

Feedback — Module 5 Quiz ****Please Note: No Grace Period****

[Help Center](#)

Thank you. Your submission for this quiz was received.

You submitted this quiz on **Fri 14 Aug 2015 10:00 PM PDT**. You got a score of **11.00** out of **11.00**.

Question 1

What does it mean to align-then-assemble?

Your Answer	Score	Explanation
<input type="radio"/> Align existing reference genomes, and then assemble the reads.		
<input type="radio"/> Assemble transcripts, and then align transcripts to an existing genome.		
<input type="radio"/> Align and assemble existing reference genomes.		
<input checked="" type="radio"/> Align reads to an existing reference genome, and then assemble transcripts from the spliced alignments.	✓ 1.00	
Total	1.00 / 1.00	

Question 2

Which of the following statements is FALSE?

Your Answer	Score	Explanation
<input type="radio"/> Align-then-assemble is not robust to variation		

☐ Align-then-assemble approach is potentially more sensitive.

☐ De-novo assembly is more computationally intensive than align-then-assemble.

☒ De-novo assembly is not robust to variation ✓ 1.00

Total 1.00 / 1.00

Question 3

What of following formats can tophat results produce?

A) BED format.

B) ADAM format.

C) BAM format.

Your Answer	Score	Explanation
<input checked="" type="radio"/> A and C ✓	1.00	
<input type="radio"/> C		
<input type="radio"/> B		
<input type="radio"/> A and B		
Total	1.00 / 1.00	

Question 4

Which tool in the cufflinks suite is used to find the differentially expressed genes?

Your Answer	Score	Explanation
<input checked="" type="radio"/> Cuffdiff ✓	1.00	

☐ Cuffquant☐ Cuffmerge☐ Cufflinks

Total

1.00 / 1.00

Question 5

One of the options is NOT a column in the output produced by Cuffdiff.

Your Answer	Score	Explanation
<input type="radio"/> q_value		
<input type="radio"/> log2 (fold change)		
<input checked="" type="radio"/> Length of the differentially expressed gene	✓ 1.00	
<input type="radio"/> gene name and gene ID		
Total	1.00 / 1.00	

Question 6

What is the main purpose of Cuffmerge and what is its input format?

Your Answer	Score	Explanation
<input type="radio"/> To merge different Cufflinks assemblies and BED files		
<input type="radio"/> To find differentially expressed genes and BED files		
<input type="radio"/> To merge different Cufflinks assemblies and SAM files.		
<input checked="" type="radio"/> To merge different Cufflinks assemblies together and GTF files.	✓ 1.00	
Total	1.00 /	

1.00

Question 7

Can we use Galaxy to run the same tophat (or other tool) job over Multiple datasets?

Your Answer	Score	Explanation
<input type="radio"/> Yes, but the datasets need to be of the same format.		
<input type="radio"/> Yes, but not with all tools.		
<input checked="" type="radio"/> Yes, the datasets need to be of the format the tool can take as input.	✓ 1.00	
<input type="radio"/> No, this is not supported, yet.		
Total	1.00 / 1.00	

Question 8

What Galaxy tool might we use to refine our Cuffdiff output to show only differentially expressed genes?

Your Answer	Score	Explanation
<input type="radio"/> Cuffmerge		
<input checked="" type="radio"/> Filter	✓ 1.00	
<input type="radio"/> Select random lines		
<input type="radio"/> Cufflinks		
Total	1.00 / 1.00	

Question 9

What comes after mapping the RNA seq data to a reference genome?

Your Answer	Score	Explanation
<input type="radio"/> Remap the reads using TopHat and continue to do differential expression analysis using the Cufflinks suite.		
<input checked="" type="radio"/> Using a reference annotation we continue to do differential expression analysis using the Cufflinks suite.	✓ 1.00	
<input type="radio"/> QC again to make sure we have mapped correctly.		
<input type="radio"/> Compare the reference annotation with the reference genome.		
Total	1.00 / 1.00	

Question 10

What is the idea behind setting the tool form “Use Reference Annotation” to “reference annotation as guide” in Cufflinks?

- A) Tells Cufflinks to use the reference annotation to guide the assembly.
- B) Results will contain referenced transcripts, novel genes and isoforms.
- C) Tells Cufflinks to remove all unannotated transcripts.

Your Answer	Score	Explanation
<input type="radio"/> B		
<input checked="" type="radio"/> A and B	✓ 1.00	
<input type="radio"/> A and C		
<input type="radio"/> C		
Total	1.00 / 1.00	

Question 11

What does the “log2(fold change)” in the gene differential expression testing result mean?

- A) Its the log-ratio of FPKM values for a pair of expressed genes.
- B) Its the log-ratio between mapped and unmapped reads.
- C) It indicates genes with significantly different expression profiles.

Your Answer	Score	Explanation
<input type="radio"/> B		
<input type="radio"/> C		
<input type="radio"/> A and B		
<input checked="" type="radio"/> A and C	✓ 1.00	
Total	1.00 / 1.00	