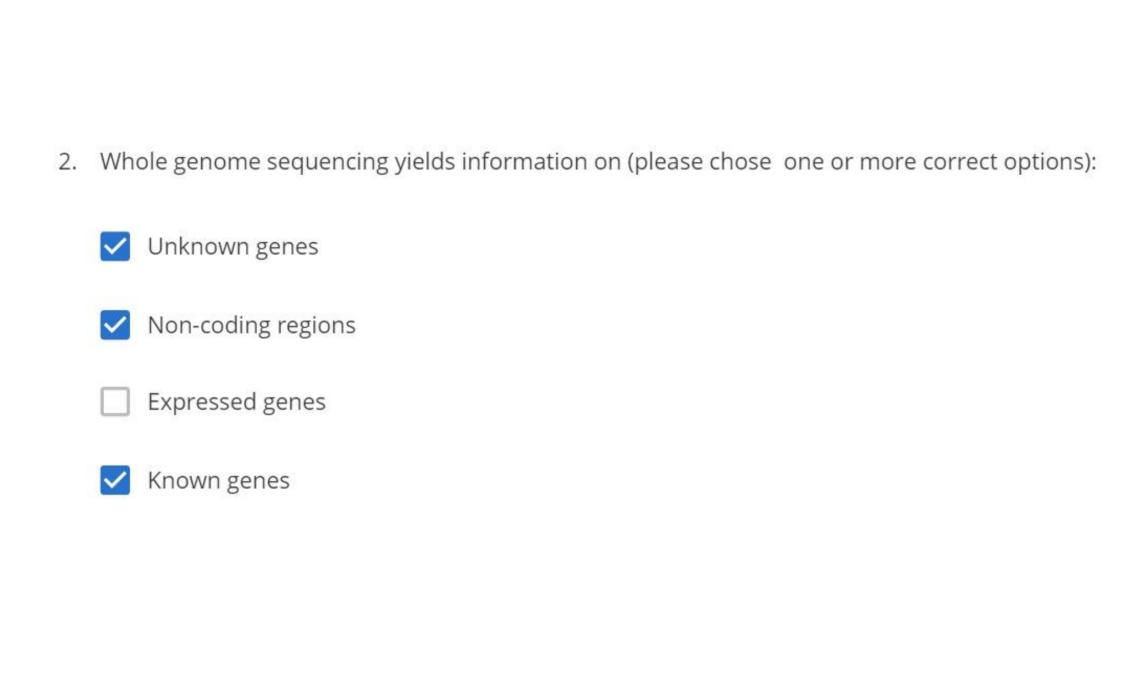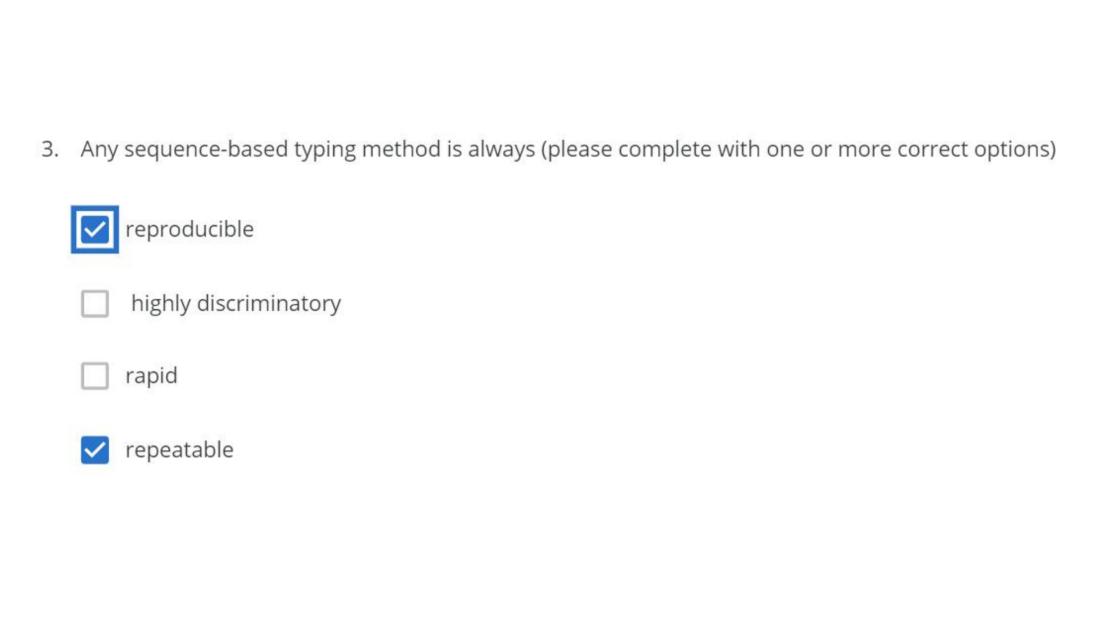1. When choosing a method for genotyping bacteria, one of the following information is necessary:

- ○ The origin of the bacteria to genotype
- ● The species of the bacteria to genotype
- ○ The time of isolation of the bacteria to genotype
- ○ The time of storage of the bacteria to genotype prior to analysis

2. Whole genome sequencing yields information on (please chose one or more correct options):

- ☑ Unknown genes

- ☑ Non-coding regions

- ☐ Expressed genes

- ☑ Known genes

3. Any sequence-based typing method is always (please complete with one or more correct options)

- ☑ reproducible
- ☐ highly discriminatory
- ☐ rapid
- ☑ repeatable

4. Two laboratories (A and B) use two different genotyping methods to characterize the same set of ten bacterial isolates. Laboratory A concludes the analysis by stating that the 10 isolates are genetically unrelated, whereas laboratory B concludes the analysis by stating that the 10 isolates cluster into three clonal groups. Which of the following statements are correct (please choose one or more options):

- ☑ It is possible that the results from both laboratories are correct

- ☑ Laboratory A used a typing method with higher discriminatory power compared to the method used by laboratory B

- ☐ It is evident that one of the laboratories made a mistake in the analysis of the genotypic data

- ☐ Laboratory B used a typing method which was more rapid compared to the method used by laboratory A

5. Five *Escherichia coli* isolates recovered from different patients in a veterinary hospital within one-week period exhibit identical antimicrobial susceptibility profiles. You need to choose a genotyping method to ascertain if there is clonal spread of *E. coli* in the hospital. Which one of the following characteristics is essential to verify if there is a clonal spread?

- ◉ High discriminatory power
- ○ Low cost
- ○ Low discriminatory power
- ○ high rapidity (speed)

6. How reliable is current phenotypic antimicrobial susceptibility testing?

○ Genotypic testing cannot be used for inferring antimicrobial susceptibility in a surveillance context

○ More reliable than genotypic testing using whole genome sequencing

○ Both pheotypic and genotypic testing provide equal reliability

● Less reliable than genotypic testing using whole genome sequencing

7. What is the name of the tool from Center for Genomic Epidemiology (CGE) that detects antimicrobial resistance genes?

  ● ResFinder

  ○ CARD

  ○ ARDB

  ○ ARG-ANNOT

8. What is the current weakness of the tools to detect antimicrobial resistance genes?

  ○   They can identify novel resistance genes and mutations

  ○ They can identify both known and novel antimicrobial resistance genes and mutations

  ○ They can only identify all known resistance genes and mutations

  ●   They can only identify known resistance genes and mutations that have been entered in their databases

9. Can the MIC (minimum inhibitory concentration) be derived and predicted from the genotypic profile?

   Yes, the MIC can be predicted and used for clinical treatment, based on genotypic profile

   Yes, the MIC can be predicted in relation to resistance genes, but not mutations

   ● No, this is not possible

   Yes, the MIC can be predicted but only used for monitoring purposes

10. What are the contents of the "toolbox" of the Center for Genomic Epidemiology (CGE)?

   ○ The toolbox is a commercially available software incontaining a repository of bioinformatic tools

   ○ The toolbox contains commercially available software for detection of antimicrobial resistance genes only

   ● The toolbox is an intuitive and freely available online repository of bioinformatic tools

   ○ The toolbox contains epidemiological software used to predict outbreaks