel' checkbox in the table. A red arrow labeled '3' points to a workflow card in the table.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input type="checkbox"/>

The 'History' panel on the right shows a list of datasets, including 'inudoshi_desu' and 'DRR024501sub_1.f astq Q30'. The workflow card in the 'Your workflows' section is highlighted with a red arrow labeled '3'.

W15-3: Show in tools panel

①左側のToolsパネルのスクロールを一番下までもっていくと、②Workflowsが見られる

The screenshot shows the Galaxy Workflows interface. On the left is the 'Tools' panel with a search bar and a list of tool categories. A red arrow labeled '2' points to the 'Workflows' category. In the center is the 'Your workflows' section with a search bar and a table of workflows. A red arrow labeled '1' points to the scroll bar of the Tools panel. On the right is the 'History' panel showing a list of datasets.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input type="checkbox"/>

W15-4: Show in tools panel

①ここにチェックを入れると、数秒で画面が切り替わって…

The screenshot shows the Galaxy Workflows interface. The main content area is titled "Your workflows" and contains a table of workflows. The table has columns for Name, Tags, Owner, # of Steps, Published, and Show in tools panel. A workflow named "Workflow constructed from history 'inudoshi_desu'" is shown with 3 steps and is not published. The "Show in tools panel" checkbox for this workflow is checked, and a red arrow with the number 1 points to it.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>

The right sidebar shows the "History" panel for the workflow "inudoshi_desu", listing several steps with their names and actions (view, edit, delete).

W15-4: Show in tools pa

こんな感じになります。一見何も変化ないようだが…①Toolsパネルのスクロールを先程と同じく一番下までもっていくと

The screenshot shows the Galaxy Workflows interface. The main content area displays 'Your workflows' with a table of workflow entries. A red arrow labeled '1' points to the 'Show in tools panel' checkbox in the first row of the table. The right sidebar shows the 'History' panel with a list of workflow steps.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>

History panel content:

- 8: Trimmomatic on DRR024501sub 1.f astq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub 1.f astq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub

① Show in tools panelの意味が、②の結果から実感できます

W15-4: Show in tools panel

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner states: 'Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)'. The main content area is titled 'Your workflows' and contains a search bar and a table of workflows. A red arrow labeled '1' points to the 'Show in tools panel' checkbox in the table. The 'Tools' panel on the left has a search bar and a list of tool categories. A red arrow labeled '2' points to the 'Workflow constructed from history 'inudoshi_desu'' link in the 'Workflows' section. The 'History' panel on the right shows a list of datasets and workflow steps, including '8: Trimmomatic on DRR024501sub 1.f astq Q30', '7: FastQC on data 5: RawData', '6: FastQC on data 5: Webpage', '5: Trimmomatic on DRR024501sub 1.f astq', '4: FastQC on data 2: RawData', '3: FastQC on data 2: Webpage', and '2: DRR024501sub'.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>

W16-1: ワークフロー実行

入力データ情報はないはずですが(W14-9)、①のワークフローを、②Runしてみる

The screenshot shows the Galaxy Workflows page. The main content area is titled "Your workflows" and contains a table of workflows. A context menu is open over the first workflow, with the "Run" option highlighted. The right sidebar shows a history of datasets, with the top entry selected.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>

History:

- 8: Trimmomatic on DRR024501sub_1.f astq Q30
- 7: FastQC on data 5: RawData
- 6: FastQC on data 5: Webpage
- 5: Trimmomatic on DRR024501sub_1.f astq
- 4: FastQC on data 2: RawData
- 3: FastQC on data 2: Webpage
- 2: DRR024501sub_

W16-2: 全貌を把握1

この画面全体を見れば、いろいろとわかる。
。まず、1つ前のスライド上でRunを押しても、
ワークフローが実行されるわけではない

Galaxy

Secure | <https://usegalaxy.org/workflows/run?id=50fb074833eb9836>

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Tools

search tools

Get Data
Send Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling

Workflow: Workflow constructed from history 'inudoshi_desu'

Run workflow

History Options

Send results to a new history

Yes No

1: FastQC (Galaxy Version 0.69)

Short read data from your current history

8: Trimmomatic on DRR024501sub_1.fastq Q30

Contaminant list

Nothing selected

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer
CAAGCAGAAGACGGCATACGA

Submodule and Limit specifying file

Nothing selected

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

History

search datasets

inudoshi_desu
7 shown, 1 deleted
474.38 MB

8: Trimmomatic on DRR024501sub_1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub_1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub

W16-2: 全貌を把握2

(やらないが)もしこのままの状態①Run workflowを押すと、②で見えているものが入力として使われて、③新規履歴(new history)に結果が格納されていかないので、④(8まである)現在の履歴一上の9以降に結果が格納されていくであろうことが容易に想像できる。がそれは望むところではない

The screenshot shows the Galaxy web interface for a workflow named 'Workflow: Workflow constructed from history 'inudoshi_desu''. The interface includes a left sidebar with tool categories, a central workflow configuration area, and a right sidebar with a history list. Red arrows and numbers 1-4 highlight specific features: 1. The 'Run workflow' button. 2. The dropdown menu for 'Short read data from your current history' showing '8: Trimmomatic on DRR024501sub_1.fastq Q30'. 3. The 'Yes' button for the 'Send results to a new history' option. 4. The '8: Trimmomatic on DRR024501sub_1.fastq Q30' entry in the history list, which is highlighted in green.

W16-2: 全貌を把握3

①をクリックすると、右側のヒストリーパネル上にある利用可能な入力データが表示される。ワークフローを用いて解析したいのは、②forward側のデータではなく、reverse側のデータ

Galaxy

Secure | https://usegalaxy.org/workflows/run?id=50fb074833eb9836

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

Galaxy has recently been upgraded to a pre-release of the next Galaxy stable release (18.01). Please report any issues you encounter using the bug icon on error (red)

Tools

search tools

Get Data
Send Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling

Workflow: Workflow constructed from history 'inudoshi_desu'

Run workflow

History Options

Send results to a new history

Yes No

1: FastQC (Galaxy Version 0.69)

Short read data from your current history

8: Trimmomatic on DRR024501sub_1.fastq Q30

8: Trimmomatic on DRR024501sub_1.fastq Q30

5: Trimmomatic on DRR024501sub_1.fastq

2: DRR024501sub_1.fastq

2

Submodule and Limit specifying file

Nothing selected

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

History

search datasets

inudoshi_desu

7 shown, 1 deleted

474.38 MB

8: Trimmomatic on DRR024501sub_1.fastq Q30

7: FastQC on data 5: RawData

6: FastQC on data 5: Webpage

5: Trimmomatic on DRR024501sub_1.fastq

4: FastQC on data 2: RawData

3: FastQC on data 2: Webpage

2: DRR024501sub_1.fastq

1

W16-3: 最短手順

この状況からの最短手順は、①reverse側のデータ(DRR024501sub_2.fastq.gz)をアップロードして、②のところに「9: DRR024501sub_2.fastq」のように表示させれば、③で選択可能になる。ここでは新規ヒストリーを作成して、全体をスッキリさせた状態で行う

The screenshot shows the Galaxy web interface for a workflow named 'Workflow: Workflow' (ID: 50fb074833eb983). The interface includes a top navigation bar with 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A notification banner at the top indicates a recent update to Galaxy version 18.01. The main content area is divided into three sections: 'Tools', 'Workflow configuration', and 'History'.

Tools: A sidebar on the left lists various tool categories such as 'Get Data', 'Send Data', 'Text Manipulation', 'Filter and Sort', and 'NGS: QC and manipulation'. A red arrow labeled '1' points to the 'Tools' section.

Workflow configuration: The central area shows the configuration for the 'Workflow: Workflow' (ID: inudoshi_desu). It includes 'History Options' (Send results to a new history: Yes/No), 'Short read data from your current history' (a dropdown menu showing '8: Trimmomatic on DRR024501sub_1.fastq Q30'), and 'Contaminant list' (Nothing selected). A red arrow labeled '3' points to the dropdown menu.

History: The right sidebar shows the 'History' panel for 'inudoshi_desu' (7 shown, 1 deleted, 474.38 MB). It lists several workflow steps, including '8: Trimmomatic on DRR024501sub_1.fastq Q30', '7: FastQC on data 5: RawData', '6: FastQC on data 5: Webpage', '5: Trimmomatic on DRR024501sub_1.fastq', '4: FastQC on data 2: RawData', '3: FastQC on data 2: Webpage', and '2: DRR024501sub'. A red arrow labeled '2' points to the '8: Trimmomatic on DRR024501sub_1.fastq Q30' step.

新規履歴を作成すべく、①History options

W17-1: 新規履歴の作成

The screenshot shows the Galaxy web interface. The main content area displays a tutorial banner for "Running Your Own Galaxy" with the subtitle "Understanding how Galaxy works" and "An in-depth tutorial". The left sidebar contains a "Tools" panel with a search bar and various tool categories like "Get Data", "Send Data", "Text Manipulation", etc. The right sidebar shows the "History" panel, which lists datasets and workflows. A red arrow with the number "1" points to the "History options" button in the top right of the History panel. The URL in the browser is <https://usegalaxy.org>.

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).

Running Your Own Galaxy

Understanding how Galaxy works

An in-depth tutorial

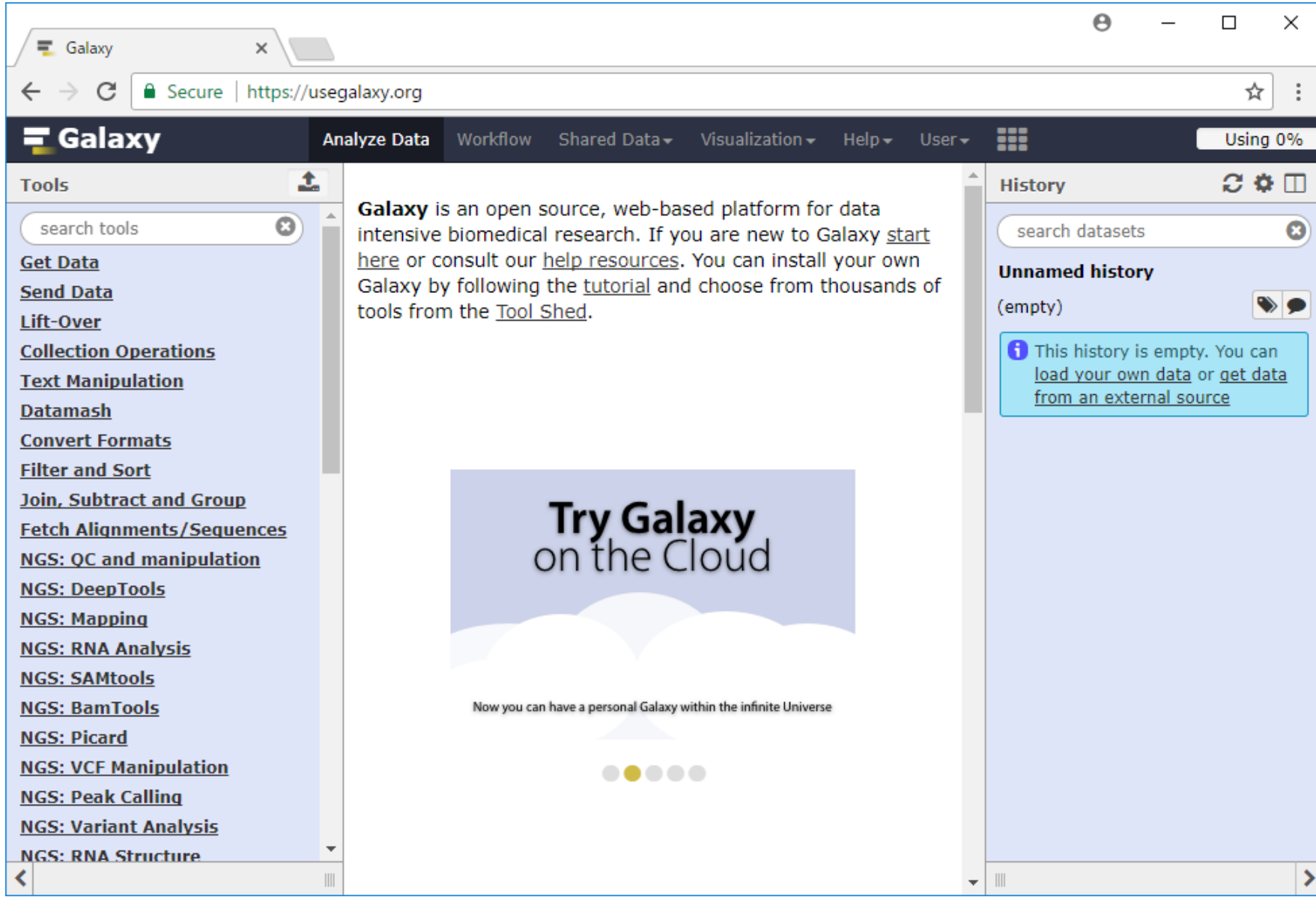
History options

Dataset/Workflow Name	Size	Actions
inudoshi_desu	474.38 MB	✓, ↵, 💬
8: Trimmomatic on DR R024501sub_1.fastq Q30		👁, ✎, ✕
7: FastQC on data 5: RawData		👁, ✎, ✕
6: FastQC on data 5: Webpage		👁, ✎, ✕
5: Trimmomatic on DR R024501sub_1.fastq		👁, ✎, ✕
4: FastQC on data 2: RawData		👁, ✎, ✕
3: FastQC on data 2: Webpage		👁, ✎, ✕
2: DRR024501sub_1.fastq		👁, ✎, ✕

W17-1: 新規ヒストリーの作成

The screenshot shows the Galaxy web interface. The main content area displays a tutorial titled "Running Your Own Understanding how Galaxy works" with the subtitle "An in-depth tutorial". On the right side, the "History" panel is open, showing a list of actions. The "Create New" option is highlighted with a red arrow and a circled number 1. The "Tools" panel on the left contains a search bar and various tool categories like "Get Data", "Send Data", "Collection Operations", etc.

W17-2: 新規ヒストリー作成後



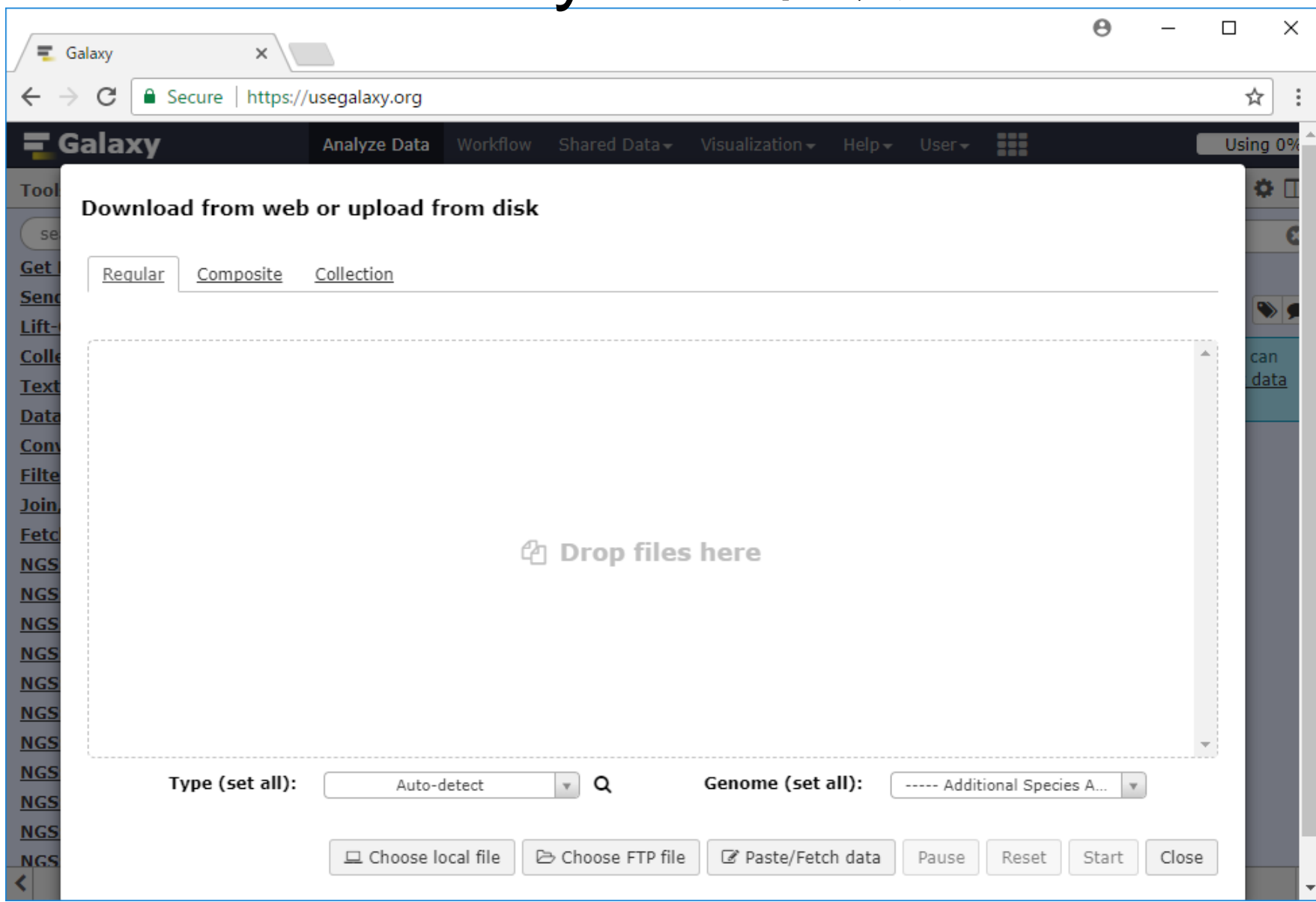
W17-3: Galaxyへの取り込み

reverse側のファイルをGalaxyに取り込みます(第11回W5-3ではアップロードと書いていますが、ここでは違うやり方を示すため表現を変えています)

The screenshot shows the Galaxy web interface. The browser address bar displays 'https://usegalaxy.org'. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A red arrow with the number '1' points to the 'Tools' menu icon. A tooltip with the text 'Download from URL or upload files from disk' is visible over the 'Tools' menu. The left sidebar lists various tool categories such as 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', 'NGS: Variant Analysis', and 'NGS: RNA Structure'. The main content area features a 'Try Galaxy on the Cloud' banner with the text 'Now you can have a personal Galaxy within the infinite Universe'. The right sidebar shows the 'History' panel, which is currently empty and contains a message: 'This history is empty. You can load your own data or get data from an external source'.

この画面は、第11回W5-3で示したforward側のファイルのアップロード時の画面と同じ

W17-3: Galaxyへの取り込み



W17-3: Galaxyへの取

第11回W5-3では、ローカル環境(自分のPC内)にあるforward側のファイルのアップロードだったので、①upload from diskのほうを行いました。ここでは、②Download from webを行います

Galaxy

Secure | https://usegalaxy.org

Galaxy Analyze Data Workflow Shared Data Visualization Help User

Using 0%

Download from web or upload from disk

Regular Composite Collection

Drop files here

Type (set all): Auto-detect Q Genome (set all): ----- Additional Species A...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

W17-3: Galaxyへの取り込み

The screenshot shows the Galaxy web interface. A dialog box titled "Download from web or upload from disk" is open. It has three tabs: "Regular", "Composite", and "Collection". The "Regular" tab is selected. In the center of the dialog is a large dashed box with the text "Drop files here". Below this box are two dropdown menus: "Type (set all):" with "Auto-detect" selected, and "Genome (set all):" with "----- Additional Species A..." selected. At the bottom of the dialog are several buttons: "Choose local file", "Choose FTP file", "Paste/Fetch data", "Pause", "Reset", "Start", and "Close". A red arrow with the number "1" inside points to the "Paste/Fetch data" button.

W17-4:ダウンロード

Galaxy

Secure | https://usegalaxy.org

Galaxy Analyze Data Workflow Shared Data Visualization Help User

Download from web or upload from disk

Regular Composite Collection

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

Name	Size	Type	Genome	Settings	Status
New File	-	Auto-dete...	----- Additional Sp...		0%

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

Type (set all): Auto-detect Genome (set all): ----- Additional Species A...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

W17-4: ダウンロード

①ボックス内にダウンロードしたいファイルのURL情報を示せ、と書いてあります

The screenshot shows the Galaxy web interface with the 'Download from web or upload from disk' dialog box open. The dialog has three tabs: 'Regular', 'Composite', and 'Collection'. Below the tabs, it says 'You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.' There is a table with columns: Name, Size, Type, Genome, Settings, and Status. The first row is 'New File' with a size of '-', type 'Auto-dete...', genome '----- Additional Sp...', and status '0%'. Below the table is a text input field with the instruction: 'You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.' A red arrow with the number '1' points to this input field. At the bottom of the dialog, there are buttons for 'Choose local file', 'Choose FTP file', 'Paste/Fetch data', 'Pause', 'Reset', 'Start', and 'Close'.

Name	Size	Type	Genome	Settings	Status
New File	-	Auto-dete...	----- Additional Sp...	⚙️	0%

reverse側のデータ(DRR024501sub_2.fastq.gz)のURL情報は、①ここで得られます

W17-5: URL

The screenshot shows a web browser window displaying a document page. The page title is "書籍 | 日本乳酸菌学会誌 | 第12回Galaxy: ヒストリーとワークフロー NEW". The page content includes a list of links and a section titled "ワークフローの実行" (Workflow Execution). A red box highlights the "ワークフローの実行" section in the main content, and a red arrow points from this box to a larger callout box on the right. The callout box contains the following text:

ワークフローの実行

- W16-2: 30万リードからなるpaired-endのreverse側のgzip圧縮FASTQファイル ([DRR024501sub_2.fastq.gz](http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz)) 連載第6回のW4-1で見えているファイルサイズと同じく、61.9 MB (64,968,861 バイト)です。

① http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz

W17-6: URLのコピー

書籍 | 日本乳酸菌学会誌 | 第12回Galaxy: ヒストリーとワークフロー NEW

日本乳酸菌学会誌の第12回分です。

- 原稿PDF
- ウェブ資料PDF
 - Windows用
 - Macintosh用...

はじめに

- Afzari et al., *Nucleic Acids Res.*, 2016
- W1: [BioStar](#)のGalaxy版でみられるQuestion: Best Browser for Galaxy?
- W2: [Galaxy main](#)
- 登場人物
 - kadota_registered
 - terada_registered
 - kadota_unregistered

履歴の共有

- W3-1: 30万リードからなるpaired-endのforward側の連続第6回のW4-1で見えているファイルサイズと同じく、61.9 MB (64,968,861 バイト)です。
- W4-4: [Published Histories](#)
- W6-2: [ヒストリー: amadoshi_dess@URL](#)
- W8-2: [Trimomatic: Bolger et al., Bioinformatics, 2014](#)
- W9-1: [FastQC: 原著論文なし](#)
- W9-6: [FastQC実行結果ファイル \(FastQC on data\)](#)

履歴の操作

- W13-7: 30万リードからなるpaired-endのforward側の連続第6回のW4-1で見えているファイルサイズと同じく、61.9 MB (64,968,861 バイト)です。

ワークフローの作成

- [乳酸菌NGS連載第6回のPDF](#)
- 連載第6回のウェブ資料PDF(約20MB)のW3-2
- [乳酸菌NGS連載第11回のPDF](#)

pt167の右下あたりに「作業の流れ」と書いてあります。

ワークフローの実行

- W16-2: 30万リードからなるpaired-endのreverse側のgzip圧縮FASTQファイル ([DRR024501sub_2.fastq.gz](http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz))
連続第6回のW4-1で見えているファイルサイズと同じく、61.9 MB (64,968,861 バイト)です。
http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz

ワークフローの実行

- W16-2: 30万リードからなるpaired-endのreverse側のgzip圧縮FASTQファイル ([DRR024501sub_2.fastq.gz](http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz))
連続第6回のW4-1で見えているファイルサイズと同じく、61.9 MB (64,968,861 バイト)です。
http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz

切り取り(T)

コピー(C) ①

貼り付け

W17-6: URLのコピペ

The screenshot shows the Galaxy web interface. The browser address bar displays 'https://usegalaxy.org'. The main navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The central dialog box is titled 'Download from web or upload from disk' and has three tabs: 'Regular', 'Composite', and 'Collection'. Below the tabs, it says 'You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.' A table with columns 'Name', 'Size', 'Type', 'Genome', 'Settings', and 'Status' is shown. The first row is for a 'New File' with a size of '76 b'. Below the table, there is a text input field containing the URL 'http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz'. A red arrow with the number '1' points to this input field. At the bottom of the dialog, there are buttons for 'Choose local file', 'Choose FTP file', 'Paste/Fetch data', 'Pause', 'Reset', 'Start', and 'Close'.

W17-6: URLのコピペ

Galaxy

Secure | <https://usegalaxy.org>

Galaxy Analyze Data Workflow Shared Data Visualization Help User

Download from web or upload from disk

Regular Composite Collection

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

Name	Size	Type	Genome	Settings	Status
New File	76 b	Auto-dete...	----- Additional Sp...		0%

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

`http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz`

Type (set all): Auto-detect Genome (set all): ----- Additional Species A...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

W17-7:ダウンロード(DL)中...

Download from web or upload from disk

Regular Composite Collection

Please wait...1 out of 1 remaining.

Name	Size	Type	Genome	Settings	Status
New File	76 b	Auto-dete...	----- Additional Sp...	⚙	Adding to history...

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

```
http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz
```

Type (set all): Auto-detect Genome (set all): ----- Additional Species A...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

W17-8: DL終了したっぽい

The screenshot shows the Galaxy web interface with a modal window titled "Download from web or upload from disk". The modal has three tabs: "Regular", "Composite", and "Collection". The "Regular" tab is active. Below the tabs is a table with columns: Name, Size, Type, Genome, Settings, and Status. A single row is visible, representing a "New File" with a size of "76 b", type "Auto-dete...", genome "---- Additional Sp...", and a status of "100%". Below the table is a text input field containing the URL "http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz". At the bottom of the modal, there are two dropdown menus for "Type (set all):" (set to "Auto-detect") and "Genome (set all):" (set to "---- Additional Species A..."). Below these are several buttons: "Choose local file", "Choose FTP file", "Paste/Fetch data", "Pause", "Reset", "Start", and "Close". A red arrow with the number "1" points to the "Close" button.

Name	Size	Type	Genome	Settings	Status
New File	76 b	Auto-dete...	---- Additional Sp...		100%

W17-9: 下準備ほぼ完了

①ダウンロードしたURL情報が完全な形で見えている。長いのでファイル名のみにしておく

The screenshot shows the Galaxy web interface. The main content area displays a message about Galaxy being an open source platform for data intensive biomedical research. Below this is a logo for '080+' and the text 'Public Galaxy Servers and still counting'. On the right side, the 'History' panel shows a list of datasets. One entry is highlighted in green and contains a long URL: '1: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq'. A red arrow with the number '1' points to this entry, indicating the focus of the annotation.

W17-10: 名前の変更1

The screenshot shows the Galaxy web interface. The main content area displays a tutorial titled "Running Your Own Understanding how Galaxy works" with the subtitle "An in-depth tutorial". The left sidebar contains a "Tools" panel with a search bar and various tool categories. The right sidebar shows a "History" panel with a search bar and a list of datasets. One dataset is highlighted in green, and a red arrow with the number "1" points to the "Edit attributes" button next to it.

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).

Running Your Own Understanding how Galaxy works
An in-depth tutorial

History

search datasets

Unnamed history
1 shown

186.06 MB

1: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501_b_2.fastq Edit attributes

https://usegalaxy.org/datasets/edit?dataset_id=bbd44e69cb8906b568cd6098db711297

W17-10: 名前の変更2

The screenshot shows the Galaxy web interface. The main content area is titled "Edit dataset attributes" and contains several sections: "Attributes" (with sub-sections for Convert, Datatypes, and Permissions), "Edit attributes" (with "Auto-detect" and "Save" buttons), "Name" (with a text input field containing a URL), "Info" (with a text area containing "uploaded fastqsanger file"), "Annotation" (with a text area and a note about annotations), and "Database/Build" (with a dropdown menu set to "unspecified (?)").

On the right side, there is a "History" panel showing "Unnamed history" with "1 shown" and a size of "186.06 MB". A single history entry is visible, highlighted in green, with a red circle and the number "1" pointing to its name: "1: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq".

The left sidebar contains a "Tools" panel with a search bar and various tool categories like "Get Data", "Send Data", "Text Manipulation", etc.

W17-10: 名前の変更3

The screenshot shows the Galaxy web interface for editing dataset attributes. The browser address bar shows the URL: https://usegalaxy.org/datasets/edit?dataset_id=bbd44e69cb8906b568cd6098db711297&_identifier=2s9xgtbtti9. The main content area is titled "Edit dataset attributes" and has tabs for "Attributes", "Convert", "Datatypes", and "Permissions". The "Attributes" tab is active, showing a form for "Edit attributes" with a "Save" button. The "Name" field contains the text "DRR024501sub_2.fastq". A red arrow labeled "1" points to the text in the "Name" field, and another red arrow labeled "2" points to the "Save" button. The "Info" field contains the text "uploaded fastqsanger file". The "Annotation" field is empty. The "Database/Build" dropdown menu is set to "unspecified (?)". On the right side, the "History" panel shows a list of datasets. The first dataset is highlighted in green and has a red arrow labeled "1" pointing to its name: "1: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq".

W17-10: 名前の変更4

①Attributes updatedとなり、②の部分(これがAttributes)も反映されています

The screenshot displays the Galaxy web interface for editing dataset attributes. The main content area is titled "Edit dataset attributes" and features a green notification bar at the top stating "Attributes updated." with a red arrow labeled "1" pointing to it. Below the notification, there are tabs for "Attributes", "Convert", "Datatypes", and "Permissions". The "Attributes" tab is active, showing a form with the following fields:

- Name:** DRR024501sub_2.fastq
- Info:** uploaded fastqsanger file
- Annotation:** (empty text area)
- Database/Build:** unspecified (?)

On the right side, the "History" panel shows a search bar and a list of datasets. The first entry, "1: DRR024501sub_2.fastq", is highlighted in green, with a red arrow labeled "2" pointing to it. The interface also includes a left sidebar with various tool categories and a top navigation bar with options like "Analyze Data", "Workflow", and "Shared Data".

①左側のツールパネル
を下にスクロールして…

W18-1: ワークフロー実行1

The screenshot displays the Galaxy web interface. The main content area is titled "Edit dataset attributes" and shows a green notification "Attributes updated." Below this, there are tabs for "Attributes", "Convert", "Datatypes", and "Permissions". The "Attributes" tab is active, showing a form with the following fields:

- Name:** DRR024501sub_2.fastq
- Info:** uploaded fastqsanger file
- Annotation:** (empty text area)
- Database/Build:** unspecified (?)

Buttons for "Auto-detect" and "Save" are visible. On the left side, the "Tools" panel is visible, with a red arrow and the number "1" pointing to it. The "History" panel on the right shows a list of datasets, with the first one highlighted in green: "1: DRR024501sub_2.fastq".

W18-1: ワークフロー実行2

The screenshot shows the Galaxy web interface. The main content area is titled "Edit dataset attributes" and displays a green notification "Attributes updated." Below this, there are tabs for "Attributes", "Convert", "Datatypes", and "Permissions". The "Attributes" tab is active, showing fields for "Name" (DRR024501sub_2.fastq), "Info" (uploaded fastqsanger file), "Annotation", and "Database/Build" (unspecified (?)).

The left-hand sidebar contains a "Tools" section with a search bar and a list of tool categories. A red arrow with the number 1 points to the "Workflow constructed from history 'inudoshi_desu'" option under the "Workflows" category.

The right-hand sidebar shows the "History" section with a search bar and a list of datasets. The first dataset is "1: DRR024501sub_2.fastq" with a size of 186.06 MB.

W18-2: 中央パネル

こんな感じになります。ヒストリーの異なるW16-2と違って、①で見えているものが、②のみになっていてステキです

The screenshot displays the Galaxy web interface for a workflow named "Workflow: Workflow constructed from history 'inudoshi_desu'". The interface is divided into several panels:

- Tools Panel (Left):** A sidebar with a search bar and a list of tool categories including "Get Data", "Send Data", "Text Manipulation", "NGS: QC and manipulation", etc.
- Workflow Configuration Panel (Center):** A dashed box highlights the "History Options" section, which includes:
 - Send results to a new history:** Radio buttons for "Yes" and "No".
 - 1: FastQC (Galaxy Version 0.69):** A dropdown menu showing "1: DRR024501sub_2.fastq" (marked with a red arrow ①).
 - Contaminant list:** A dropdown menu showing "Nothing selected".
 - Submodule and Limit specifying file:** A dropdown menu showing "Nothing selected".
- History Panel (Right):** A panel titled "History" showing a search bar and a list of datasets. The first item is "1: DRR024501sub_2.fastq" (marked with a red arrow ②), which is highlighted in green.

W18-3: History Options

①新規ヒストリーを作る必要がないので、デフォルトの②Noのままでよい

The screenshot shows the Galaxy web interface for a workflow named 'Workflow: Workflow constructed from history 'inudoshi_desu''. The 'History Options' section is highlighted with a red box and a red arrow labeled '1'. This section contains the option 'Send results to a new history' with 'Yes' and 'No' buttons. A red arrow labeled '2' points to the 'No' button. Below this, the workflow is identified as 'I: C (Galaxy Version 0.69)'. The 'Short read data from your current history' section shows a dropdown menu with '1: DRR024501sub_2.fastq'. The 'Contaminant list' section shows 'Nothing selected'. The 'Submodule and Limit specifying file' section also shows 'Nothing selected'. On the right side, the 'History' panel shows an 'Unnamed history' with 1 shown, 186.06 MB, and a dataset '1: DRR024501sub_2.fastq'.

W18-4: Step1

(計3ステップからなるワークフローの) Step1である①FastQCの、②入力ファイルは、③でよい

The screenshot displays the Galaxy web interface for configuring a workflow step. The main panel is titled "Workflow: Workflow constructed from history 'inudoshi_desu'". A red box highlights the configuration for step "1: FastQC (Galaxy Version 0.69)".

- ①** Points to the "Tools" sidebar on the left, specifically to the "FastQC" tool.
- ②** Points to the "Short read data from your current history" dropdown menu, which is set to "1: DRR024501sub_2.fastq".
- ③** Points to the "Run workflow" button at the top right of the configuration panel.

The "History Options" section includes a "Send results to a new history" toggle set to "No". The "Contaminant list" and "Submodule and Limit specifying file" sections are currently set to "Nothing selected".

The right sidebar shows the "History" panel with an "Unnamed history" containing one dataset: "1: DRR024501sub_2.fastq".

W18-5: Step2

①中央パネル上で下にスクロールして、② Step2であるTrimmomaticのところを表示

The screenshot displays the Galaxy web interface. The main panel shows a workflow step configuration for '2: Trimmomatic (Galaxy Version 0.36.3)'. The configuration includes the following options:

- Single-end or paired-end reads?: Single-end
- Input FASTQ file: 1: DRR024501sub_2.fastq
- Perform initial ILLUMINACLIP step?: true
- Adapter sequences to use: TruSeq3 (single-ended, for MiSeq and HiSeq)
- Maximum mismatch count which will still allow a full match to be performed: 2
- How accurate the match between the two 'adapter ligated' reads must be for PE palindrome read alignment: 30
- How accurate the match between any adapter etc.

Two red arrows with numbers indicate the steps described in the text: Arrow ① points to the scroll bar on the right side of the workflow step configuration, and Arrow ② points to the step title '2: Trimmomatic (Galaxy Version 0.36.3)'.

W18-5: Step2

ここの①入力ファイルも、②でよい。③アダプター除去用として指定したTruSeq3も、第11回W12-2で指定したものがそのまま残っていますね

The screenshot displays the Galaxy web interface for a workflow titled "Workflow: Workflow constructed from history 'inudoshi_desu'". The workflow step "2: Trimmomatic (Galaxy Version 0.36.3)" is highlighted with a red dashed box. The configuration for this step is as follows:

- Single-end or paired-end reads?: Single-end
- Input FASTQ file: 1: DRR024501sub_2.fastq (marked with ①)
- Perform initial ILLUMINACLIP step?: true (marked with ②)
- Adapter sequences to use: TruSeq3 (single-ended, for MiSeq and HiSeq) (marked with ③)
- Maximum mismatch count which will still allow a full match to be performed: 2
- How accurate the match between the two 'adapter ligated' reads must be for PE palindrome read alignment: 30
- How accurate the match between any adapter etc. (checkbox checked)

The right sidebar shows the "History" panel with "Unnamed history" containing 1 dataset: "1: DRR024501sub_2.fastq" (186.06 MB).

W18-5: Step2

①またちょっと下にスクロール。②アダプター配列以外のオプションは当時は変更していないので、②このワークフロー中でのTrimmomaticの、③Average quality requiredの閾値はデフォルトの20です

Galaxy

Secure | https://usegalaxy.org/workflows/run?id=50fb074833eb9836

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

Tools

search tools

Get Data
Send Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling
NGS: Variant Analysis
NGS: RNA Structure

Workflow: Workflow constructed from history mudoshi_desu

Run workflow

How accurate the match between the two 'adapter ligated' reads must be for PE palindrome read alignment

30

How accurate the match between any adapter etc. sequence must be against a read

10

Trimmomatic Operation

1: Trimmomatic Operation

Select Trimmomatic operation to perform

Sliding window trimming (SLIDINGWINDOW)

Number of bases to average across

4

Average quality required

20

3: FastQC (Galaxy Version 0.69)

History

search datasets

Unnamed history

1 shown

186.06 MB

1: DRR024501sub_2.f astq

W18-6: Step3

①一番下までスクロール。②Step3は、Step2実行結果ファイルを入力としてFastQCを実行するところ。③の表記を見て大丈夫だろうと安心する

The screenshot shows the Galaxy web interface for a workflow titled "Workflow: Workflow constructed from history 'inudoshi_desu'". The interface includes a left sidebar with tool categories, a central workflow editor, and a right sidebar with history. The central editor shows a step configuration for "3: FastQC (Galaxy Version 0.69)". The configuration includes a dropdown menu for "Contaminant list" and a scrollable area for "Submodule and Limit specifying file". Three red arrows point to specific elements: arrow 1 points to the bottom of the scrollable area, arrow 2 points to the step title, and arrow 3 points to the "Contaminant list" dropdown menu.

W18-7: Run workflow

The screenshot shows the Galaxy web interface. The browser address bar displays <https://usegalaxy.org/workflows/run?id=50fb074833eb9836>. The main content area is titled "Workflow: Workflow constructed from history 'inudoshi_desu'". A blue button with a checkmark and the text "Run workflow" is visible, with a red arrow and the number "1" pointing to it. Below the title, the workflow configuration is shown, including a parameter "Average quality required" set to 20. A step titled "3: FastQC (Galaxy Version 0.69)" is highlighted in yellow. The "History" panel on the right shows "1: DRR024501sub_2.f astq" in a green row.

①Sending...になっているのがわかります

W18-8: ジョブ投げ中...

The screenshot shows the Galaxy web interface. The browser address bar displays <https://usegalaxy.org/workflows/run?id=50fb074833eb9836>. The main content area is titled "Workflow: Workflow constructed from history 'inudoshi_desu'". A blue button labeled "Sending..." is positioned above the workflow steps, with a red arrow and the number "1" pointing to it. The workflow steps include:

- 4
- Average quality required
- 20
- 3: FastQC (Galaxy Version 0.69)**

The "FastQC" step description reads: "Short read data from your current history", "Output dataset 'fastq_out' from step 2", "Contaminant list" (Nothing selected), and "Submodule and Limit specifying file" (Nothing selected). The right sidebar shows the "History" panel with "search datasets" and "Unnamed history" (1 shown, 186.06 MB). A dataset is listed: "1: DRR024501sub_2.f astq".

W18-9: Successfully invoked

①無事ワークフローを呼び出す (invoke) ことができたようです

The screenshot shows the Galaxy web interface. A green notification box with a red arrow pointing to it contains the following text:

① Successfully invoked workflow **Workflow constructed from history 'inudoshi_desu'**.
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.

The History pane on the right shows a list of jobs:

- 6: FastQC on data 4: RawData
- 5: FastQC on data 4: Webpage
- 4: Trimmomatic on DRR024501sub 2.fast q
- 3: FastQC on data 1: RawData
- 2: FastQC on data 1: Webpage
- 1: DRR024501sub 2.fastq

The job '1: DRR024501sub 2.fastq' is highlighted in green, indicating it is the current job.

このときは、まず①Step2
のTrimmomaticが終了した

W18-10: Step2終了

The screenshot shows the Galaxy web interface. A green notification box in the center reads: "Successfully invoked workflow **Workflow constructed from history 'inudoshi_desu'**. 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." The History pane on the right shows a list of datasets. The dataset "4: Trimmomatic on DR R024501sub 2.fastq" is highlighted in green and has a red arrow with the number "1" pointing to it. Other datasets in the history include "6: FastQC on data 4: RawData", "5: FastQC on data 4: Webpage", "3: FastQC on data 1: RawData", "2: FastQC on data 1: Webpage", and "1: DRR024501sub 2.fastq". The left sidebar shows various tool categories like "Get Data", "Send Data", "Text Manipulation", etc.

W18-11: Step1終了

Galaxy

Secure | https://usegalaxy.org/workflows/run?id=50fb074833eb9836

Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

search tools

Get Data
Send Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling
NGS: Variant Analysis
NGS: RNA Structure

Successfully invoked workflow **Workflow constructed from history 'inudoshi_desu'**.
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.

History

search datasets

Unnamed history
6 shown
186.06 MB

6: FastQC on data 4: RawData

5: FastQC on data 4: Webpage

4: Trimmomatic on DR R024501sub_2.fastq

3: FastQC on data 1: RawData

2: FastQC on data 1: Webpage

1: DRR024501sub_2.fastq

W18-12: Step3終了

Galaxy

Secure | <https://usegalaxy.org/workflows/run?id=50fb074833eb9836>

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

Tools

search tools

Get Data
Send Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling
NGS: Variant Analysis
NGS: RNA Structure

Successfully invoked workflow **Workflow constructed from history 'inudoshi_desu'**.
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.

History

search datasets

Unnamed history
6 shown
327.16 MB

6: FastQC on data 4: R awData

5: FastQC on data 4: W ebpage

4: Trimmomatic on DR R024501sub_2.fastq

3: FastQC on data 1: R awData

2: FastQC on data 1: W ebpage

1: DRR024501sub_2.fastq

W19-1: ワークフロー編集画面

Galaxy | Workflows

Secure | <https://usegalaxy.org/workflow/list>

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

Tools

search tools

Get Data
Send Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling
NGS: Variant Analysis
NGS: RNA Structure

Your workflows

search for workflow... +

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudosh/desu'		You	3	No	<input checked="" type="checkbox"/>

Edit
Run
Share
Download
Copy
Rename
View
Delete

History

search datasets

Unnamed history
6 shown
327.16 MB

- 6: FastQC on data 4: RawData
- 5: FastQC on data 4: Webpage
- 4: Trimmomatic on DR R024501sub_2.fastq
- 3: FastQC on data 1: RawData
- 2: FastQC on data 1: Webpage
- 1: DRR024501sub_2.fastq

<https://usegalaxy.org/workflow/editor?id=50fb074833eb9...>

①ワークフローエディタをロードしている…ようです

W19-1: ワークフロー編集画面

The screenshot shows the Galaxy Workflow Editor interface. The browser address bar displays the URL: <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The main workspace is titled "Workflow Canvas | Workflow constructed from history" and shows a loading progress bar with a red arrow and the number "1" pointing to it. The left sidebar contains tool categories such as "Inputs", "Get Data", "Send Data", "Lift-Over", "Collection Operations", "Text Manipulation", "Datamash", "Convert Formats", "Filter and Sort", "Join, Subtract and Group", "Fetch Alignments/Sequences", "NGS: QC and manipulation", "NGS: DeepTools", "NGS: Mapping", "NGS: RNA Analysis", "NGS: SAMtools", "NGS: BamTools", "NGS: Picard", "NGS: VCF Manipulation", "NGS: Peak Calling", and "NGS: Variant Analysis". The right sidebar shows "Edit Workflow Attributes" with fields for "Name:" (Workflow constructed from history 'inudoshi_desu') and "Tags:". Below the main workspace, a tool palette is visible with tools like "FastQC", "Trimmomatic", and "Input FASTQ file".

W19-2: 編集画面

The screenshot displays the Galaxy Workflow Editor interface. The browser address bar shows the URL: <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and a 'Using 0%' indicator.

The interface is divided into three main sections:

- Tools:** A sidebar on the left with a search bar and a list of tool categories including Inputs, Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, and NGS: Variant Analysis.
- Workflow Canvas:** The central area titled 'Workflow Canvas | Workflow constructed from history'. It shows a grid with several tool nodes. The 'FastQC' tool is highlighted in orange, with its configuration panel open, showing options like 'Short read data from your current history', 'Contaminant list', 'Submodule and Limit specifying file', and 'Input FASTQ file'. Below these are output fields: 'fastq_out_paired', 'fastq_out_unpaired', 'fastq_out_r1_paired', 'fastq_out_r2_paired', and 'fastq_out_r1_unpaired'. A blue box highlights a portion of the output fields.
- Details:** A panel on the right titled 'Details' with a sub-section 'Edit Workflow Attributes'. It shows the workflow name as 'Workflow constructed from history' and 'inudoshi_desu'. It also includes a 'Tags' section with a search icon and a description: 'Apply tags to make it easy to search for and find items with the same tag.' Below that is an 'Annotation / Notes' section with the instruction: 'Describe or add notes to workflow. Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.'

W19-2: 編集画面

W19-3: Tips

Galaxy | Workflow Editor

Secure | https://usegalaxy.org/workflow/editor?id=50fb074833eb9836

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

Tools

search tools

Inputs

- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

FastQC

- Short read data from your current history
- Contaminant list
- Submodule and Limit specifying file

Trimmomatic

- Input FASTQ file
- fastq_out_paired
- fastq_out_unpaired
- fastq_out_r1_paired
- fastq_out_r2_paired
- fastq_out_r1_unpaired

Details

Edit Workflow Attributes

Name:
Workflow constructed from history 'inudoshi_desu'

Tags:

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

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

W19-3: Tips

The screenshot shows the Galaxy Workflow Editor interface. The browser address bar displays `https://usegalaxy.org/workflow/editor?id=50fb074833eb9836`. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and a 'Using 0%' indicator.

The interface is divided into three main sections:

- Tools:** A sidebar on the left with a search bar and a list of tool categories: Inputs, Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, and NGS: Variant Analysis.
- Workflow Canvas:** The central area titled 'Workflow Canvas | Workflow constructed from history'. It shows a grid with two tool nodes: 'FastQC' and 'Trimmomatic'. The 'FastQC' node has inputs for 'Short read data from your current history' and 'Contaminant list'. The 'Trimmomatic' node has an input for 'Input FASTQ file' and outputs for 'fastq_out_paired', 'fastq_out_unpaired', 'fastq_out_r1_paired', 'fastq_out_r2_paired', and 'fastq_out_r1_unpaired'. Lines connect the output of 'FastQC' to the input of 'Trimmomatic'.
- Details:** A panel on the right titled 'Edit Workflow Attributes'. It shows:
 - Name:** Workflow constructed from history 'inudoshi_desu'
 - Tags:** A field with a plus icon and a text box containing the instruction: 'Apply tags to make it easy to search for and find items with the same tag.'
 - Annotation / Notes:** A text area with the instruction: 'Describe or add notes to workflow. Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.'

W19-3: Tips

The screenshot shows the Galaxy Workflow Editor interface. The browser address bar indicates the URL: <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 0%'. The 'Tools' panel on the left lists various bioinformatics tools under categories like 'Inputs', 'Text Manipulation', and 'NGS: Mapping'. The 'Workflow Canvas' in the center shows a workflow with steps like 'FastQC' and 'Trimmomatic'. A red arrow with the number '1' points to a small icon at the bottom of the canvas, which is used to return to the previous step.

W19-4: 自動で再レイアウト

①設定、②Auto Re-layoutというのがあるのでやってみましょう

The screenshot displays the Galaxy Workflow Editor interface. The browser address bar shows the URL <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', and 'Help'. A red arrow labeled '①' points to the 'Workflow' menu icon. A context menu is open over the workflow canvas, with a red arrow labeled '②' pointing to the 'Auto Re-layout' option. The workflow canvas shows a 'FastQC' tool step with its configuration panel open, listing inputs like 'Short read data from your current history' and 'Contaminant list', and outputs like 'fastq_out_unpaired' and 'fastq_out_r1_unpaired'. A 'Trimmomatic' tool step is also visible below it. The left sidebar contains a 'Tools' section with a search bar and various tool categories such as 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'. The right sidebar shows 'Workflow Attributes' and 'Annotation / Notes'.

W19-4: 自動で再レイアウト

こんな感じになりました。確かに重なっていたのがちょっと見やすくなったような気がします。①を押してみる

The screenshot shows the Galaxy Workflow Editor interface. The browser address bar displays `https://usegalaxy.org/workflow/editor?id=50fb074833eb9836`. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', 'User', and 'Using 0%'. The left sidebar lists various tool categories such as 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'. The main 'Workflow Canvas' shows a workflow constructed from history with two tool nodes: 'FastQC' and 'Trimmomatic'. The 'FastQC' node has inputs for 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file', with outputs for 'html_file (html)' and 'text_file (txt)'. The 'Trimmomatic' node has an input for 'Input FASTQ file' and outputs for 'fastq_out_paired' and 'fastq_out_unpaired'. A red arrow labeled '1' points to a button at the bottom right of the canvas.

おお！確かにW19-2で見えていたときよりも見やすい

W19-4: 自動で再レイアウト

The screenshot displays the Galaxy Workflow Editor interface. The browser address bar shows the URL <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A 'Using 0%' indicator is visible on the right.

The interface is divided into three main sections:

- Tools:** A sidebar on the left with a search bar and a list of tool categories including Inputs, Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, and NGS: Variant Analysis.
- Workflow Canvas:** The central area titled 'Workflow Canvas | Workflow constructed from history'. It features a grid background. Two tool cards are visible:
 - FastQC:** A card with a key icon and a close button. It lists inputs: 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. It also shows output fields for 'html_file (html)' and 'text_file (txt)'.
 - Trimmomatic:** A card with a key icon and a close button. It lists an input: 'Input FASTQ file' and output fields for 'fastq_out_paired' and 'fastq_out_unpaired'.
- Details:** A panel on the right titled 'Details' with a sub-section 'Edit Workflow Attributes'. It contains:
 - Name:** 'Workflow constructed from history' and 'inudoshi_desu'.
 - Tags:** A section with a tag icon and a text input field. Below it, a note reads: 'Apply tags to make it easy to search for and find items with the same tag.'
 - Annotation / Notes:** A section with a note icon and a text input field. Below it, a note reads: 'Describe or add notes to workflow. Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.'

W19-5: 計3ステップなので

①がおそらくStep1で、②で見えているFastQCなのでしょ

The screenshot displays the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy | Workflow Editor', a search bar, and menu items like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The main area is divided into three panels: 'Tools', 'Workflow Canvas', and 'Details'. The 'Tools' panel on the left lists various categories such as 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'. The 'Workflow Canvas' panel shows a grid with two tool nodes: 'FastQC' and 'Trimmomatic'. The 'FastQC' node is highlighted with a red arrow labeled '2' and has its configuration window open, showing inputs like 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. The 'Trimmomatic' node is highlighted with a red arrow labeled '1' and has its configuration window open, showing an 'Input FASTQ file' input. The 'Details' panel on the right shows 'Edit Workflow Attributes' with fields for 'Name' (Workflow constructed from history 'inudoshi_desu'), 'Tags', and 'Annotation / Notes'.

W19-5: 計3ステップなので

①は間違いなくStep2で、②で見えているTrimmomatic

The screenshot displays the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The main workspace is divided into three panels: 'Tools', 'Workflow Canvas', and 'Details'. The 'Tools' panel on the left lists various categories such as 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'. The 'Workflow Canvas' panel shows a workflow constructed from history, featuring two tool steps: 'FastQC' and 'Trimmomatic'. The 'FastQC' tool step is highlighted with a red arrow labeled '2', and the 'Trimmomatic' tool step is highlighted with a red arrow labeled '1'. The 'Details' panel on the right shows the 'Edit Workflow Attributes' section, including fields for 'Name', 'Tags', and 'Annotation / Notes'. The 'Name' field contains 'Workflow constructed from history 'inudoshi_desu''. The 'Tags' field is empty. The 'Annotation / Notes' field contains the text: 'Describe or add notes to workflow. Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.'

W19-6: Step3は...

(たぶんこれだろうと思われる) Step3のFastQCはどうやって見るんだらうと思いつつ、①のあたりをクリックすると...

The screenshot shows the Galaxy Workflow Editor interface. The 'Tools' panel on the left lists various bioinformatics tools. The 'Workflow Canvas' in the center shows a workflow with a 'FastQC' tool highlighted. A red arrow with the number '1' points to a specific input field in the 'FastQC' tool configuration. The 'Details' panel on the right shows the workflow's attributes, including its name and tags.

Tools

- search tools
- Inputs**
- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

- FastQC
 - Short read data from your current history
 - Contaminant list
 - Submodule and Limit specifying file
 - html_file (html)
 - text_file (txt)
- Trimmomatic
 - Input FASTQ file
 - fastq_out_paired
 - fastq_out_unpaired

W19-6: Step3は...

The screenshot displays the Galaxy Workflow Editor interface. The central 'Workflow Canvas' shows a 'FastQC' tool node with the following configuration options:

- Short read data from your current history
- Contaminant list
- Submodule and Limit specifying file
- html_file (html)
- text_file (txt)

A red arrow with the number '1' points to a small icon in the bottom right corner of the canvas area. The left sidebar contains a 'Tools' menu with categories like 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'. The right sidebar shows 'Details' for the workflow, including 'Edit Workflow Attributes' with fields for Name, Tags, and Annotation/Notes.

W19-7: Step間の関係性

①のあたりをクリックしてみると、Step間の関係性の理解がより深まってくる

The screenshot displays the Galaxy Workflow Editor interface. The main canvas shows a workflow constructed from history, featuring two 'FastQC' steps and one 'Trimmomatic' step. The 'FastQC' steps are connected to the 'Trimmomatic' step. A red arrow with the number 1 points to a specific connection point between the 'FastQC' steps and the 'Trimmomatic' step. The interface includes a 'Tools' sidebar on the left, a 'Details' panel on the right, and a navigation bar at the top.

Tools

- search tools
- Inputs**
- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

- FastQC**
 - Short read data from your current history
 - Contaminant list
 - Submodule and Limit specifying file
 - html_file (html)
 - text_file (txt)
- FastQC**
 - Short read data from your history
 - Contaminant list
 - Submodule and Limit specifying file
 - html_file (html)
 - text_file (txt)
- Trimmomatic**
 - Input FASTQ file
 - fastq_out_paired
 - fastq_out_unpaired
 - fastq_out_r1_paired
 - fastq_out_r2_paired
 - fastq_out_r1_unpaired
 - fastq_out_r2_unpaired
 - fastq_out

Details

Edit Workflow Attributes

Name:
Workflow constructed from history 'inudoshi_desu'

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

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

W19-7: Step間の関係性

赤矢印のあたりを掴んで、矢印の方向に矢印の長さ分だけ移動した結果。この結果から、黒枠がStep1だという確定診断が下る

The screenshot shows the Galaxy Workflow Editor interface. The main canvas displays a workflow with two steps: 'FastQC' and 'Trimmomatic'. The 'FastQC' step is highlighted with a red arrow pointing to its left side. The 'Trimmomatic' step is highlighted with a blue box. A yellow callout box explains that by moving the red arrow in the direction of the arrow's length, a determination can be made that the black box represents Step 1.

Galaxy | Workflow Editor

Secure | <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>

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

Tools

search tools

Inputs

- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

QC

- Read data from your current history
- Contaminant list
- Module and Limit specifying file
- File (html)
- File (txt)

FastQC

- Short read data from your current history
- Contaminant list
- Submodule and Limit specifying file
- html_file (html)
- text_file (txt)

Trimmomatic

- Input FASTQ file
- fastq_out_paired
- fastq_out_unpaired
- fastq_out_r1_paired
- fastq_out_r2_paired
- fastq_out_r1_unpaired
- fastq_out_r2_unpaired
- fastq_out

Details

FastQC Read

Quality reports (Galaxy Version 0.69)

Label

Add a step label.

Annotation

Add an annotation or notes to this step. Annotations are available when a workflow is viewed.

Short read data from your current history

Data input 'input_file' (fastq, fastq.gz, fastq.bz2, bam or sam)

Contaminant list

Data input 'contaminants' (tabular)

tab delimited file with 2 columns: name and sequence. For example:

W19-7: Step間の関係性

ちょこちょこ移動させて全体が見られるようにしたところ。Step間の関係性が分かりやすいですね

The screenshot displays the Galaxy Workflow Editor interface. The main canvas shows a workflow with three steps: a top FastQC step, a Trimmomatic step, and a bottom FastQC step. The top FastQC step is connected to the Trimmomatic step, which in turn connects to the bottom FastQC step. The Trimmomatic step has multiple output ports labeled 'fastq_out_paired' through 'fastq_out_r2_unpaired' and 'fastq_out'. The bottom FastQC step is connected to the 'fastq_out' output of the Trimmomatic step. The details panel on the right shows the configuration for the selected FastQC step, including options for quality reports, labels, and annotations.

Galaxy | Workflow Editor x

Secure | <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>

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

Tools

search tools

Inputs

Get Data

Send Data

Lift-Over

Collection Operations

Text Manipulation

Datamash

Convert Formats

Filter and Sort

Join, Subtract and Group

Fetch Alignments/Sequences

NGS: QC and manipulation

NGS: DeepTools

NGS: Mapping

NGS: RNA Analysis

NGS: SAMtools

NGS: BamTools

NGS: Picard

NGS: VCF Manipulation

NGS: Peak Calling

NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

FastQC

Short read data from your current history

Contaminant list

Submodule and Limit specifying file

html_file (html)

text_file (txt)

Trimmomatic

Input FASTQ file

fastq_out_paired

fastq_out_unpaired

fastq_out_r1_paired

fastq_out_r2_paired

fastq_out_r1_unpaired

fastq_out_r2_unpaired

fastq_out

FastQC

Short read data from your current history

Contaminant list

Submodule and Limit specifying file

html_file (html)

text_file (txt)

Details

FastQC Read Quality reports (Galaxy Version 0.69)

Label

Add a step label.

Annotation

Add an annotation or notes to this step. Annotations are available when a workflow is viewed.

Short read data from your current history

Data input 'input_file' (fastq, fastq.gz, fastq.bz2, bam or sam)

Contaminant list

Data input 'contaminants' (tabular) tab delimited file with 2 columns: name and sequence. For example:

W19-8: 右側が詳細情報

- ①何気なしにStep2を黒枠にしてみると、
- ②この部分が変わっていることに気づく

The screenshot displays the Galaxy Workflow Editor interface. On the left is a 'Tools' sidebar with a search bar and various tool categories. The central 'Workflow Canvas' shows a workflow with three steps: 'FastQC', 'Trimmomatic', and another 'FastQC'. The 'Trimmomatic' step is highlighted with a black border and a red arrow labeled '1'. The right-hand 'Details' panel shows the configuration for the selected 'Trimmomatic' step, including its description, label field, annotation field, and a dropdown for 'Single-end or paired-end reads?'. A red arrow labeled '2' points to the top of the details panel.

W19-8: 右側が詳細情報

①Detailsの書いているので、ここでTrimmomaticのオプションをいろいろといじれるのでしょうか

The screenshot displays the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy | Workflow Editor', a secure URL, and menu items like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A 'Using 0%' indicator is visible on the right. The main area is divided into three sections: 'Tools' on the left with a search bar and categorized tool lists; 'Workflow Canvas | Workflow constructed from history' in the center, showing a workflow with 'FastQC' and 'Trimmomatic' steps; and 'Details' on the right, which is highlighted with a red box and a red arrow labeled '1'. The 'Details' panel for 'Trimmomatic' includes a title, a description, a 'Label' input field, an 'Annotation' text area, a 'Single-end or paired-end reads?' dropdown menu (set to 'Single-end'), and an 'Input FASTQ file' section with a description of the data input.

W19-8: 右側が詳細情報

①ちょっと下にスクロール。②除去したいアダプター配列を変更できそうですね

The screenshot displays the Galaxy Workflow Editor interface. The main window is titled "Workflow Canvas | Workflow constructed from history". It shows a workflow with three tools: "FastQC", "Trimmomatic", and another "FastQC". The "Trimmomatic" tool is highlighted with a blue border. The right-hand side of the interface shows the "Details" panel for the selected tool, which is "FastQC". The "Details" panel is scrolled down to show the "Adapter sequences to use" section, where "TruSeq3 (single-ended, fo..." is selected. A red arrow labeled "1" points to the "Input FASTQ file" section, and another red arrow labeled "2" points to the "Adapter sequences to use" section.

Galaxy | Workflow Editor x

Secure | https://usegalaxy.org/workflow/editor?id=50fb074833eb9836

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

Tools search tools

Inputs

- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

FastQC

- Short read data from your current history
- Contaminant list
- Submodule and Limit specifying file
- html_file (html)
- text_file (txt)

Trimmomatic

- Input FASTQ file
- fastq_out_paired
- fastq_out_unpaired
- fastq_out_r1_paired
- fastq_out_r2_paired
- fastq_out_r1_unpaired
- fastq_out_r2_unpaired
- fastq_out

FastQC

- Short read data from your current history
- Contaminant list
- Submodule and Limit specifying file
- html_file (html)
- text_file (txt)

Details

Single-end or paired-end reads?

Single-end

Input FASTQ file

Data input 'fastq_in' (fastqsanger or fastqsanger.gz)

Perform initial ILLUMINACLIP step?

Yes No

Cut adapter and other illumina-specific sequences from the read

Adapter sequences to use

TruSeq3 (single-ended, fo...

Maximum mismatch count which will still allow a full match to be performed

2

How accurate the match between the two 'adapter ligated' reads must be for PE palindrome read alignment

30

W19-9: Attributes 1

実験系じゃなくてもわかりづらい表現だと思いますが、①設定、②Edit Attributes

The screenshot displays the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and a settings icon (1). The main area is the 'Workflow Canvas | Workflow constructed from history'. It shows a workflow with three tools: 'FastQC' (top), 'Trimmomatic' (middle), and another 'FastQC' (bottom). The top 'FastQC' tool is selected, and a context menu is open over it, with 'Edit Attributes' highlighted (2). The 'Trimmomatic' tool has several output ports connected to the bottom 'FastQC' tool. The right sidebar shows the configuration for the selected 'FastQC' tool, including options for 'Perform initial ILLUMINACLIP step?' (Yes/No), 'Adapter sequences to use' (TruSeq3), 'Maximum mismatch count' (2), and 'How accurate the match' (30).

W19-9: Attributes2

こんな感じになります。①のあたりをみることで、このワークフローがどういうことをやるものかがわかりやすいようにタグ付けするところなのでしょう。②のあたりをクリック

The screenshot shows the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy | Workflow Editor', a search bar, and a 'Secure' indicator. The main area is divided into three sections: 'Tools', 'Workflow Canvas', and 'Details'. The 'Tools' section on the left lists various categories like 'Inputs', 'Get Data', 'Send Data', etc. The 'Workflow Canvas' in the center shows a workflow with two 'FastQC' tools and a 'Trimmomatic' tool. The 'Details' panel on the right is titled 'Edit Workflow Attributes' and contains fields for 'Name', 'Tags', and 'Annotation / Notes'. Red callout boxes with circled numbers 1 and 2 point to the 'Annotation / Notes' field and the 'Tags' field, respectively.

Galaxy | Workflow Editor x

Secure | https://usegalaxy.org/workflow/editor?id=50fb074833eb9836

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

Tools

search tools

Inputs

Get Data

Send Data

Lift-Over

Collection Operations

Text Manipulation

Datamash

Convert Formats

Filter and Sort

Join, Subtract and Group

Fetch Alignments/Sequences

NGS: QC and manipulation

NGS: DeepTools

NGS: Mapping

NGS: RNA Analysis

NGS: SAMtools

NGS: BamTools

NGS: Picard

NGS: VCF Manipulation

NGS: Peak Calling

NGS: Variant Analysis

Workflow Canvas | Workflow constructed from history

FastQC

Short read data from your current history

Contaminant list

Submodule and Limit specifying file

html_file (html)

text_file (txt)

Trimmomatic

Input FASTQ file

fastq_out_paired

fastq_out_unpaired

fastq_out_r1_paired

fastq_out_r2_paired

fastq_out_r1_unpaired

fastq_out_r2_unpaired

fastq_out

FastQC

Short read data from your current history

Contaminant list

Submodule and Limit specifying file

html_file (html)

text_file (txt)

Details

Edit Workflow Attributes

Name:

Workflow constructed from history 'inudoshi_desu'

Tags:

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

Annotation / Notes:

Describe or add notes to workflow. Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

W19-9: Attributes3

こんな感じになるので、①Quality Controlなどと書いておけばいいでしょう

The screenshot displays the Galaxy Workflow Editor interface. The browser address bar shows the URL: <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The interface includes a top navigation bar with 'Galaxy' and various menu items like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A 'Using 0%' indicator is present in the top right.

The main workspace is divided into three panels:

- Tools:** A sidebar on the left with a search bar and a list of tool categories including 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'.
- Workflow Canvas:** The central area showing a workflow graph. It contains three tool nodes:
 - FastQC (top):** Inputs include 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. It has two output ports: 'html_file (html)' and 'text_file (txt)'.
 - Trimmomatic (bottom left):** Input is 'Input FASTQ file'. It has multiple output ports: 'fastq_out_paired', 'fastq_out_unpaired', 'fastq_out_r1_paired', 'fastq_out_r2_paired', 'fastq_out_r1_unpaired', 'fastq_out_r2_unpaired', and 'fastq_out'.
 - FastQC (bottom right):** Identical to the top FastQC node.Connections are shown between the Trimmomatic outputs and the FastQC inputs.
- Details:** A panel on the right titled 'Edit Workflow Attributes'. It shows:
 - Name:** Workflow constructed from history 'inudoshi_desu'
 - Tags:** An empty text input field.
 - Annotation / Notes:** A text area with the instruction: 'Describe or add notes to workflow. Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.'

W19-9: Attributes4

Quality Controlと打って、こんな感じになったところ。QualityとControlが分断された結果にうろたえつつw、こういうノリなら、FastQCとTrimmomaticにしたほうがよりわかりやすいんじゃないかと思い、変更する

The screenshot shows the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy | Workflow Editor', a search bar, and a URL: 'https://usegalaxy.org/workflow/editor?id=50fb074833eb9836'. The main area is divided into three panels: 'Tools', 'Workflow Canvas', and 'Details'.

- Tools Panel:** Lists various tool categories such as 'Inputs', 'Get Data', 'Send Data', 'Lift-Over', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'.
- Workflow Canvas:** Displays a workflow graph with two 'FastQC' tools and one 'Trimmomatic' tool. The top 'FastQC' tool has inputs: 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. The 'Trimmomatic' tool has an input 'Input FASTQ file' and outputs: 'fastq_out_paired', 'fastq_out_unpaired', 'fastq_out_r1_paired', 'fastq_out_r2_paired', 'fastq_out_r1_unpaired', 'fastq_out_r2_unpaired', and 'fastq_out'. The bottom 'FastQC' tool has the same inputs as the top one. Connections show the 'fastq_out' from Trimmomatic feeding into the 'Short read data from your current history' input of the bottom FastQC tool.
- Details Panel:** Shows 'Edit Workflow Attributes' for the workflow 'Workflow constructed from history 'inudoshi_desu''. It includes a 'Name' field, a 'Tags' section with 'Quality' and 'Control' tags, and an 'Annotation / Notes' section with a text area.

W19-9: Attributes5

The screenshot displays the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy | Workflow Editor', a secure URL, and a 'Using 0%' indicator. The main workspace is divided into three panels: 'Tools', 'Workflow Canvas', and 'Details'.

- Tools Panel:** Lists various tool categories such as 'Inputs', 'Get Data', 'Send Data', 'Collection Operations', 'Text Manipulation', 'Datamash', 'Convert Formats', 'Filter and Sort', 'Join, Subtract and Group', 'Fetch Alignments/Sequences', 'NGS: QC and manipulation', 'NGS: DeepTools', 'NGS: Mapping', 'NGS: RNA Analysis', 'NGS: SAMtools', 'NGS: BamTools', 'NGS: Picard', 'NGS: VCF Manipulation', 'NGS: Peak Calling', and 'NGS: Variant Analysis'.
- Workflow Canvas:** Shows a workflow graph with two 'FastQC' tools and one 'Trimmomatic' tool. The top 'FastQC' tool is connected to 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. The 'Trimmomatic' tool is connected to 'Input FASTQ file' and multiple 'fastq_out_*' outputs. The bottom 'FastQC' tool is connected to 'Short read data from your current history', 'Contaminant list', 'Submodule and Limit specifying file', 'html_file (html)', and 'text_file (txt)'.
- Details Panel:** Titled 'Edit Workflow Attributes', it shows the workflow name 'Workflow constructed from history 'inudoshi_desu''. The 'Tags' section has a red arrow pointing to a 'Quality' tag with a red '1' in a circle next to its close button (×). Below the tags is a text area for 'Annotation / Notes'.

W19-9: Attributes6

The screenshot displays the Galaxy Workflow Editor interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', and 'Help'. The main area is the 'Workflow Canvas | Workflow constructed from history', which contains two tool nodes: 'FastQC' and 'Trimmomatic'. The 'FastQC' node is connected to the 'Trimmomatic' node. A context menu is open over the 'FastQC' node, with options: 'Save', 'Save As', 'Run', 'Edit Attributes', 'Auto Re-layout', and 'Close'. A 'Workflow Attributes' panel is open on the right, showing a search bar and a text area for annotations. Red arrows point to the 'Save' option in the context menu (labeled 2), the 'Workflow Attributes' panel (labeled 1), and the 'Save' option in the context menu (labeled 3).

W19-10: Save中

The screenshot shows the Galaxy Workflow Editor interface. A modal dialog box titled "Saving workflow" is centered on the screen, featuring a blue progress bar. The background workflow diagram includes a "Trimmomatic" tool with inputs for "Input FASTQ file" (with sub-inputs: fastq_out_paired, fastq_out_unpaired, fastq_out_r1_paired, fastq_out_r2_paired, fastq_out_r1_unpaired, fastq_out_r2_unpaired, fastq_out) and a "FastQC" tool with inputs for "Short read data from your current history", "Contaminant list", and "Submodule and Limit specifying file" (with sub-inputs: html_file (html), text_file (txt)). The interface also shows a left sidebar with tool categories, a top navigation bar, and a right sidebar with "Tags" (FastQC, Trimmomatic) and "Annotation / Notes" sections.

W19-11: Save完了

The screenshot displays the Galaxy Workflow Editor interface. The browser address bar shows the URL: <https://usegalaxy.org/workflow/editor?id=50fb074833eb9836>. The interface includes a top navigation bar with 'Galaxy' and various menu items like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A 'Using 0%' indicator is visible in the top right.

The main workspace is divided into three panels:

- Tools:** A sidebar on the left with a search bar and a list of tool categories including Inputs, Get Data, Send Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, and NGS: Variant Analysis.
- Workflow Canvas:** The central area showing a workflow graph. It contains three tool nodes:
 - FastQC:** A top node with inputs: 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. It has two output ports: 'html_file (html)' and 'text_file (txt)'.
 - Trimmomatic:** A middle node with input: 'Input FASTQ file'. It has eight output ports: 'fastq_out_paired', 'fastq_out_unpaired', 'fastq_out_r1_paired', 'fastq_out_r2_paired', 'fastq_out_r1_unpaired', 'fastq_out_r2_unpaired', and 'fastq_out'.
 - FastQC:** A bottom node with inputs: 'Short read data from your current history', 'Contaminant list', and 'Submodule and Limit specifying file'. It has two output ports: 'html_file (html)' and 'text_file (txt)'.
- Details:** A panel on the right titled 'Edit Workflow Attributes'. It shows:
 - Name:** Workflow constructed from history 'inudoshi_desu'
 - Tags:** 'FastQC' and 'Trimmomatic' (with a plus icon to add more).
 - Annotation / Notes:** A section for describing or adding notes to the workflow.

W19-12: Close

The screenshot displays the Galaxy Workflow Editor interface. The browser address bar shows the URL `https://usegalaxy.org/workflow/editor?id=50fb074833eb9836`. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and a settings icon. A red arrow labeled '1' points to the settings icon. Below the navigation bar, the 'Tools' sidebar is visible on the left, and the 'Workflow Canvas' is in the center. A context menu is open over a 'FastQC' tool node, with a red arrow labeled '2' pointing to the 'Close' option. The context menu includes 'Save', 'Save As', 'Run', 'Edit Attributes', 'Auto Re-Layout', and 'Close'. The workflow canvas shows two 'FastQC' tools and one 'Trimmomatic' tool connected by lines. The 'Details' panel on the right shows 'Workflow Attributes' and 'Annotation / Notes'.

W19-13: Close後

The screenshot shows the Galaxy Workflows interface. The main content area displays a table of workflows under the heading "Your workflows".

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>

On the right side, the "History" panel shows a list of datasets:

- 6: FastQC on data 4: RawData
- 5: FastQC on data 4: Webpage
- 4: Trimmomatic on DR R024501sub_2.fastq
- 3: FastQC on data 1: RawData
- 2: FastQC on data 1: Webpage
- 1: DRR024501sub_2.fastq

W20-1: ワークフロー公開

①をクリックして、②Share。
中央パネルがこうになってない
ヒトは、③Workflowをクリック

The screenshot shows the Galaxy Workflows interface. The browser address bar shows the URL <https://usegalaxy.org/workflow/list>. The main panel displays a table of workflows. A context menu is open over the workflow 'Workflow constructed from history 'inudoshi_desu'', with the 'Share' option highlighted. The 'History' panel on the right shows a list of datasets.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>

History:

- 6: FastQC on data 4: RawData
- 5: FastQC on data 4: Webpage
- 4: Trimmomatic on DR R024501sub_2.fastq
- 3: FastQC on data 1: RawData
- 2: FastQC on data 1: Webpage
- 1: DRR024501sub_2.fastq

W20-1: ワークフロー公開

こんな感じになります。W4-3と同じような見栄えと選択肢ですね。特に隠さないといけないものでもないなので、誰でも見られるように①公開しちゃいます

Galaxy | x

Secure | <https://usegalaxy.org/workflow/sharing?id=50fb074833eb9836>

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

[Go back to Workflows List](#)

Workflow ' Workflow constructed from history 'inudoshi_desu''

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.

① [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

W20-2: 公開完了

①がURL。②Published Workflows
からも辿れる。②を押してみる

The screenshot shows a web browser window with the URL <https://usegalaxy.org/workflow/sharing?id=50fb074833eb9836>. The page title is "Workflow 'Workflow constructed from history 'inudoshi_desu''". Under the "Share" section, it states "This workflow is currently accessible via link and published." and provides a URL: https://usegalaxy.org/u/aaribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu. A red arrow with the number 1 points to this URL. Below this, it says "This workflow is publicly listed and searchable in Galaxy's [Published Workflows](#) section." and has a button "Unpublish Workflow" with a red arrow and the number 2 pointing to it. Other buttons include "Disable Access to Workflow via Link and Unpublish" and "Share with a user". The "Export" section has a "Download" button.

W20-3: Published Workflows

The screenshot displays the Galaxy web interface at https://usegalaxy.org/workflows/list_published. The interface includes a navigation bar with options like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A left sidebar lists various tool categories such as 'Get Data', 'Send Data', 'Text Manipulation', and 'NGS: QC and manipulation'. The main content area shows a list of published workflows in a table format, with a 'History' panel on the right displaying details for the selected workflow.

Workflow ID	Workflow Name	View	Edit	Delete
6	FastQC on data 4: RawData			
5	FastQC on data 4: Webpage			
4	Trimmomatic on DR R024501sub_2.fastq			
3	FastQC on data 1: RawData			
2	FastQC on data 1: Webpage			
1	DRR024501sub_2.fastq			

W20-3: Published

じきにこんな感じになります。このときは①inudoshi_desuのワークフロー公開直後に見たので、この位置にありました。もし、後日見たい場合は、②でinudoshi_desuでキーワード検索するとよいでしょう。①をクリック

The screenshot shows the Galaxy web interface. The browser address bar displays https://usegalaxy.org/workflows/list_published. The main content area is titled "Published Workflows" and contains a search bar with the placeholder text "search name, annotation" and a magnifying glass icon. A red arrow with the number "2" points to the search bar. Below the search bar is a table of workflows with columns "Name" and "Annotation". The first row is highlighted in orange and contains the text "Workflow constructed from history 'inudoshi_desu'", with a red arrow and the number "1" pointing to it. The right sidebar shows a "History" panel with a search bar and a list of datasets, including "6: FastQC on data 4: RawData", "5: FastQC on data 4: Webpage", "4: Trimmomatic on DR R024501sub_2.fastq", "3: FastQC on data 1: RawData", "2: FastQC on data 1: Webpage", and "1: DRR024501sub_2.fastq".

W20-4: inudoshi_desu

こんな感じになります。
①下のほうにスクロール

Galaxy | Published Workf x

Secure | https://usegalaxy.org/u/agribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu

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

Published Workflows | agribio t t desu | Workflow constructed from history 'inudoshi_desu'

Galaxy Workflow 'Workflow constructed from history 'inudoshi_desu''

Step	Annotation
Step 1: FastQC Short read data from your current history <i>select at runtime</i> Contaminant list <i>select at runtime</i> Submodule and Limit specifying file <i>select at runtime</i>	
Step 2: Trimmomatic Single-end or paired-end reads? Single-end Input FASTQ file <i>select at runtime</i> Perform initial ILLUMINACLIP step? True Adapter sequences to use	

About this Workflow

Author
agribio_t_t_desu

Related Workflows
[All published workflows](#)
[Published workflows by agribio t t desu](#)

Rating
Community: ★★★★★ (0 ratings, 0.0 average)
Yours: ★★★★★

Tags
Community: none
Yours:

W20-4: inudoshi_desu

①Step3あたりの記述は、W18-6と似ていてわかりやすいですね

Galaxy | Published Workf x

Secure | https://usegalaxy.org/u/agribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu

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

Published Workflows | agribio t t desu | Workflow constructed from history 'inudoshi_desu'

30

How accurate the match between any adapter etc. sequence must be against a read

10

Trimmomatic Operations

Trimmomatic Operation 1

Select Trimmomatic operation to perform
Sliding window trimming (SLIDINGWINDOW)

Number of bases to average across
4

Average quality required
20

Step 3: FastQC

Short read data from your current history
Output dataset 'fastq_out' from step 2

Contaminant list
select at runtime

Submodule and Limit specifying file
select at runtime

About this Workflow

Author
agribio_t_t_desu

Related Workflows

All published workflows
Published workflows by agribio t t desu

Rating

Community ★★★★★
(0 ratings, 0.0 average)

Yours ★★★★★

Tags

Community: none

Yours:

3分割の通常画面に戻りたいときは、①Analyze Data

W20-5: 通常画面に...

The screenshot shows the Galaxy web interface. The browser address bar displays the URL: https://usegalaxy.org/u/agribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu. The Galaxy navigation bar includes the following items: Galaxy logo, Analyze Data (highlighted with a red circle and arrow labeled '1'), Workflow, Shared Data, Visualization, Help, User, and a grid icon. The 'Using 0%' indicator is visible in the top right. The main content area is divided into two columns. The left column shows the workflow steps, including 'Trimmomatic Operations' and 'Step 3: FastQC'. The right column displays 'About this Workflow' information, including the author 'agribio_t_t_desu', related workflows, and a rating section.

W20-5: 通常画面に...

The screenshot shows the Galaxy web interface. The main content area features a banner that reads "Try Galaxy on the Cloud" with the subtext "Now you can have a personal Galaxy within the infinite Universe". Above the banner, there is introductory text: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)."

The interface includes a left sidebar with a "Tools" section containing a search bar and a list of tool categories such as "Get Data", "Send Data", "Lift-Over", "Collection Operations", "Text Manipulation", "Datamash", "Convert Formats", "Filter and Sort", "Join, Subtract and Group", "Fetch Alignments/Sequences", "NGS: QC and manipulation", "NGS: DeepTools", "NGS: Mapping", "NGS: RNA Analysis", "NGS: SAMtools", "NGS: BamTools", "NGS: Picard", "NGS: VCF Manipulation", "NGS: Peak Calling", "NGS: Variant Analysis", and "NGS: RNA Structure".

On the right side, there is a "History" panel with a search bar and a list of recent jobs. The jobs listed are:

- 6: FastQC on data 4: RawData
- 5: FastQC on data 4: Webpage
- 4: Trimmomatic on DR R024501sub_2.fastq
- 3: FastQC on data 1: RawData
- 2: FastQC on data 1: Webpage
- 1: DRR024501sub_2.fastq

W21-1:メール送信

①履歴を共有する登録済みユーザー terada_registered に、②公開したワークフローと、③入力ファイル情報をメール

ワークフローを公開しました - メッセージ (テキスト形式)

ファイル メッセージ 挿入 オプション 書式設定 校閲 実行したい作業を入力してください

宛先... tomoko.terada@iu.a.u-tokyo.ac.jp ①

C C (C)...

B C C (B)...

件名(U) ワークフローを公開しました

送信(S)

terada_registered さま

FastQC --> Trimmomatic --> FastQC

の3ステップからなるワークフローを公開しました。

https://usegalaxy.org/u/agribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu ②

尚、確認用の「30万リードからなる paired-end の forward 側の gzip 圧縮 FASTQ ファイル」

の URL は下記の通りです。

http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq.gz ③

ご確認よろしくお願いたします。

kadota_registered

W21-2: ログイン

メールを受け取った
terada_registeredがログイン

Galaxy | x

Secure | https://usegalaxy.org/user/login?use_panels=True

Galaxy Analyze Data Workflow Shared Data Visualization Help Login or Register Using 0 bytes

Login

Username / Email Address:

tomoko.terada@iu.a.u-tokyo.ac.jp

Password:

.....|

[Forgot password?](#) [Reset here](#)

Login

OpenID Login

OpenID URL:

Or, authenticate with your **GenomeSpace** account.

Login

[Terms and Conditions for use of this service](#)

W21-3: ログイン後

terada_registeredのログイン後の状態。右側のヒストリーパネルには、①Trimというヒストリー名で何か作業をやった結果が残っている(ということを書いてあるだけで、何か過去にやったものがある状態で行いますよということを書いたいただけです)

The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed." Below this is a logo for "Public Galaxy Servers and still counting" with a "080+" graphic.

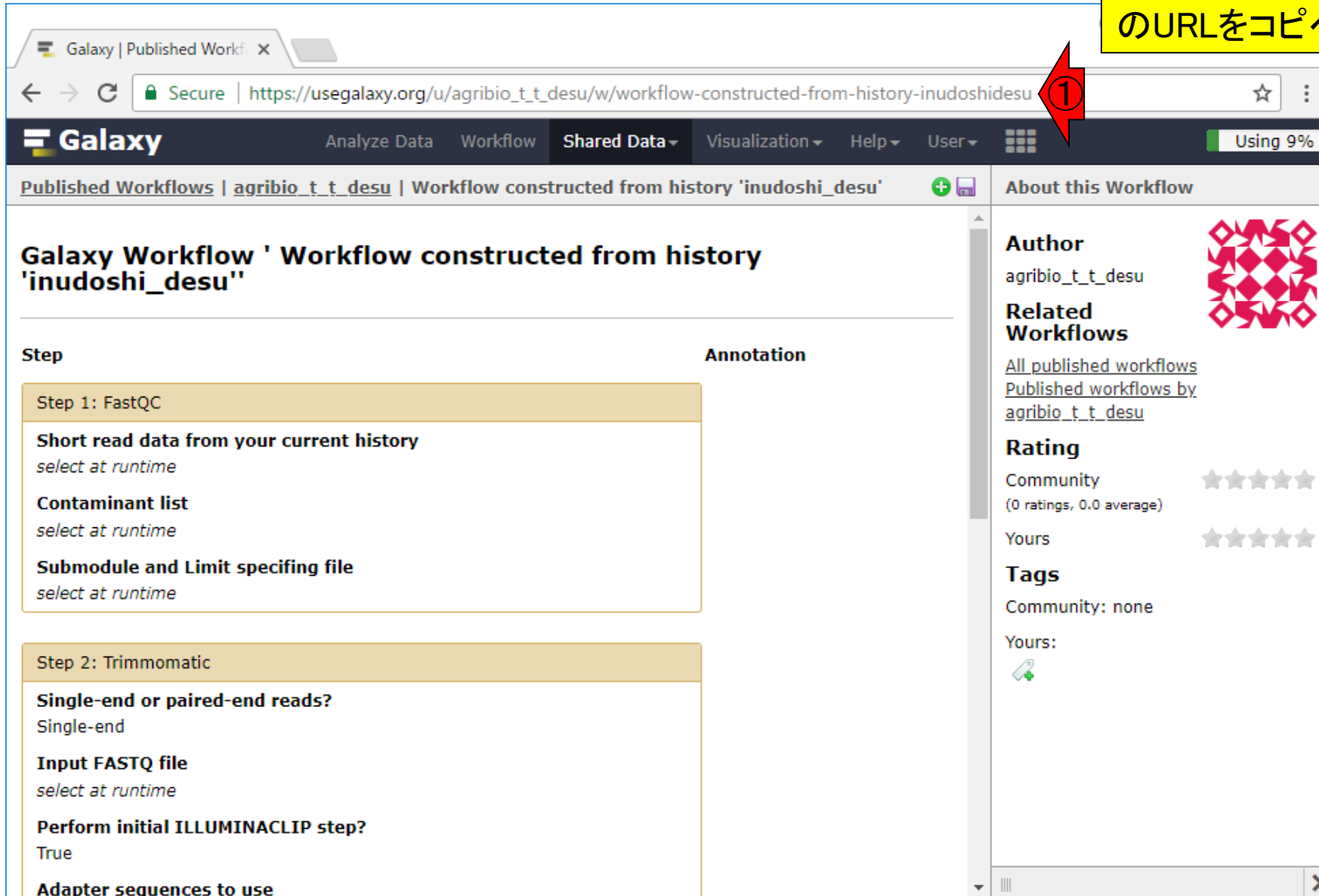
The right-hand "History" panel is highlighted with a red box. It contains a search bar and a list of history items:

- Trim (7 shown, 1 deleted)
- 7: getorf on data 1
- 6: plotorf on data 1
- 5: Trim on data 3
- 4: Trim on data 3
- 3: multi_FASTA_demo 3.fasta
- 2: Trim on data 1
- 1: demo0_seq.txt

A red arrow with the number "1" points to the "Trim" history item.

W21-4: ワークフローURL

terada_registeredさんが、(kadota_registeredからメールで送られた)①ワークフローのURLをコピペした結果



The screenshot shows a web browser displaying a Galaxy workflow page. The address bar contains the URL: https://usegalaxy.org/u/agribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu. A red arrow with the number '1' points to this URL. The page title is "Galaxy Workflow 'Workflow constructed from history 'inudoshi_desu'". The main content area is divided into two columns: "Step" and "Annotation".

Step	Annotation
Step 1: FastQC	
Short read data from your current history <i>select at runtime</i>	
Contaminant list <i>select at runtime</i>	
Submodule and Limit specifying file <i>select at runtime</i>	
Step 2: Trimmomatic	
Single-end or paired-end reads? Single-end	
Input FASTQ file <i>select at runtime</i>	
Perform initial ILLUMINACLIP step? True	
Adapter sequences to use	

The right sidebar contains metadata for the workflow:

- Author:** agribio_t_t_desu (with profile picture)
- Related Workflows:** [All published workflows](#), [Published workflows by agribio_t_t_desu](#)
- Rating:** Community (0 ratings, 0.0 average) (5 stars), Yours (5 stars)
- Tags:** Community: none, Yours: (with tag icon)

W21-5: インポート

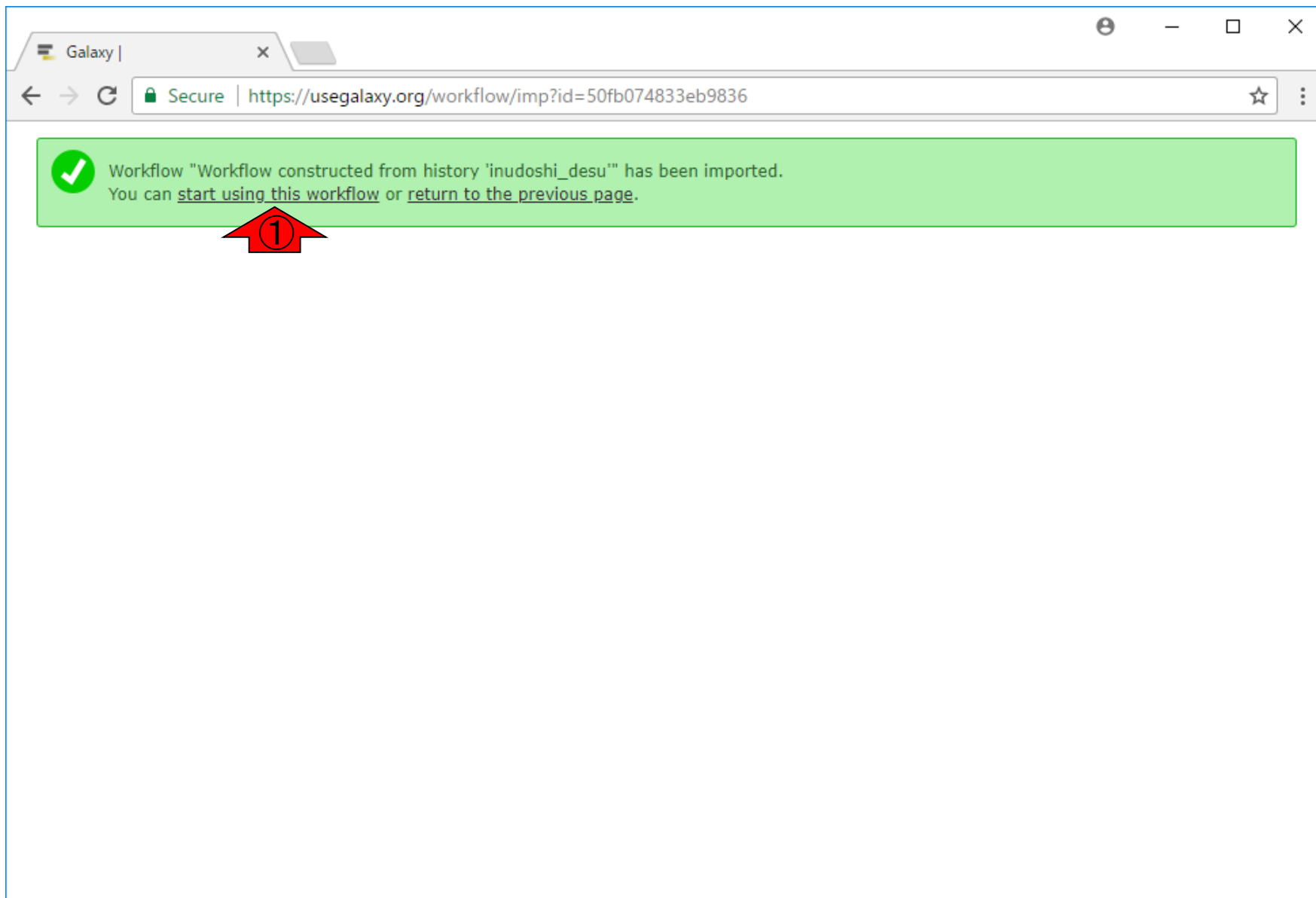
①ワークフローをインポート(取り込み)して使えるようにします

The screenshot shows the Galaxy web interface. The browser address bar displays the URL: https://usegalaxy.org/u/agribio_t_t_desu/w/workflow-constructed-from-history-inudoshidesu. The navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', and 'Help'. A red arrow with a circled '1' points to the 'Import workflow' button, which is located next to the workflow title 'Workflow constructed from history 'inudoshi_desu''. The main content area shows the workflow details, including two steps: 'Step 1: FastQC' and 'Step 2: Trimmomatic'. The right sidebar contains information about the workflow, including the author 'agribio_t_t_desu', related workflows, and a rating section.

Step	Annotation
Step 1: FastQC	
Short read data from your current history <i>select at runtime</i>	
Contaminant list <i>select at runtime</i>	
Submodule and Limit specifying file <i>select at runtime</i>	
Step 2: Trimmomatic	
Single-end or paired-end reads? Single-end	
Input FASTQ file <i>select at runtime</i>	
Perform initial ILLUMINACLIP step? True	

W21-6: インポート後

インポートに成功すると、こんな感じになります。①start using this workflow



W21-7: Your workflows

terada_registeredさんは、沢山ワークフローを持っているので、中央パネルがこんな感じに見えます

The screenshot shows the Galaxy Workflows interface. The main panel displays a list of workflows under the heading "Your workflows". The list has columns for Name, Tags, Owner, # of Steps, Published, and Show in tool panel. The workflows listed are:

Name	Tags	Owner	# of Steps	Published	Show in tool panel
imported: Workflow constructed from history 'inudoshi_desu'		You	3	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_0130_1'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_used'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393'		You	9	No	<input type="checkbox"/>

On the right, the History panel shows a list of datasets with their names and actions (view, edit, delete). The datasets listed are:

- Trim (7 shown, 1 deleted, 7.5 KB)
- 7: getorf on data 1
- 6: plotorf on data 1
- 5: Trim on data 3
- 4: Trim on data 3
- 3: multi_FASTA_demo 3.fasta
- 2: Trim on data 1
- 1: demo0_seq.txt

W21-7: Your workflows

もし以前にワークフローを作成したことがなければ、①のみが見えているはず

The screenshot shows the Galaxy Workflows interface. The main panel displays a table of workflows. The first workflow is highlighted with a red box and a red circle with the number 1. The history panel on the right shows a list of datasets, with the first dataset also highlighted with a red circle and the number 1.

Name	Tags	Owner	# of Steps	Published	Show in tool panel
imported: Workflow constructed from history 'inudoshi_desu'		You	3	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_0130_1'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_used'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393'		You	9	No	<input type="checkbox"/>

History panel:

- Trim (7 shown, 1 deleted) - 7.5 KB
- 7: getorf on data 1
- 1: plotorf on data 1
- 6: Trim on data 3
- 4: Trim on data 3
- 3: multi_FASTA_demo 3.fasta
- 2: Trim on data 1
- 1: demo0_seq.txt

W15-4と同じく、①Show in tools panelにチェックを入れる

W21-8: Show in tools panel

The screenshot shows the Galaxy Workflows interface. On the left is a 'Tools' panel with a search bar and various tool categories. The main area is titled 'Your workflows' and contains a table of workflow entries. On the right is a 'History' panel showing a list of datasets.

Name	Tags	Owner	# of Steps	Published	Show in tool panel
imported: Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>
Workflow constructed from history 'ERR519393_0130_1'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_used'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393'		You	9	No	<input type="checkbox"/>

The 'History' panel on the right shows a list of datasets with their names and actions (view, edit, delete). The first dataset is '7: getorf on data 1', which is highlighted in green. A red arrow with the number '1' points to the 'Show in tool panel' checkbox in the workflow table.

W21-9: Galaxyへの取り込み

①解析データのGalaxyへの取り込み (W17-3と同じ)

The screenshot shows the Galaxy Workflows interface. A red arrow with the number '1' points to the 'Analyze Data' button in the top navigation bar. A tooltip above this button reads 'Download from URL or upload files from disk'. The main content area displays a table of workflows with columns for Name, Tags, Owner, # of Steps, Published, and Show in tool panel. The History panel on the right shows a list of datasets with their names and actions.

Name	Tags	Owner	# of Steps	Published	Show in tool panel
imported: Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>
Workflow constructed from history 'ERR519393_0130_1'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_used'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393'		You	9	No	<input type="checkbox"/>

History panel contents:

- Trim (7 shown, 1 deleted, 7.5 KB)
- 7: getorf on data 1
- 6: plotorf on data 1
- 5: Trim on data 3
- 4: Trim on data 3
- 3: multi_FASTA_demo_3.fasta
- 2: Trim on data 1
- 1: demo0_seq.txt

W21-9: Galaxyへの取り込み

The screenshot shows the Galaxy web interface with a dialog box titled "Download from web or upload from disk". The dialog has three tabs: "Regular", "Composite", and "Collection". The "Regular" tab is selected. Inside the dialog, there is a large dashed box with the text "Drop files here". Below this box, there are two dropdown menus: "Type (set all):" with "Auto-detect" selected, and "Genome (set all):" with "----- Additional Species A..." selected. At the bottom of the dialog, there are several buttons: "Choose local file", "Choose FTP file", "Paste/ Fetch data", "Pause", "Reset", "Start", and "Close". A red arrow with the number "1" points to the "Paste/ Fetch data" button.

W21-10: ダウンロード (DL)

The screenshot shows the Galaxy Workflows interface. The browser address bar displays <https://usegalaxy.org/workflows/list>. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The 'Download from web or upload from disk' dialog box is open, showing the 'Regular' tab selected. A message states: 'You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.' Below this is a table with columns: Name, Size, Type, Genome, Settings, and Status. The table contains one entry: 'New File' with size '-', type 'Auto-dete...', genome '----- Additional Sp...', and status '0%'. Below the table is a text input area with the instruction: 'You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.' At the bottom of the dialog, there are controls for 'Type (set all): Auto-detect', 'Genome (set all): ----- Additional Species A...', and buttons for 'Choose local file', 'Choose FTP file', 'Paste/Fetch data', 'Pause', 'Reset', 'Start', and 'Close'.

W21-11: URLのコピペ

①メールで指定された確認用データファイルのURLをコピペして、②Start

The screenshot shows the Galaxy web interface. The main dialog box is titled "Download from web or upload from disk". It has three tabs: "Regular", "Composite", and "Collection". Below the tabs, it says "You added 1 file(s) to the queue. Add more files or click 'Start' to proceed." There is a table with columns: Name, Size, Type, Genome, Settings, and Status. The table contains one row for a "New File" with a size of "76 b". Below the table, there is a text input field containing the URL "http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fasta.gz". A red arrow with the number "1" points to this input field. At the bottom of the dialog, there are several buttons: "Choose local file", "Choose FTP file", "Paste/Fetch data", "Pause", "Reset", "Start", and "Close". A red arrow with the number "2" points to the "Start" button.

Name	Size	Type	Genome	Settings	Status
New File	76 b	Auto-dete...	----- Additional Sp...	⚙️	0%

Type (set all): Auto-detect Genome (set all): ----- Additional Species A...

Buttons: Choose local file, Choose FTP file, Paste/Fetch data, Pause, Reset, Start, Close

W21-12:DL終了

The screenshot shows the Galaxy Workflows interface. A modal window titled "Download from web or upload from disk" is open. It has three tabs: "Regular", "Composite", and "Collection". The "Regular" tab is selected. Below the tabs is a table with columns: Name, Size, Type, Genome, Settings, and Status. The table contains one row for a "New File" with a size of "76 b", type "Auto-dete...", genome "---- Additional Sp...", and a status of "100%". Below the table is a text input field containing the URL: `http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fasta.gz`. At the bottom of the modal, there are two dropdown menus for "Type (set all):" (set to "Auto-detect") and "Genome (set all):" (set to "---- Additional Species A..."). At the very bottom are buttons for "Choose local file", "Choose FTP file", "Paste/Fetch data", "Pause", "Reset", "Start", and "Close". A red arrow with the number "1" points to the "Close" button.

Name	Size	Type	Genome	Settings	Status
New File	76 b	Auto-dete...	---- Additional Sp...		100%

W22-1: 下準備ほぼ完了

W17-9では①の部分の名前を変更しましたが、ここではそのままやります。
②ツールパネルで③下にスクロール

The screenshot shows the Galaxy Workflows interface. The 'Tools' panel on the left is expanded, and the 'Your workflows' table is visible. A red arrow labeled '1' points to the 'Tools' header, another labeled '3' points to the scroll bar of the 'Tools' panel, and a third labeled '1' points to the 'History' panel on the right.

Name	Tags	Owner	# of Steps	Published	Show in tool panel
imported: Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>
Workflow constructed from history 'ERR519393_0130_1'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_used'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393'		You	9	No	<input type="checkbox"/>

History panel content:

- Trim (8 shown, 1 deleted)
- 9: http://www.iu.a-u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq
- 7: getorf on data 1
- 6: plotorf on data 1
- 5: Trim on data 3
- 4: Trim on data 3
- 3: multi_FASTA_demo_3.fasta
- 2: Trim on data 1
- 1: demo0_seq.txt

W22-2: ワークフロー実行

The screenshot shows the Galaxy web interface. The main content area displays a list of workflows under the heading "Your workflows". A search bar is present above the list. The list has columns for Name, Tags, Owner, # of Steps, Published, and Show in tool panel. A red arrow with the number 1 points to the first workflow entry: "imported: Workflow constructed from history 'inudoshi_desu'".

Name	Tags	Owner	# of Steps	Published	Show in tool panel
imported: Workflow constructed from history 'inudoshi_desu'		You	3	No	<input checked="" type="checkbox"/>
Workflow constructed from history 'ERR519393_0130_1'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393_used'		You	9	No	<input type="checkbox"/>
Workflow constructed from history 'ERR519393'		You	9	No	<input type="checkbox"/>

The right sidebar shows the "History" panel with a search bar and a list of datasets. The top dataset is "Trim" (186.07 MB) with 8 shown and 1 deleted. Below it are several other datasets, including "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq", "7: getorf on data 1", "6: plotorf on data 1", "5: Trim on data 3", "4: Trim on data 3", "3: multi_FASTA_demo 3.fasta", "2: Trim on data 1", and "1: demo0_seq.txt".

W22-3: 中央パネル

中央パネルはこんな感じになります。①の部分は、個々人の履歴リーパネルの状態によって異なる

The screenshot displays the Galaxy web interface for a workflow. The central panel shows the workflow configuration for 'inudoshi_desu'. A red arrow labeled '1' points to the '1: FastQC (Galaxy Version 0.69)' step. The right panel shows a history list with datasets. A red box highlights the last five items in the history list: '7: getorf on data 1', '6: plotorf on data 1', '5: Trim on data 3', '4: Trim on data 3', and '3: multi_FASTA_demo 3.fasta'.

W22-3: 中央パネル

重要なのは、①解析したい入力ファイルが、②で見えているということ

The screenshot displays the Galaxy web interface for configuring a workflow. The central panel, titled "Workflow: imported: Workflow constructed from history 'inudoshi_desu'", contains several configuration sections:

- History Options:** Includes a "Send results to a new history" section with "Yes" and "No" radio buttons.
- 1: FastQC (Galaxy Version 0.69):** A section for "Short read data from your current history" with a text input field containing a URL: "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR0245...". A red arrow labeled "2" points to this input field.
- Contaminant list:** A dropdown menu currently showing "Nothing selected".
- Submodule and Limit specifying file:** Another dropdown menu showing "Nothing selected".

A red arrow labeled "1" points to the "Run workflow" button at the top right of the central panel. The right-hand panel, titled "History", shows a list of datasets and tools, including "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq", "7: getorf on data 1", "6: plotorf on data 1", "5: Trim on data 3", "4: Trim on data 3", "3: multi_FASTA_demo 3.fasta", "2: Trim on data 1", and "1: demo0_seq.txt".

W22-4: History Options

但し、今は①は無関係なので、新しい履歴にワークフロー実行結果を格納すべく、②Yesに変更

The screenshot shows the Galaxy web interface. The main content area displays a workflow titled "Workflow: imported: Workflow constructed from history 'inudoshi_desu'". A "Run workflow" button is visible. Below the title, there are several sections:

- History Options:** A section with a red arrow labeled "2" pointing to the text "results to a new history". Below this text are two buttons: "Yes" and "No".
- 1: FastQC (Galaxy Version 0.69):** A section with a red arrow labeled "1" pointing to the title. It contains a dropdown menu with the value "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR0245...".

The right sidebar shows the "History" panel, which lists several datasets and workflows. A red box highlights the following items:

- 7: getorf on data 1
- 6: plotorf on data 1
- 5: Trim on data 3
- 4: Trim on data 3
- 3: multi_FASTA_demo 3.fasta
- 2: Trim on data 1
- 1: demo0_seq.txt

The top navigation bar includes "Galaxy", "Analyze Data", "Workflow", "Shared Data", "Visualization", "Help", "User", and "Using 9%". The left sidebar lists various tool categories such as "Get Data", "Text Manipulation", "NGS: QC and manipulation", etc.

W22-4: History Options

Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 9%

Tools

search tools

Get Data
Lift-Over
Collection Operations
Text Manipulation
Datamash
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
NGS: QC and manipulation
NGS: DeepTools
NGS: Mapping
NGS: RNA Analysis
NGS: SAMtools
NGS: BamTools
NGS: Picard
NGS: VCF Manipulation
NGS: Peak Calling
NGS: Variant Analysis
NGS: RNA Structure
NGS: De Novo

Workflow: imported: Workflow constructed from history 'inudoshi_desu'

Run workflow

History Options

Results to a new history

Yes No

History name

imported: Workflow constructed from history 'inudoshi_desu'

1: FastQC (Galaxy Version 0.69)

Short read data from your current history

9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR0245...

Contaminant list

Nothing selected

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

Submodule and Limit specifying file

Nothing selected

History

search datasets

Trim

8 shown, 1 deleted

186.07 MB

9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq

7: getorf on data 1

6: plotorf on data 1

5: Trim on data 3

4: Trim on data 3

3: multi_FASTA_demo_3.fasta

2: Trim on data 1

1: demo0_seq.txt

ここでは①inudoshi_desu
reverse_dataと変更した

W22-5: ヒストリー名変更

The screenshot shows the Galaxy web interface. The main content area displays the configuration for a workflow named "imported: Workflow constructed from history 'inudoshi_desu'". A red arrow points to the "History name" input field, which contains the text "inudoshi_desu reverse_data" and a circled "1". The "History Options" section includes a "Send results to a new history" toggle (set to "Yes"), a "History name" input field, and a "1: FastQC (Galaxy Version 0.69)" tool selection. The "Short read data from your current history" dropdown is set to "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR0245...". The "Contaminant list" dropdown is set to "Nothing selected". The "Submodule and Limit specifying file" dropdown is also set to "Nothing selected". The right sidebar shows a "History" panel with a search bar and a list of datasets, including "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq", "7: getorf on data 1", "6: plotorf on data 1", "5: Trim on data 3", "4: Trim on data 3", "3: multi_FASTA_demo_3.fasta", "2: Trim on data 1", and "1: demo0_seq.txt".

W22-6: Run workflow

Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 9%

Workflow: imported: Workflow constructed from history 'inudoshi_desu'

Run workflow

History Options

Send results to a new history

Yes No

History name

inudoshi_desu reverse_data

1: FastQC (Galaxy Version 0.69)

Short read data from your current history

9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR0245...

Contaminant list

Nothing selected

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

Submodule and Limit specifying file

Nothing selected

History

search datasets

Trim

8 shown, 1 deleted

186.07 MB

9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq

7: getorf on data 1

6: plotorf on data 1

5: Trim on data 3

4: Trim on data 3

3: multi_FASTA_demo_3.fasta

2: Trim on data 1

1: demo0_seq.txt

W22-7: ジョブ投げ中...

① Sending... になっているのがわかります (W18-8)

The screenshot shows the Galaxy web interface. The browser address bar displays `https://usegalaxy.org/workflows/run?id=380a2a1cc7d4370a`. The main content area is titled "Workflow: imported: Workflow constructed from history 'inudoshi_desu'". A blue button labeled "Sending..." is positioned above the workflow options, with a red arrow and the number "1" pointing to it. The workflow options include "History Options" with a "Send results to a new history" toggle set to "Yes", a "History name" field containing "inudoshi_desu reverse_data", and a selected tool "1: FastQC (Galaxy Version 0.69)". The right-hand "History" panel shows a list of datasets, including "9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq" and "7: getorf on data 1".

W22-7: Successfully invoked

①無事ワークフローを呼び出す (invoke) ことができたようです。W18-9とほぼ同じだが

The screenshot shows the Galaxy web interface. The browser address bar displays `https://usegalaxy.org/workflows/run?id=380a2a1cc7d4370a`. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. A 'Using 9%' indicator is visible on the right.

The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: Get Data, Lift-Over, Collection Operations, Text Manipulation, Datamash, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, NGS: QC and manipulation, NGS: DeepTools, NGS: Mapping, NGS: RNA Analysis, NGS: SAMtools, NGS: BamTools, NGS: Picard, NGS: VCF Manipulation, NGS: Peak Calling, NGS: Variant Analysis, NGS: RNA Structure, and NGS: De Novo.

The main content area features a green notification box with a checkmark icon. The text reads: 'Successfully invoked workflow imported: Workflow constructed from history 'inudoshi_desu'. 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.'

The right sidebar shows the 'History' pane with a search bar and a list of workflow steps. The steps are numbered 1 through 9, each with a status icon (eye, pencil, or X) and a delete icon (X). The steps are: 1: demo0_seq.txt, 2: Trim on data 1, 3: multi_FASTA_demo 3.fasta, 4: Trim on data 3, 5: Trim on data 3, 6: plotorf on data 1, 7: getorf on data 1, 9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq. Above the list, it says 'Trim' with '8 shown, 1 deleted' and '186.07 MB'.

W22-8: 待てど暮らせど...

①Refresh historyをやろうが、何も変化はありません。理由は明確で、これは②Trimというヒストリーだから

The screenshot shows the Galaxy web interface. The browser address bar is <https://usegalaxy.org/workflows/run?id=380a2a1cc7d4370a>. The main content area displays a green notification box with a checkmark icon and the text: "Successfully invoked workflow imported: Workflow constructed from history 'inudoshi_desu'. 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." The History panel on the right shows a list of steps, with 'Trim' selected. A red arrow labeled '1' points to the 'Refresh history' button in the History panel. Another red arrow labeled '2' points to the 'Trim' step in the History panel.

Step	Tool	View	Edit	Delete
9	http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq	👁	✎	✖
7	getorf on data 1	👁	✎	✖
6	plotorf on data 1	👁	✎	✖
5	Trim on data 3	👁	✎	✖
4	Trim on data 3	👁	✎	✖
3	multi_FASTA_demo_3.fasta	👁	✎	✖
2	Trim on data 1	👁	✎	✖
1	demo0_seq.txt	👁	✎	✖

W23-1 : View all histories

W22-5を思い出すとピンとくるが、ワークフロー実行結果はinudoshi_desu reverse_dataに格納されているはずなので、②View all historiesで確認

The screenshot shows the Galaxy web interface. The browser address bar displays <https://usegalaxy.org/workflows/run?id=380a2a1cc7d4370a>. The main content area features a green notification box with a checkmark icon and the text: "Successfully invoked workflow imported: Workflow constructed from history 'inudoshi_desu'. 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." To the right, the "History" panel is visible, containing a search bar and a list of workflow steps. Step 9 is highlighted in green and contains the URL: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq. A red arrow labeled "1" points to the "View all histories" button in the top right corner of the history panel.

W23-2: 実行結果を無事発見

The screenshot shows the Galaxy web interface with three panels of dataset history. The middle panel, titled "inudoshi_desu reverse_data", has a red arrow pointing to its "Switch to" dropdown menu, which is labeled with a circled "1".

Panel Title	Dataset List
Trim	8 shown, 1 deleted 186.07 MB 9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq 7: getorf on data 1 6: plotorf on data 1 5: Trim on data 3 4: Trim on data 3 3: multi_FASTA_demo3.fasta 2: Trim on data 1 1: demo0_seq.txt
inudoshi_desu reverse_data	5 shown 141.11 MB 5: FastQC on data 3: RawData 4: FastQC on data 3: Webpage 3: Trimmomatic on http://www.iu.a.u-tokyo.ac.jp/Xkadota/book/DRR024501/DRR024501sub_2.fastq 2: FastQC on data 9: RawData 1: FastQC on data 9: Webpage
ERR519385_0201_2	18 shown, 1 hidden 1.2 GB 18: Trinity on data 10 and data 9: Assembled Transcripts 17: Trinity on data 10 and data 9: log 16: FastQC on data 10: RawData 15: FastQC on data 10: Webpage 14: FastQC on data 9: RawData 13: FastQC on data 9: Webpage 12: Trimmomatic on ERR519385_2.fastq (R2 unpaired)

①Switch toで、②Current Historyのところに移動

W23-3: Switch to

The screenshot shows the Galaxy web interface with three panels. The top panel is the 'Switch to' dropdown menu, which is currently open and shows a list of datasets. A red arrow labeled '1' points to the 'Switch to' dropdown. The middle panel is the 'Current History' dropdown menu, which is currently open and shows a list of history items. A red arrow labeled '2' points to the 'Current History' dropdown. The bottom panel is the main content area, which is currently empty.

Galaxy | Histories x

Secure | https://usegalaxy.org/history/view_multiple

Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 9%

Done search histories datasets Create new

Current History Switch to Switch to

Trim
8 shown, 1 deleted
186.07 MB
search datasets
Drag datasets here to copy them to the current history

9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq

7: [getorf on data 1](#)

6: [plotorf on data 1](#)

5: [Trim on data 3](#)

4: [Trim on data 3](#)

3: [multi_FASTA_demo3.fasta](#)

2: [Trim on data 1](#)

1: [demo0_seq.txt](#)

inudoshi_desu reverse_data
5 shown
141.11 MB
search datasets

5: [FastQC on data 3: RawData](#)

4: [FastQC on data 3: Webpage](#)

3: [Trimmomatic on http://www.iu.a.u-tokyo.ac.jp/Xkadota/book/DRR024501/DRR024501sub_2.fastq](#)

2: [FastQC on data 9: RawData](#)

1: [FastQC on data 9: Webpage](#)

ERR519385_0201_2
18 shown, 1 hidden
1.2 GB
search datasets

18: [Trinity on data 10 and data 9: Assembled Transcripts](#)

17: [Trinity on data 10 and data 9: log](#)

16: [FastQC on data 10: RawData](#)

15: [FastQC on data 10: Webpage](#)

14: [FastQC on data 9: RawData](#)

13: [FastQC on data 9: Webpage](#)

12: [Trimmomatic on ERR519385_2.fastq \(R2 unpaired\)](#)

無事移動完了です。
この状態で、①Done

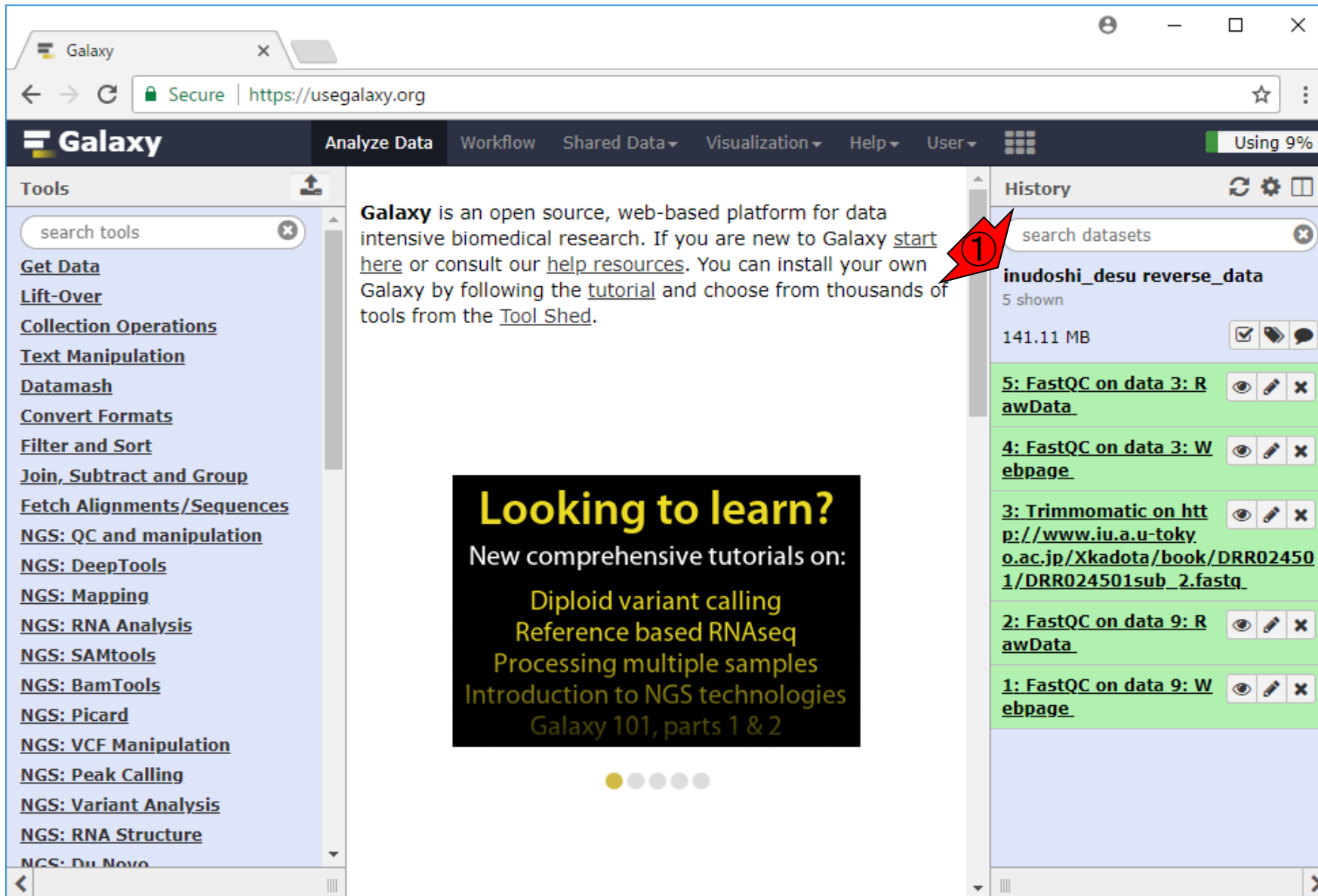
W23-4: 移動完了

The screenshot shows the Galaxy web interface with three history panels. A red arrow with the number 1 points to the 'inudoshi_desu reverse_data' panel. The interface includes a search bar, navigation tabs, and a list of datasets with their respective workflow steps.

History Panel	Name	Size	Items
inudoshi_desu reverse_data	5 shown	141.11 MB	5: FastQC on data 3: RawData, 4: FastQC on data 3: Webpage, 3: Trimmomatic on http://www.iu.a.u-tokyo.ac.jp/Xkadota/book/DRR024501/DRR024501sub_2.fastq, 2: FastQC on data 9: RawData, 1: FastQC on data 9: Webpage
Trim	8 shown, 1 deleted	186.07 MB	9: http://www.iu.a.u-tokyo.ac.jp/~kadota/book/DRR024501/DRR024501sub_2.fastq, 7: getorf on data 1, 6: plotorf on data 1, 5: Trim on data 3, 4: Trim on data 3, 3: multi_FASTA_demo3.fasta, 2: Trim on data 1, 1: demo0_seq.txt
ERR519385_0201_2	18 shown, 1 hidden	1.2 GB	18: Trinity on data 10 and data 9: Assembled Transcripts, 17: Trinity on data 10 and data 9: log, 16: FastQC on data 10: RawData, 15: FastQC on data 10: Webpage, 14: FastQC on data 9: RawData, 13: FastQC on data 9: Webpage, 12: Trimmomatic on ERR519385_2.fastq (R2 unpaired)

無事通常画面上に、①ワークフロー実行結果が反映されました

W23-5: 反映完了



The screenshot shows the Galaxy web interface. The main content area displays a welcome message: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#)." A red arrow with the number 1 points to the top of the History panel on the right.

History

- search datasets
- inudoshi_desu reverse_data**
5 shown
141.11 MB
- 5: FastQC on data 3: RawData**
- 4: FastQC on data 3: Webpage**
- 3: Trimmomatic on http://www.iu.a.u-tokyo.ac.jp/Xkadota/book/DRR024501/DRR024501sub_2.fastq**
- 2: FastQC on data 9: RawData**
- 1: FastQC on data 9: Webpage**

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Reference based RNAseq
Processing multiple samples
Introduction to NGS technologies
Galaxy 101, parts 1 & 2