GENOMIC EPIDEMIOLOGY — DAY 5			
Time	**Activity Description**	**Intended Learning Outcomes** *After completion, trainees will (be able to):*	**Relevance** *Why this is important for you as:*
0930-1100	Gene-by-gene approach Part 2: cgMLST applications using EnteroBase (Carolina Nodari)	Comprehend the principles and applications in epidemiological surveillance and outbreak investigation of gene-by-gene approaches, including cgMLST Master the utilization of Enterobase for epidemiological surveillance and outbreak investigation and surveillance	**Bioinformaticians** will apply their knowledge on gene-by-gene approaches, including cgMLST, and on tools such as Enterobase to support microbiologists and epidemiologists in analyzing and interpreting genetic data and understanding disease transmission patterns. **Microbiologists and epidemiologists** will couple their knowledge of basic microbiology and epidemiology with gene-by-gene approaches for epidemiological surveillance and outbreak investigation, collaborating with bioinformaticians to interpret genetic data and inform public health interventions.
1400-1500	Genomic Epidemiology applied to Listeria and cluster detection (Alexandra Moura)	Background information on the biology of Listeria monocytogenes (genomic and molecular aspects, virulence, global distribution, clinical aspects, diagnostics methods and treatments) Know how to integrate genomic and epidemiological data using tools such as BIGSdb, GrapeTree, and ReporTree to analyze transmission patterns and identify sources of Listeria infection during disease outbreaks Learn techniques for *Listeria* cluster detection, characterization, surveillance, and risk assessment in relation to *Listeria* infections and foodborne disease outbreaks	**Bioinformaticians** will learn how to visualize *Listeria* phylogenetic trees and associated epidemiological data using tools like BIGSdb, GrapeTree and ReporTree. **Microbiologists** will deepen their knowledge about the biology of *Listeria* and use it to support epidemiological investigation, integrating it with genomic and epidemiological data and cluster detection. **Epidemiologists** will collaborate with bioinformaticians and microbiologists to analyze *Listeria* transmission patterns thanks to their knowledge on epidemiology, and they will learn to apply this to genomic data analysis, facilitating the identification of transmission routes, cluster detection,

Details

Gene-by-gene approach Part 2: cgMLST applications using EnteroBase

The course on "Gene-by-Gene Approach Part 2: cgMLST applications using EnteroBase" provides participants with a comprehensive practical training on the cgMLST approach and its applications in epidemiological surveillance and outbreak investigation of foodborne pathogens. Participants will learn to use Enterobase for analyzing genomic data effectively and interpreting transmission patterns. Additionally, the course will cover practical aspects of cgMLST in Enterobase, including data input, parameter selection, and result interpretation. By the end of the course, participants will have acquired the skills necessary to apply cgMLST to sequence data within Enterobase effectively, which will help them to address public health challenges related to outbreak investigation, surveillance, and transmission analysis.

Genomic epidemiology applied to *Listeria monocytogenes* and cluster detection

This course provides participants with a comprehensive training in visualizing phylogenetic trees and integrating genomic and epidemiological data relative to *Listeria* using tools like BIGSdb, GrapeTree, and ReporTree. Additionally, the course will cover practical aspects including detecting and interpreting transmission patterns, as well as identifying sources of *Listeria* infection and detecting clusters. By the end of the course, participants will have acquired the skills necessary to analyze genetic and epidemiological information and apply their knowledge to address public health challenges related to *Listeria* transmission, cluster detection and outbreak investigation.