1. Why is whole genome sequencing combined with bioinformatic tools seen as revolutionizing diagnostics and surveillance?

- ○ Whole genome sequencing combined with bioinformatic tools can only be used by state of the art high profile laboratories
- ○ Whole genome sequencing combined with bioinformatic tools can only be used for bacteria
- ○ Whole genome sequencing combined with bioinformatic tools is only for research
- ◉ Whole genome sequencing combined with bioinformatic tools can be used for all organisms

2. What is one of the advances with whole genome sequencing combined with bioinformatic tools?

- ○ Overall, the time spent from sample to results (species ID, typing, virulence and relatedness tests) increases and it is less expensive than conventional methodologies combined
- ◉ Overall, the time spent from sample to results (species ID, typing, virulence and relatedness tests) decreases and it is less expensive than conventional methodologies combined
- ○ Overall, the time spent from sample to results (species ID, typing, virulence and relatedness tests) decreases and it is more expensive than conventional methodologies combined
- ○ Overall, the time spent from sample to results (species ID, typing, virulence and relatedness tests) increases and it is more expensive than conventional methodologies combined

3. What was the aim for Center for Genomic Epidemiology (CGE) project

- ○ To develop a bioinformatics tool to detect only the bacterial species, virulence properties, antimicrobial resistance genes and relatedness to other strains
- ○ To develop a commercial available bioinformatics tool for diagnostic
- ◉ To provide a foundation for web based solutions that are easy to use
- ○ To develop a bioinformatics tool for research

4. Does the Center for Genomic Epidemiology (CGE) have a tool that combines several tools?

- ○ No, this was not part of the strategy, all tools are single stand-alone tools
- ◉ Yes, It is called the batch upload tool
- ○ Yes, but it is only used by DTU
- ○ No, but it is in a development phase

5. Why the urgent need to use whole genome sequencing ?

- ○ To avoid that developing counties embrace the technology
- ○ To agree on using only one brand of sequencing platform, globally
- ◉ To initiate and improve standardization and quality control
- ○ To enhance the resolution beyond the genome level

6. Which sequencing technology produces long read sequences ?

- ○ Illumina MiSeq
- ○ Illumina HiSeq
- ○ Ion Torrent
- ◉ Oxford Nanopore

7. In library preparation for NGS, If you sequence more than one isolate/sample. What part in adapter helps you to distinguish the isolates/samples ?

- ○ Sequencing primer
- ○ Amplification primer
- ◉ Barcode
- ○ None of above

8. What is the format used to store raw read sequences (NGS data) ?

- ○ FASTA
- ○ GENBANK
- ◉ FASTQ
- ○ All of above

9. What is the purpose for 'Trimming' of raw reads ?

- [x] To get rid of low quality sequences or reads
- [ ] To assemble reads to contigs
- [ ] To transform from FASTQ to FASTA format
- [ ] All of above

10. What is the purpose of mapping reads to a reference genome to identify variance ?

- [ ] To identify core gene
- [ ] To assemble reads to contigs
- [ ] To search for genes
- [x] To identify SNPs

11. What is the parameter for checking genome quality ?

- ○ N50
- ○ Number of contigs
- ○ Total size of genomes
- ◉ All of above

12. N50 is often used as a quality measure for assemblies. What does it describe?

- ○ 50% of the total assembly size
- ○ The total assembly size
- ○ The size of the longest contig
- ◉ The median of the contig sizes in the assembly

13. What does it mean "to do de-novo assembly"?

- (●) The assembly is created using only the raw read data.
- ( ) The assembly is done using Velvet.
- ( ) The assembly is partly based upon a reference sequence.
- ( ) The assembly is based upon a reference sequence.

14. When using the CGE Assembler with Illumina data, what assembler will do the assembly?

- ( ) Mira
- ( ) Newbler
- ( ) A combination of Velvet and Newbler
- (●) Velvet

15. When using the CGE Assembler with Ion Torrent sequencing data, what assembler will do the assembly?

- ○ Velvet
- ◉ Newbler
- ○ A combination of Velvet and Newbler
- ○ Mira