Feedback — Module 4 Quiz

Help Center

Thank you. Your submission for this quiz was received.

You submitted this quiz on **Wed 30 Sep 2015 10:30 PM PDT**. You got a score of **10.00** out of **10.00**.

Question 1

Which of the following is FALSE:

Your Answer		Score	Explanation
○ Splice isoforms result from different combinations of a gene's exons.			
○ A codon is a nucleotide triplet that is translated into one amino acid.			
◉ A human gene can express at most 12 splice variants.	✔	1.00	
○ Alternative splicing can create multiple protein and/or mRNA isoforms from the same gene.			
Total		1.00 / 1.00	

Question 2

Which of the following is FALSE about the organization of a eukaryotic gene:

Your Answer	Score	Explanation
○ Genes that have only one exon are not alternatively spliced.		
○ Some eukaryotic genes are single exon.		

The length of the coding region in a transcript must be a multiple of 3.		
The length of an intron cannot be a multiple of 3.	✔	1.00
Total		1.00 / 1.00

Question 3

What programs could you use to align RNA-seq reads to: i) a reference genome, and ii) a transcript database?

Your Answer		Score	Explanation
tophat, bowtie	✔	1.00	
bowtie, tophat			
tophat, bcftools			
bowtie, bcftools			
Total		1.00 / 1.00	

Question 4

Which of the following is FALSE:

Your Answer		Score	Explanation
Spliced reads can be used to determine the introns in a gene.			
Unspliced reads can be used to determine the introns of a gene.	✔	1.00	
'Transfrag' stands for 'transcript fragments', a reference to the fact than transcript assemblers cannot always reconstruct full-length splice variants.			

As measures of gene expression, RPKM is determined at the level of reads and FPKM is determined at the level of fragments.	
Total	1.00 / 1.00

Question 5

What programs could be used to: i) assemble transcripts from RNA-seq reads, and ii) identify potentially novel transcripts and genes?

Your Answer		Score	Explanation
cufflinks, cuffmerge			
cuffdiff, cuffdiff			
igv, cuffdiff			
cufflinks, cuffcompare	✔	1.00	
Total		1.00 / 1.00	

Question 6

Which of the following is FALSE about the gene annotations in the following GTF snippet:

```
chr1    MGF     gene    3413609 3671498 .       -       .       gene_id "MG
051951";
chr1    MGF     transcript      3413609 3416344 .       -       .gene_id "M
G051951"; transcript_id "MT162897";
chr1    MGF     exon    3413609 3416344 .       -       .       gene_id "MG
051951"; transcript_id "MT162897";
chr1    MGF     transcript      3421702 3671498 .       -       .       gen
e_id "MG051951"; transcript_id "MT070533";
chr1    MGF     exon    3670552 3671498 .       -       .       gene_id "MG
051951"; transcript_id "MT070533";
```

```
chr1    MGF     CDS     3670552 3671348 .       -       0       gene_id "MG
051951"; transcript_id "MT070533";
chr1    MGF     exon    3421702 3421901 .       -       .       gene_id "MG
051951"; transcript_id "MT070533";
chr1    MGF     CDS     3421792 3421901 .       -       1       gene_id "MG
051951"; transcript_id "MT070533";
```

Your Answer		Score	Explanation
○ The coding sequence (CDS) for transcript MT070533 contains two exons.			
◉ The two transcripts for gene MG051951 overlap on the genome.	✔	1.00	
○ The gene spans the interval chr1:3413609-3671498.			
○ Transcript MT070533 is designated as coding.			
Total		1.00 / 1.00	

Question 7

What does the following code NOT do:

```
BWT2IDX=/home/me/genomes/hg20/hg20
ANNOT=/home/me/genomes/hg20/myannot.gtf
ANNOTIDX=/home/me/genomes/hg20/myannot/myannot

mkdir -p /home/me/SRR100000
tophat2 -o /home/me/SRR100000 -p 10 --max-multihits 10 \
        -r 26 --mate-std-dev 25 \
        -a 6 \
        -G $ANNOT --transcriptome-index $ANNOTIDX \
        $BWT2IDX \
        /home/me/SRR100000_1.fastq.gz /home/me/SR100000_2.fastq.gz
```

Your Answer		Score	Explanation
(•) Report spliced reads with at most 6 mismatches in the anchor site	✔	1.00	
( ) Create the output in the /home/me/SRR100000 directory			
( ) Report only reads with 10 or fewer alignments on the genome			
( ) Use a minimum anchor of 6 bases on either side of the intron for spliced reads			
Total		1.00 / 1.00	

Question 8

What does the following code NOT do:

```
TOPHATDIR=/home/florea/Tophat/

mkdir –p Test1
cd Test1
ln –s $TOPHATDIR/accepted_hits.bam .
cufflinks -L Test1 -p 8 –j 0.10 –F 0.05 accepted_hits.bam
```

Your Answer		Score	Explanation
( ) Generate a file named transcripts.gtf in directory Test1, containing all assembled transfrags			
(•) Use the default reference transcript annotation to guide assembly	✔	1.00	
( ) Use 0.10 as the minimum level for intra-intronic transcripts			
( ) Label cufflinks transcripts with the prefix ‘Test1’			
Total		1.00 / 1.00	

Question 9

Which of the following is NOT described in the following summary file produced by tophat:

```
Left reads:
          Input     :  60586968
           Mapped   :  58163843 (96.0% of input)
            of these:   6832240 (11.7%) have multiple alignments (359075 ha
ve >10)
Right reads:
          Input     :  60586968
           Mapped   :  56969290 (94.0% of input)
            of these:   6668479 (11.7%) have multiple alignments (358573 ha
ve >10)
95.0% overall read mapping rate.

Aligned pairs:  55880048
     of these:   6491876 (11.6%) have multiple alignments
                 2795712 ( 5.0%) are discordant alignments
87.6% concordant pair alignment rate.
```

Your Answer		Score	Explanation
◉ The reads were 100 bp long	✔	1.00	
○ 94.0% of the mate 2 reads were mapped			
○ The number of read pairs in which both mates were aligned is 55,880,048			
○ Of the aligned pairs, 6,491,876 had multiple matches on the genome			
Total		1.00 / 1.00	

Question 10

Which of the following is NOT TRUE about the output below, obtained from a cuffdiff differential expression analysis:

```
XLOC_000002     XLOC_000002     AT1G01020       1:5927-8737     q1      q2
OK      1.13032 3.48406 1.62404 0.694576        0.5277  0.998846        no
XLOC_000004     XLOC_000004     AT1G01073       1:44676-44787   q1      q2
NOTEST  0       0       0       0       1       1       no
XLOC_000042     XLOC_000042     AT1G01580       1:209394-213041 q1      q2
OK      1.59512 0       -inf    nan     5e-05   0.0096703       yes
```

Your Answer		Score	Explanation
○ Locus XLOC_000002 is located on the genomic axis '1', between positions 5927 and 8737			
○ Locus XLOC_000002 is differentially expressed between the two conditions			
◉ There are too many alignments for testing for differential expression at locus XLOC_000004	✔	1.00	
○ The q-value, or false discovery rate (FDR), at locus XLOC_000002 is 0.998846			
Total		1.00 / 1.00	