RESISTANCE ELEMENTS — DAY 6			
Time	**Activity Description**	**Intended Learning Outcomes** *After completion, trainees will (be able to):*	**Relevance** *Why this is important for you as:*
0930-1100	Antibiotic resistance genes (Carla Rodrigues)	Understand the diversity of antibiotic resistance genes and their associated mechanisms Gain knowledge about resistance genes databases	**Bioinformaticians** will gain knowledge on resistance gene databases to consult in order to download AMR gene sequences to perform analysis of genomic data. **Microbiologists and epidemiologists** will deepen their knowledge of antibiotic resistance genes and their mechanisms, and they will gain more understanding on the importance of such genes for public health.
1110-1240	Antibiotic resistance genes or mutations (Carla Rodrigues)	Practical analysis for *in silico* detection of antibiotic resistance genes and mutations leading to resistance with tools such as ResFinder, CARD, etc Performing BLAST searches on nucleotide or amino acid sequences to detect AMR genes Visualization and location of the AMR genes in the genome using BANDAGE	**Bioinformatician**s will gain practical skills on detection of AMR genes in NGS data with tools such as ResFinder and BLAST, leveraging on public AMR databases, to predict antibiotic resistance profiles. **Microbiologists and epidemiologists** will learn to interpret the genomic data relative to antimicrobial resistance and to track AMR trends and spread in order to support public health interventions and inform therapeutic choices.

Details

Antibiotic resistance genes

This course provides participants with a comprehensive theoretical overview of antimicrobial resistance genes, resistance mechanisms, and the resistance genes databases. Participants will learn about the diversity of AMR genes and their associated mechanisms, they will explore the resources and functionalities of resistance genes databases.

Antibiotic resistance genes or mutations

This module provides participants with practical training to learn how to use antimicrobial resistance gene databases (e.g., CARD) and *in silico* detection tools like ResFinder and CARD to detect AMR genes or mutations associated with AMR in genome assemblies or raw reads. Participants will learn the principles and applications of ResFinder and BLAST, with practical exercises to analyze genomic data and predict AMR profiles. By the end of the course, participants will have acquired the skills necessary to effectively leverage resistance databases and *in silico* AMR detection tools and they will be able to apply their knowledge to address public health challenges related to antibiotic resistance and microbial epidemiology.