

Genome Assembly Assessment

Add questions, at least two answer alternatives and choose correct answers (at least one). Have fun creating your awesome quiz!

See an example question below (don't forget to overwrite this with your first question!)

	Question	Answer 1	Answer 2	Answer 3	Answer 4	- choose at least one
1	Which of the following can cause issues with genome assembly (multiple correct answers)?	Age of the organism sampled	Read length of sequencing	Low quality sequencing reads		2,3
2	What does a N50 value of 1Mb mean?	50% of sequences in the assembly are less than 1Mb in size	The assembly is made up of 50 contigs 1Mb in size	50 contigs in the assembly are larger than 1Mb in size	50% of sequences in the assembly are larger than 1Mb in size	4
3	What is scaffolding?	Identifying repetitive DNA	The process of ordering contigs into larger peices of DNA	Assessing a genome with Hi-C sequencing	Assembling individual sequencing reads into larger pieces	2
4	How does Nanopore sequencing determine the sequence of a piece of DNA?	By measuring the electric current across a membrane as DNA passes through a pore	By binding a flourophore to a growing DNA strand which changes color	By passing DNA through a pore which changes color	By running DNA on a agarose gel	1
5	When was the sequence of the human genome first published?	1995	2001	2010	2021	2
6	The entire sequence of the human genome is known.	TRUE	FALSE			2
7	How many contigs are there?	750	23000	500	2000	3
8	What is the approximate length of repeats in the final assembly?	1000 basepairs	200 kilobases	390 kilobases	390 megabases	3
9	In the canu.vcf file generated as part of exercise 6.2, what is the REF base for the variant located at position 37307?	G	A	TAAAAAA	C	1
10	Run the following command: bcfutils view canu.vcf.gz "tig0000001:105301", what did this do?	It displayed all variants in the file canu.vcf.gz	It displayed the variant at position 105301	It printed just the genotype information from the canu.vcf.gz file	It generated a new file called canu.vcf.gz.tbi	2
11	What is something that can be annotated in an assembled genome?	Coding Sequence	Repetitive DNA	Noncoding RNAs	All of the above	4
12	How many DNA nucleotides is one codon?	2	5	3	6	3
13	What proportion of the human genome is made up of repetitive sequence?	30%	60%	70%	2%	2
14	Eukaryotic genes always have introns.	TRUE	FALSE			2
15	LacZ helps bacteria to...	Use fructose as an energy source	Regulate glucose production	Use lactose as an energy source	Regulate transposon jumping	3
16	What is a way to confirm gene discovery performed by an algorithm (multiple correct answers)?	Visualisation	Count the total number of genes	Determine the proportion of the genome that contains coding genes	Functional experiments	1,4
17	What is the goal of the Darwin Tree of Life project?	To assemble the genomes of all <i>Lepidoptera</i> species	To develop new sequencing technologies	To assemble the genomes of all organisms found on the British Isles	To assemble the genomes of Darwin's finches	3
18	In the PB.contigs.polished.reheader.fasta.out file created as the output of exercise 3.3, what is the repeat unit of the repeat starting at position 605984?	A	AATATAT	TATAA	TA	2
19	In the gth.gff3 file created as the output of exercise 5.2, how many exons does gene90 have?	4	1	10	6	1
20	What is the start coordinate of the first mate for the read named "ERR2234744.965848"	8547411	2481	2620	27852	2

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