Thank you for agreeing to take part in our follow-up survey. In order to continuously improve modules, we ask participants for their views. We would greatly appreciate you taking just a few minutes to complete this online survey. The questionnaire should take approximately between 15 to 45 minutes to complete. Please be assured that all of your answers are strictly confidential and responses will be reported in aggregates only.

**Section 1**

Questions marked with an asterisk (\*) are mandatory for the completion of the survey.

* 1. Full Name (First Name, Initials, Last Name) \*:
  2. Affiliation/Employer\*:
  3. Email address\*:
  4. Phone number\*:
  5. Educational background\* For example, molecular biology, pharmacy, botany, zoology, ...etc Highest educational degree obtained \* (Mark only one oval.)

a.) BSc

b.) MSc

c.) PhD

d.) Other. Please specify:

* 1. What is your profession and/or your professional background? \* Please choose only one of the following that fits best.
* Microbiologist/laboratory scientist - directly involved in handling and/or testing specimens (pathogen expert)
* Molecular biologist - using advanced techniques to study organisms at the molecular level
* Clinical biologist - involved in clinical diagnostics (patient samples)
* Bioinformatician - developing computational approaches/algorithms to analyse genomic data from pathogens
* Epidemiologist/public health professional - work with data to understand patterns in disease occurrence (at the population level)
* Infection control practitioner - local prevention and control of infectious diseases in the community (frontline, including field epidemiologists)
* Hospital hygienist - prevention and control of healthcare associated infections (frontline, including field epidemiologists)
* Clinician: infectiology - directly involved in patient care and/or case management
* Clinician: other - directly involved in patient care and/or case management
* Public health policy maker - the making and implementing of decisions to improve the health of the public

1. **Section 2**
   1. **To what extent do you agree or disagree with the following statements about the course you attended last year? (5 point Likert scale).**

**The course:**

* provided useful experience on the latest research
* provided me with useful experience on the latest diagnostic technique in my subject area
* provided a high-quality learning environment
* provided the opportunity to meet and network with experts in my subject area
* provided the knowledge that enabled me to explore new areas of research, diagnostics and/or clinical practice
* [Free text box - explain your responses further]
  1. **To what extent do you feel the training has - (5 point Likert scale)**
* Helped you progress to the next stage of your career
* Helped you apply for grants/funding
* Contributed to any papers that have been or are due to be published
* Enhanced your collaborations and building networks
* [Free text box - explain your responses further]
  1. **Have you been able to apply what you learnt during the course to your own work? [Yes][No]**

• If you answered Yes, how have you been able to apply what you learnt? [Free text box]

• If you answered No, why have you not been able to apply what you learnt? [Free text box]

* 1. **How useful were the following seminars/topics/discussions to you (or your work/research) since the end of the course?**

|  | Very useful | Fairly useful | Not useful | Not relevant to my current work |
| --- | --- | --- | --- | --- |
| Online bioinformatics software tools and platforms for AMR surveillance |  |  |  |  |
| Introduction to Nextflow Tower, AMR pipeline, hAMRonization |  |  |  |  |
| Analysis and Interpretation of AMR analysis data using the Nextflow Tower |  |  |  |  |
| Introduction to the Command line |  |  |  |  |
| Application of the Command-line in the analysis of sequence data |  |  |  |  |

* 1. **Given your answers above, please provide any explanation to help us understand your response**
  2. **To what extent do you agree or disagree that attendance of this virtual course last year has given you the skills to:**

|  | Strongly agree | Slightly agree | Slightly disagree | Strongly disagree | Unable to judge |
| --- | --- | --- | --- | --- | --- |
| Leverage on your understanding of data analysis (using web-based tools (e.g., Pathogenwatch, ResFinder), and visualization in Microreact? |  |  |  |  |  |
| Carry out antimicrobial resistance gene prediction analysis using the Nextflow Tower platform |  |  |  |  |  |
| Be confident in the use of the command line |  |  |  |  |  |
| Apply command-line approaches in the analysis of sequence data (particularly antimicrobial resistance gene analysis) |  |  |  |  |  |

* 1. **Given your answers above, please provide any explanation to help us understand your response (For instance, which of the steps/skills above have been most/least useful to you since last year? How have these skills been useful?**
  2. **Have you shared what you learnt with others? [Yes][No]**

• If you answered Yes, how have you shared what you learnt? [Free text box]

• If you answered No, how have you been able to apply what you learnt? [Free text box]

* 1. If you have trained anyone on the use of the bioinformatics in the last year, please complete the following

What is your role? Lead trainer, course content contributor [Free text box]

What stage is the training? Planning, training, completed [Free text box]

What is the training about? Please list the tools you used during the training [Free text box]

Which of the following topics were covered during the training?

1. Microbial Whole Genome Sequencing (an overview)
2. Bacterial genome assembly (using the CGI Assembler (https://cge.cbs.dtu.dk/services/Assembler/))
3. Pre-assembly quality check (using FastQC and/or MultiQC)
4. Post-assembly quality check (using QUAST)
5. Bacterial Species Identification (using the CGE tools SpeciesFinder and/or KmerFinder, PathogenWatch)
6. Prediction of Antimicrobial Resistance Genes, virulence genes, and/or plasmid replicon genes (using the CGE tools ResFinder (<https://cge.cbs.dtu.dk/services/ResFinder/>), VirulenceFinder (<https://cge.cbs.dtu.dk/services/VirulenceFinder/>), and/or PlasmidFinder (<https://cge.cbs.dtu.dk/services/PlasmidFinder/)>)
7. Construction/Generation of a Phylogenetic Tree (CSIPhylogeny (<https://cge.cbs.dtu.dk/services/CSIPhylogeny/)> and Microreact)
8. Multilocus Sequence Typing (MLST (<https://cge.food.dtu.dk/services/MLST/>) and/or Pathogenwatch (<https://pathogen.watch/)>)
9. Interpretation of data generated using any of the aforementioned tools
10. Introduction to the command-line
11. Introduction and use of Nextflow Tower for sequence data analyses
12. Prediction of Antimicrobial Resistance Genes, virulence genes, and/or plasmid replicon genes via the command-line route (e.g., using the ariba software tool)

Who were the participants?

What was/is the date of the training?  ~~[Free text box]~~

* 1. **Have you applied the knowledge and skills from the course to contribute to the assembly or implementation of a bioinformatics pipeline for whole genome data analysis for AMR surveillance?**

[Yes],Provide details on what has been done or planned. [Free text box]

No

* 1. **Have you applied the knowledge and skills from the course to contribute to the interpretation of Whole Genome Sequence (WGS) data generated from pathogens recovered from patients visiting your hospital/laboratory?**

Provide details on what has been done or planned…

* 1. **How has the bioinformatics course impacted your work? What is different now? What are you doing now which you were not doing before, or doing differently or better?** [Free text box]
  2. **What are some of the challenges and barriers to implementing what you have learnt in the course that you have encountered?** [Free text box]
  3. **If applicable, how have you overcome these challenges and barriers?** [Free text box]

* 1. **Any other information which you would like to share?** [Free text box]

The questionnaire was adapted from the post-course survey of the Train-the-trainer Course (Abrudan et al., 2021; https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8634536/pdf/ciab770.pdf)