| GENOMIC EPIDEMIOLOGY — DAY 3 | | | |
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| **Time** | **Activity Description** | **Intended Learning Outcomes**<br><br>*After completion, trainees will (be able to):* | **Relevance**<br><br>*Why this is important for you as:* |
| 1040-1200 | Gene-by-gene approach Part 1: BIGSdb (Sylvain Brisse) | Acquire proficiency in utilizing gene-by-gene approaches such as cgMLST and wgMLST<br><br>Learn more about the BIGSdb platform and its role in epidemiological surveillance and outbreak investigation<br><br>Gain knowledge on how to use tools like GrapeTree for analyzing genomes and interpreting genetic relationships within pathogen populations | **Bioinformaticians** must master gene-by-gene approaches like cgMLST and wgMLST, utilizing platforms such as BIGSdb to analyze genomic data and provide essential support for microbiologists and epidemiologists in characterizing and tracking microbial strains during epidemiological surveillance and outbreak investigations.<br><br>**Microbiologists** must learn how to use tools like GrapeTree to interpret genetic relationships between pathogens, supporting the understanding of transmission patterns during disease outbreaks.<br><br>**Epidemiologists** must leverage bioinformaticians' and microbiologists' insights to integrate genomic data into epidemiological studies, enabling a comprehensive understanding of disease transmission dynamics and facilitating effective outbreak control measures. |
| 1330-1530 | Visualization and Epidemiology theory and practice (Chiara Crestani) | Learn to integrate genomic and epidemiological data with Microreact<br><br>Gain knowledge in visualizing and analyzing genomic data with Pathogenwatch and manipulating phylogenetic trees using Microreact.<br><br>Apply new knowledge and skills with a case study using a simple published dataset of a foodborne pathogen and using | **Bioinformaticians and epidemiologists** must understand visualization and analysis tools like Pathogenwatch and Microreact to interpret genomic data and integrate it with epidemiological data for outbreak tracking.<br><br>**Microbiologists** will use these tools to investigate pathogen evolution and population dynamics, essential for microbial research and surveillance. |

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| | | Pathogen Watch and/or MicroReact | |

## Details

Gene-by-gene approach 1: BIGSdb

The course "Gene-by-gene Approach 1: BIGBSdb" offers participants an in-depth exploration of gene-by-gene typing methods such as cgMLST and wgMLST, with a focus on their application in epidemiological surveillance and outbreak investigation. Through an interactive session, participants will learn how to leverage the BIGSdb platform for analyzing genomic data and interpreting genetic relationships within pathogen populations. Additionally, participants will gain hands-on experience in analyzing genomes using tools like GrapeTree, allowing them to visualize the genetic diversity and relatedness of microbial strains. By the end of the course, participants will have acquired the skills necessary to apply gene-by-gene approaches effectively in microbiological research and epidemiological practice, enhancing their ability to characterize and track microbial strains during disease outbreaks.

Visualisation and epidemiology theory and practice

This course provides participants with comprehensive training on open-access tools for visualization and analysis crucial for epidemiological research. Attendees will learn to integrate genomic and epidemiological data using platforms like Pathogenwatch and Microreact, gaining proficiency in visualizing genomic data and manipulating phylogenetic trees.

Participants will then apply their new skills to a case study involving a simple published dataset of a foodborne pathogen, using Pathogen Watch and/or MicroReact for analysis.