

# SEQAFRICA Virtual Training Course

## Course information

**Title:** Introduction to Whole Genome Sequencing (WGS) in Antimicrobial Resistance (AMR).

**Language of instruction:** English.

**Offered as:** Webinar with lectures, exercises and panel discussion.

**Duration of course:** 6 x ½ days. Originally held 15 Feb – 26 Feb 2021.

**Responsible:** Rene S. Hendriksen (DTU), [rshe@food.dtu.dk](mailto:rshe@food.dtu.dk)

**Course co-responsible:** Pernille Nilsson (DTU), Anthony Smith (NICD, South Africa), Jinal Bhiman (NICD, South Africa), Marco van Zwetselaar (KCRI, Tanzania), Beverly Eygir (NMIMR, Ghana), Iruka N. Okeke (UI, Nigeria).

## General course objectives:

The course provides an introduction to Whole Genome Sequencing (WGS) and its use in Antimicrobial resistance (AMR) surveillance.

The participant will upon completion of the course i) know what WGS is and how it can be used and ii) be able to use freely available online tools to perform simple bioinformatics analysis and interpret results.

## Learning objectives:

A participant who has met the objectives of the course will be able to:

- Describe the potential uses of WGS in public health microbiology
- Describe the different sequencing platforms and the technology behind using the correct terminology
- Plan sampling/surveillance appropriate for with WGS studies with epidemiology in mind
- Perform drag-and-drop bioinformatics using online analysis tools and interpret the results

## Content:

The course covers sampling strategies for doing WGS in AMR, sequencing terminology, detailing state-of-the-art technology including technical specifics of whole genome sequencing to give the participants a thorough understanding. Furthermore the course covers what the output data looks like, the importance of quality control and the use of online tools to analyse the data for species identification and AMR detection.

The course is comprised of lectures and hands-on exercises that the participants complete on their own. Self-evaluation is possible through responding to surveys related to the exercises.

## Course literature:

No literature required.

## Audience:

None and novel users.

| Day 1: Why and how to bring WGS into AMR                            |   |  |                       |
|---|---|--|-----------------------|
| Links to <a href="#">Presentation</a> and <a href="#">Recording</a> |   |  |                       |
| Speaker/Presenter   | Content/Activity  | Slides   | Video                 |
| Pernille Nilsson (DTU, Denmark)                                     | <b>Welcome and Introduction</b> (15 min)  |  |                       |
| Rene S. Hendriksen (DTU, Denmark)                                   | [1] <b>The present and future in AMR surveillance.</b><br>The potential of using WGS in AMR surveillance (30 min)   | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Rene S. Hendriksen (DTU, Denmark)                                   | [2] <b>Application of WGS in public health microbiology:</b> Cholera and Haiti.<br>Genomic epidemiology of the Haitian Cholera outbreak. (30 min)   | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Alessandro Foddai (DTU, Denmark)                                    | [3] <b>Taking epidemiology into account –what to sequence and how much?</b> (30 min)<br><br><b>Note:</b> Attendants are encouraged to review the treatment guidelines for syndromes/pathogens or organisms in their country (to know what data will help clinicians and public health people in their country or region)                              | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Jette Sejer Kjeldgaard (DTU, Denmark)                               | [4] <b>Overview of terminology and different sequencing platforms:</b> Illumina, Ion Torrent, Pacific Biosciences (PacBio), Oxford Nanopore Technologies (30 min)   | <a href="#">PDF</a>  | <a href="#">Video</a> |
|   | <b>Q&amp;A and Wrap-up</b> (15 min)   |  |                       |
| Day 2: Quality control and identification/characterization          |   |  |                       |
| Links to <a href="#">Presentation</a> and <a href="#">Recording</a> |   |  |                       |
|   | <b>Welcome and Introduction</b> (15 min)  |  |                       |
| Mushal Allam (NICD, South Africa)                                   | [5] <b>Basic quality control of raw reads</b> (30 min)  | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Mushal Allam (NICD, South Africa)                                   | [5E] <b>Exercise: Basic quality control of raw reads using FastQC.</b><br>A tutorial where you learn how to import, view and check the quality of sequenced data using FastQC. (15-30 min introduction)<br><br><b>Note:</b> You will perform the exercise on your own computer and can submit replies through the link to the right to self-evaluate. | <a href="#">PDF</a><br><br><a href="#">Files</a><br><br><a href="#">Exercise sub</a> |                       |
| Marco van Zwetselaar (KCRI, Tanzania)                               | [6] <b>Bioinformatics Basics:</b> General introduction to bioinformatics and introducing genome assembly. (60 min)  | <a href="#">PDF</a>  | <a href="#">Video</a> |
|   | <b>Q&amp;A and Wrap-up</b> (15 min)   |  |                       |

| Day 3: Bioinformatics with online tools                                     |   |  |                       |
|---|---|--|-----------------------|
| Links to <a href="#">Presentation</a> and <a href="#">Recording</a>         |   |  |                       |
|   | <b>Welcome and Introduction</b> (15 min)  |  |                       |
| Stanford Kwenda<br>(NICD, South Africa)                                     | [7] <b>Online tools 1:</b> Introduction to online tools. Kmers, MLST and serotyping of <i>Salmonella</i> and <i>E.coli</i> . (30 min).  | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Tolbert Sonda (KCRI,<br>Tanzania)   | [8] <b>Online tools 2:</b> CGE Online Bioinformatics Tools. SpeciesFinder, KmerFinder, ResFinder. (30 min).   | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Anthony Smith<br>(NICD, South Africa)                                       | [9] <b>Online tools 3:</b> Presentation of online tools available for microbial identification using sequence analysis: Pathogenwatch, autoMLST, pubMLST-ribosomal MLST. (30 min).  | n/a  | <a href="#">Video</a> |
| Anthony Smith<br>(NICD, South Africa)                                       | [9E] <b>Exercise using online tools:</b> Participants will download sequence data and tasked to perform analysis using the presented online tools. (15 min introduction).<br><br><b>Note:</b> You will perform the exercise on your own computer and can submit replies through the link to the right to self-evaluate. | <a href="#">PDF</a><br><a href="#">Files</a><br><a href="#">Exercise sub</a> |                       |
|   | <b>Q&amp;A and Wrap-up</b> (15 min)   |  |                       |
| Day 4: Phylogeny and Genotype to phenotype                                  |   |  |                       |
| Links to <a href="#">Presentation</a> and <a href="#">Recording</a>         |   |  |                       |
|   | <b>Welcome and Introduction</b> (15 min)  |  |                       |
| Erkison Odih (UI,<br>Nigeria)   | [10] <b>Phylogeny:</b> construction, visualization and interpretation. Tools: Microreact (60 min)   | <a href="#">PDF</a>  | <a href="#">Video</a> |
| Erkison Odih (UI),<br>Sonda Tolbert (KCRI)<br>and Ayorinde Afolayan<br>(UI) | [10E] <b>Exercise on phylogeny:</b> Participants will be given an exercise on phylogeny (30 min introduction).<br><br><b>Note:</b> You will perform the exercise on your own computer and can submit replies through the link to the right to self-evaluate   | <a href="#">PDF</a><br><a href="#">Files</a><br><a href="#">Exercise sub</a> |                       |
| Jette Sejer Kjeldgaard<br>(DTU, Denmark)                                    | [11] <b>Genotype to Phenotype:</b> Prediction of AMR by WGS (30 min)  | n/a  | <a href="#">Video</a> |
| Jette Sejer Kjeldgaard<br>(DTU, Denmark)                                    | [11E] <b>Exercise Phenotype based on genotype:</b> Determining phenotype based on genotype. (15 min introduction).<br><br><b>Note:</b> The sequence analysis output files mentioned in the exercise description are no longer available. You need to run  | <a href="#">PDF</a><br><a href="#">Files</a><br><a href="#">Excel</a>        |                       |

|  |  |                     |                              |
|--|--|---------------------|------------------------------|
|  | the six sequence files through <a href="#">ResFinder</a> before you can evaluate the presence of AMR genes and the predicted phenotypes.<br>You will perform the exercise on your own computer and can submit replies through the link to the right to self-evaluate |                     | <a href="#">Exercise sub</a> |
|  | <b>Q&amp;A and Wrap-up</b> (15 min)  |                     |                              |
| <b>Day 5: Results and Nagoya protocol</b><br>Links to <a href="#">Presentation</a> and <a href="#">Recording</a> |  |                     |                              |
|  | <b>Welcome and Introduction</b> (15 min)   |                     |                              |
|  | <b>Going through results from all exercises</b> (90 min)   |                     |                              |
| Carolina Dos Santos Ribeiro (RIVM)   | [12] <b>The Nagoya protocol: An introduction.</b> (45 min)   | <a href="#">PDF</a> | <a href="#">Video</a>        |
|  | <b>Q&amp;A and Wrap-up</b> (15 min)  |                     |                              |
| <b>Day 6: Friday Genomic surveillance</b><br>Links to <a href="#">Presentation</a> and <a href="#">Recording</a> |  |                     |                              |
|  | <b>Welcome and Introduction</b> (15 min)   |                     |                              |
| Anthony Smith (NICD, South Africa)   | [13] <b>Practical examples of genomic surveillance</b><br>1. NICD, South Africa: Genomic surveillance of enteric pathogens (20 min)  | n/a                 | <a href="#">Video</a>        |
| Errol Strain (FDA, USA)  | [13] <b>Practical examples of genomic surveillance</b><br>2. FDA, USA: Genomic and metagenomics based surveillance of AMR in the United States under the National Antimicrobial Resistance Monitoring System (NARMS). (20 min).                                      | n/a                 | <a href="#">Video</a>        |
| Rene S. Hendriksen (DTU, Denmark),   | [13] <b>Practical examples of genomic surveillance</b><br>3. DTU, Denmark: WGS surveillance in Europe. (20 min).   | n/a                 | <a href="#">Video</a>        |
| Sofonias K. Tessema (Africa Union, ACDC),  | [13] <b>Practical examples of genomic surveillance</b><br>4. Africa Union/Africa CDC: Pathogen Genomics for Infectious Disease Control and Elimination in Africa. (20 min).  | n/a                 | <a href="#">Video</a>        |
| Jorge Raul Matheu Alvarez (WHO)  | [13] <b>Practical examples of genomic surveillance</b><br>5. WHO: Integrated surveillance of AMR and the ESBL Ec tricycle project. (20 min).   | n/a                 | <a href="#">Video</a>        |

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|------------------------|--|--|--|
|                        | <p><b>[14] Panel Discussion: Genomic Surveillance (Live)</b></p> <p>Moderator: Iruka N. Okeke</p> <p>Panel:</p> <ul style="list-style-type: none"> <li>• Anthony Smith (NICD, South Africa)</li> <li>• Errol Strain (FDA, USA)</li> <li>• Rene S. Hendriksen (DTU, Denmark)</li> <li>• Sofonias K. Tessema (Africa Union/ACDC)</li> <li>• Jorge Raul Matheu Alvarez (WHO)</li> </ul> |  |  |
| Pernille Nilsson (DTU) | <b>Concluding remarks and close (15 min)</b>   |  |  |