	Question	Answer 1	Answer 2	Answer 3	Answer 4	Correct answer(s) - choose at least one
1	Which tool is can be used for mapping reads to reference	bctools	samtools	bwa	none	3
2	Which of the following tools can be used for determining pairwise SNP difference	samtools	snp-sites	snp-dists	snpEff	3
3	Which submodule of samtools we use for generating alignment stats	samtools index	samtools view	samtools stats	samtools depth	3
4	Which of the following is correct for "mapped and properly paired" in the stats f	both read pairs mapped irrespective of distance between them	both read pairs mapped and the distance between them is within the insert size limits	both paired and upaired reads that have mapped	unpaired reads that have mapped	2
5	Why do we need to filter the varaints called from an alignment? Choose the option that is most relevant	to remove erroneous calls/variants	to remove indels	to remove SNPs	to annotate the variants	1
6	Which of the following is true	can be inferred from phylogenetic tree	from the multifasta alignment of genomes	calualted from annotation files	none	2
7	In a phylogentic tree which of the following option doesnot carry any meaning	horizontal banch	clade	root	vertical branch	4
8	The characteristic of a monophyletic clade is	single common ancestor	mutiple common ancestor	mutiple nodes	none	1
9	Which one of the following does not affect the choice of mapping reference	chromosome length	species	completeness of genome	availability of the genome sequence	1
10	What is an STR?	Small Transposon Reductase	Short Tandem Repeat	STRreptococcus	Send Tiny Rinos	2
11	Incorrect base calls are a result of:	PCR errors	Overall low quality of single pass long read sequencing	Quality drop-off towards the end of the read as the flow cell degrades	All of the above	4
12	What type of mutations are tools like SAMtools cuurenty NOT able to detect	Large chromosomal inversions	Indels	Missense mutations	Frameshift mutations	1
13	What does the QUAL column generally represent	The number of reads with the variant	The average quality of the reads	The phred-scaled probability the ALT is wrong	The phred-scaled probability the ALT is correct	3
14	What information does SnpEff NOT give?	Upstream/downstream variants	The ID of affected genes	The effect of the mutation	Annotation information from other strains	4
15	SnpEff can be used to:	antimicrobial resistance genes	Investigate causes of gene differential expression	Neither of the above	Both of the above	4
16						
17						
18						