Which of the following sentences is TRUE?

○ Genomic epidemiology is the genetic analysis of the host of the infectious disease.

○ Phylogenetic trees can not show evolutionary relatedness between samples.

● Genomic epidemiology is the epidemiological investigation of infectious disease cases, supplemented by genomic data.

○ Evergreen Online aims to detect airborne disease outbreaks.

How are MGEs often regulated by the bacteria?

○ They are not regulated

⦿ Regulation is coupled to the SOS response systems

○ Regulation is coupled to the citric acid cycle

Question

How are MGEs being predicted?

- ⦿ By sequence similarity to known MGEs

- ◯ By using deep learning neural networks

- ◯ By looking for SNPs in core genes

What is k-mer ?

○ Complete genome

○ Draft genome

◉ A contiguous sequence of k bases

○ Raw reads

Why might we want to replace some phenotypical methods in the future (please chose the most correct option)

◉ phenotypical methods might take longer time and are prone to mistakes

◯ sequencing is not reliable or repeatable

◯ sequencing requires a lot of knowledge

◯ phenotypical methods are easy and practical

- [x] SNP (Single nucleotide polymorphism) genotyping is a sequence-based method for typing of bacteria

- [x] MLST (Multi Locus Sequence typing) is a sequence-based method for typing of bacteria

- [x] MLVA (Multiple Loci Variable number of Tandem Repeats analysis) is a band-based method for typing of bacteria

- [x] PFGE (Pulsed-Field Gel Electrophoresis) is a band-based method for typing of bacteria

If we take a bacteria and test for sugar fermentation patterns (biochemical tests) how can we classify these tests?

○ Phenotypic

○ Genotypic

What is the format for your own sequence database ?

- ◉ Nucletotide sequences in FASTA

- ○ Nucleotide sequences in Genbank

- ○ Protein sequences in FASTA

- ○ Protein sequences in Genbank

What is MLST configuration based on ?

○ Kingdom

● Species

○ Resistance profile

○ Serotype

Which of the following sentences is TRUE ?

○ The bioinformatic pipeline downloads assembled genomes from public repositories.

○ All columns with unknown bases are removed before genetic distance calculation.

○ The pipeline re-calculates all output each time it runs.

◉ Phylogenetic trees are part of the output of the pipeline.

What is the difference between FASTQ and FASTA ?

- ○ There is no difference

- ● FASTQ contain quality scores

- ○ FASTA contains sequences but FASTQ doesn't contain sequences

- ○ FASTA contain quality scores

✓ **Correct**

FASTQ contain both sequences and quality score

What does ResFinder 4.0 do ?

○ Detect the presence of whole resistance genes

○ Detect chromosomal point mutations causing resistance

○ Provide in silico antibiograms

● All of above

What does PlasmidFinder do ?

○ Identify ST type

○ Identity plasmid ST type

◉ Identify plasmid replicons

○ Identify whole plasmid sequences

✓ **Correct**

PlasmidFinder

If you want to identify gene, what process you should do ?

○ Mapping reads to a reference genome

◉ De novo assembly

○ Quality check

○ None of above

✓ **Correct**
To merge reads to contigs and identify genes or other genetic markers

Which mobile elements are capable of transporting within a bacterial cell AND carrying accessory genes?

○ Insertion sequences and Integrons

◉ Unit transposons and Composite transposons

○ Unit transposons and Integrative Conjugative Elements (ICE)

What is more-less the cost of sequencing a whole bacterial genome nowadays?

○ 200-500 Euro

○ 100-200 Euro

◉ 50-100 Euro

○ More than 500 Euro