

## Feedback — Module 3 Quiz

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Thank you. Your submission for this quiz was received.

You submitted this quiz on **Wed 12 Aug 2015 10:10 PM PDT**. You got a score of **28.00** out of **28.00**.

### Question 1

Where are basic analyses you can perform found in the Galaxy interface?

Your Answer	Score	Explanation
<input type="radio"/> Data Libraries		
<input type="radio"/> The History		
<input type="radio"/> The Workflow Tab		
<input checked="" type="radio"/> The Tool Panel	✓ 1.00	
Total	1.00 / 1.00	

### Question 2

Where are the datafiles and output of analysis you have performed located in the Galaxy interface?

Your Answer	Score	Explanation
<input type="radio"/> The Workflow Tab		
<input type="radio"/> The Tool Panel		
<input type="radio"/> Data Libraries		

<input checked="" type="radio"/> The History	✓	1.00
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Total	1.00 / 1.00
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## Question 3

Where can I find tools that download or upload data to Galaxy?

Your Answer	Score	Explanation
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<input type="radio"/> In the Galaxy History		
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<input type="radio"/> The Workflow Tab		
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<input type="radio"/> Shared Data tab in Galaxy's top navigation bar		
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<input checked="" type="radio"/> Get Data in the tool panel	✓	1.00
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Total	1.00 / 1.00
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## Question 4

What file format was used for both the exon and repeat data in the exercise?

Your Answer	Score	Explanation
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<input type="radio"/> GFF file format		
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<input type="radio"/> FASTA file format		
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<input type="radio"/> TXT file format		
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<input checked="" type="radio"/> BED file format	✓	1.00
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Total	1.00 / 1.00
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## Question 5

What information is not contained within a BED file?

Your Answer	Score	Explanation
<input type="radio"/> A name for each feature		
<input type="radio"/> Position on chromosome for each feature		
<input checked="" type="radio"/> The genome the feature belongs to	✓ 1.00	
<input type="radio"/> The strand on which the feature is encoded		
Total	1.00 / 1.00	

## Question 6

What does the “Operate on Genomic Intervals: Join” tool do?

Your Answer	Score	Explanation
<input checked="" type="radio"/> Join overlapping region from two or more datasets	✓ 1.00	
<input type="radio"/> Combine overlapping regions within a single dataset		
<input type="radio"/> Match rows in one or more datasets that share the same key		
<input type="radio"/> Combine regions that are located close to each other along the chromosome		
Total	1.00 / 1.00	

## Question 7

What question are we trying to answer using the exon and repeat data?

Your Answer	Score	Explanation
<input type="radio"/> How many exons in each gene?		
<input type="radio"/> Which exons overlap a repetitive element?		
<input checked="" type="radio"/> How many repeat regions overlap each exon region?	✓ 1.00	
<input type="radio"/> How many exons overlap each repeat region?		
Total	1.00 / 1.00	

## Question 8

Which of the following can be done with the group tool?

Your Answer	Score	Explanation
<input type="radio"/> Combine columns based on common values		
<input checked="" type="radio"/> Count the occurrence of each record or data field within a file	✓ 1.00	
<input type="radio"/> Identify datasets with similar characteristics		
<input type="radio"/> Combine datasets based on similar fields		
Total	1.00 / 1.00	

## Question 9

How does Galaxy assist in the reproducibility of analysis?

Your Answer	Score	Explanation
<input checked="" type="radio"/> All of these options	✓ 1.00	
<input type="radio"/> Archives data from external databases that may change		

☐ Allows repeating the entire analysis

☐ Automatically maintains records of tools and parameters

Total

1.00 / 1.00

## Question 10

The “pencil” icon in the Galaxy history allows you to do all but

Your Answer	Score	Explanation
<input checked="" type="radio"/> Edit a dataset’s contents	✓ 1.00	
<input type="radio"/> Modify metadata about a datasets		
<input type="radio"/> Provide an annotation for a datasets		
<input type="radio"/> Modify the name of a datasets		
Total	1.00 / 1.00	

## Question 11

The file [Quiz3\\_Genes.bed](#) contains locations of how many transcripts?

Your Answer	Score	Explanation
<input type="radio"/> 1810		
<input type="radio"/> 1510		
<input type="radio"/> 1620		
<input checked="" type="radio"/> 1720	✓ 1.00	
Total	1.00 / 1.00	

## Question 12

The file [Quiz3\\_Genes.bed](#) contains locations of how many genes?

Your Answer	Score	Explanation
<input checked="" type="radio"/> 1510	✓ 1.00	
<input type="radio"/> 1810		
<input type="radio"/> 1320		
<input type="radio"/> 1620		
Total	1.00 / 1.00	

## Question 13

What is a workflow?

Your Answer	Score	Explanation
<input type="radio"/> A tutorial for analyzing a type of data		
<input type="radio"/> A summary of the provenance of a given piece of data		
<input type="radio"/> A description of how to carry out an analysis on a specific dataset		
<input checked="" type="radio"/> An abstract representation of a multi-step analysis	✓ 1.00	
Total	1.00 / 1.00	

## Question 14

How can a workflow be added to a Galaxy instance?

**Your Answer****Score****Explanation**☒ All of these options 1.00☐ Import a workflow from a file☐ Create a new workflow from scratch with the workflow editor☐ Create a workflow from an existing history

Total

1.00 /  
1.00

## Question 15

Which of the following statements is true?

**Your Answer****Score****Explanation**☐ Files can be uploaded as part of running a workflow☒ Galaxy allows sending workflow data to a new history 1.00☐ Workflows cannot run multiple tools in parallel☐ A workflow can only operate on one type of data

Total

1.00 / 1.00

## Question 16

Which are advanced options available in workflows?

**Your Answer****Score****Explanation**☒ Both of these options 1.00☐ Rename output datasets

☐ Neither of these options

☐ Hide datasets that represent intermediate steps

Total

1.00 / 1.00

## Question 17

Which of the following is true of tags?

**Your Answer**

**Score**

**Explanation**

☐ They can only be attached to datasets

☒ An item can have more than one of them



1.00

☐ They can contain arbitrary free form text

☐ They can only be created by a Galaxy administrator

Total

1.00 / 1.00

## Question 18

Which of the following is true of annotations?

**Your Answer**

**Score**

**Explanation**

☐ They can only be created by a Galaxy administrator

☒ They can contain arbitrary free form text



1.00

☐ An item can have more than one of them

☐ They can only be attached to datasets

Total

1.00 / 1.00



## Question 19

Which of the following is true of tags and annotations?

Your Answer	Score	Explanation
<input type="radio"/> They allow users to provide additional information about entities in Galaxy		
<input type="radio"/> They can be used for search		
<input checked="" type="radio"/> All of these options	✓ 1.00	
<input type="radio"/> They can be attached to Datasets, Histories, and Workflows		
Total	1.00 / 1.00	

## Question 20

What does it mean to share a galaxy history?

Your Answer	Score	Explanation
<input type="radio"/> Make the history automatically available on any Galaxy server		
<input type="radio"/> Automatically send an email/tweet/facebook with a link to it		
<input checked="" type="radio"/> Only certain users will be able to access it	✓ 1.00	
<input type="radio"/> Make is possible to download an entire history		
Total	1.00 / 1.00	

## Question 21

What does it mean to publish a galaxy history?

Your Answer	Score	Explanation
<input type="radio"/> Post it on social media (twitter/facebook)		
<input checked="" type="radio"/> The history will be listed in a central, public place within Galaxy and all users can access it	✓ 1.00	
<input type="radio"/> Email the history		
<input type="radio"/> Post it on a blog		
Total	1.00 / 1.00	

## Question 22

What do you need to share a history with just one user?

Your Answer	Score	Explanation
<input type="radio"/> It cannot be done; a history can only be shared with all users		
<input type="radio"/> Galaxy administrator access		
<input type="radio"/> Access to a server where the data can be uploaded to		
<input checked="" type="radio"/> The email associated with the user's Galaxy account	✓ 1.00	
Total	1.00 / 1.00	

## Question 23

Who can see a history that's been made 'accessible'?

Your Answer	Score	Explanation
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☐ It is visible on the 'Published Histories' page so anyone that clicks on the history name

☒ Anyone who knows the URL (the browser address) ✓ 1.00

☐ Only people I have given explicit permission

☐ Only the person that owns (i.e., has created) this history

Total 1.00 /  
1.00

## Question 24

Where are published histories found on Galaxy?

Your Answer	Score	Explanation
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☐ All of these options

☐ In a Data Library

☐ On the Galaxy's wiki

☒ Shared Data -> Published Histories ✓ 1.00

Total 1.00 / 1.00

## Question 25


What can you do if you no longer want a history to be accessible?

Your Answer	Score	Explanation
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☐ Rename the history

☐ It must be deleted


☐ Need to send an email to helpdesk and ask to make it private

- ☒ From the same interface used to make it accessible: use the 'Share or Publish' link in the history options  1.00

Total 1.00 / 1.00


## Question 26

What do Galaxy pages allow you to do?

Your Answer	Score	Explanation
<input type="radio"/> Embed histories		
<input checked="" type="radio"/> All of these options	 1.00	
<input type="radio"/> Add and format text		
<input type="radio"/> None of these options		
Total	1.00 / 1.00	

## Question 27

Why can annotations be important in a Galaxy page?

Your Answer	Score	Explanation
<input type="radio"/> They are required to share the page with others		
<input checked="" type="radio"/> They can be used to describe why an analysis was performed in a particular way	 1.00	
<input type="radio"/> They provide machine readable provenance information		
<input type="radio"/> They are needed to attach histories and workflow to a page		
Total	1.00 / 1.00	

## Question 28

What are Data Libraries?

Your Answer	Score	Explanation
<input checked="" type="radio"/> Another way to share data and make it easy to find	✓ 1.00	
<input type="radio"/> Where all data that is shared by users can be found		
<input type="radio"/> How you search through data you have created in Galaxy		
<input type="radio"/> A way to get data from external databases		
Total	1.00 / 1.00	