

1. What method is used by the SeqSero tool?

- ☐ None of the above
- ☐ Indirect targets
- ☐ Both direct and indirect targets



Direct targets

2. Was the SeqSero tool developed by the Center For Genomic Epidemiology (CGE)?

- ☐ Yes, but it is also hosted at the Deng Lab
- ☐ It was developed in collaboration with the Deng Lab
- ☒ No, It was developed at the Deng Lab (Zang S. *et al*)
- ☐ Yes

3. What type of data is to be preferred as input to SeqSero?

- ☒ Raw data is preferred
- ☐ A combination of assembled data and raw data is preferred
- ☐ No data type is preferred, they are equally good
- ☐ Assembled data is preferred

4. SeqSero sometimes output two possible serotypes, how might that be resolved?

- ☐ By investigating the O antigen
- ☐ It can't be resolved
- ☒ By checking the MLST as the obtained ST can be compared to the serotyped isolates in Enterobase
- ☐ By investigating the H antigens

5. What method is used by the SeroTypeFinder?



Direct targets



Indirect targets



None of the above



Both direct and indirect targets

6. In which cases will SeroTypeFinder output a genotype that is inconsistent with the phenotype (please chose all options that apply):



Bacterial strains characterized as "non-motile"



Bacterial strains characterized as "non-typable"



E. coli with the phenotype O157:H7



Bacterial strains characterized as "Rough"

7. What type of input data can be used for SerotypeFinder (please chose all that apply):

☒ Assembled data (FASTA format)

☐ SNP calls (VCF format)

☒ Read data (FASTQ format)

☐ Mapped reads (BAM format)

8. In case you wish to use the assembly-based CGE tool ResFinder and SerotypeFinder, and you only had raw data, how could you optimize your work-flow? (please chose all options that apply)

☐ Reduce the number of reads in your FASTQ files and upload those instead

☐ It cannot be optimized

☒ Get an assembly first by using the CGE assembler and then upload that assembly to ResFinder and SerotypeFinder

☒ Get an assembly first by using a local assembler of your own choice and then upload that assembly to ResFinder and SerotypeFinder

9. What is the plasmid replicon found in the unknown sample using PlasmidFinder with default parameters and choosing Enterobacteriaceae ?

unknown_sample.fasta.zip

Please note that the sequence file need to be **unzipped** prior uploading to the web tool.

☒ *incFII(S)*

☐ *ind1*

☐ *incQ1*

☐ *incP*

10. What is the plasmid ST type for the unknow sample using pMLST tool with default parameters ?

Please use the unknown sequence as in Question 9.

☐ ST-19

☐ ST-1

☒ S1:A-B17

☐ S1:A-B20