BIODIVERSITY — DAY 4			
Time	**Activity Description**	**Intended Learning Outcomes**	**Relevance**
0930-1100	Phylogeny Part 1 (Julien Guglielmini)	Understand the basic principles of phylogeny, including substitutions models, optimality criteria and branch support How to read a phylogenetic tree Learn the impacts of recombination on phylogenetic inference	**Bioinformaticians** will gain knowledge of phylogenetic methods to support microbiologists and epidemiologists in understanding genetic relationships within microbial populations and tracking the spread of pathogens during outbreaks. **Microbiologists and epidemiologists** will learn how to interpret phylogenies to investigate disease transmission patterns, collaborating with bioinformaticians to track outbreaks.
1110-1240	Phylogeny Part 2 (Julien Guglielmini)	Gain knowledge about easy-to-use tools for phylogenetic tree generation Practical interpretation of trees to investigate transmission dynamics of bacterial pathogens Interpretation of genetic relationships within microbial populations through phylogenetic methods Practical exercises on how to interpret phylogenetic trees or classification graphs	**Bioinformaticians** will gain a practical understanding of alignment and phylogeny tools to support microbiologists and epidemiologists in interpreting NGS data for outbreak investigation and in understanding evolutionary relationships among microbial strains. **Microbiologists** can leverage tools to study microbial evolution and population structure, collaborating with bioinformaticians and epidemiologists to interpret genetic data accurately. **Epidemiologists** will be able to interpret phylogenetic trees to analyze transmission patterns, working closely with bioinformaticians and microbiologists to integrate genetic data into epidemiological investigations and inform public health interventions.

Details

Phylogeny

The course on "Phylogeny" offers participants theoretical and practical training on basic phylogenetic analysis principles. They will learn the principles for inference, such as choosing substitution models, tree building, and evaluating trees, alongside understanding recombination's impact on phylogenetic relationships.

Participants will gain hands-on experience using phylogenetic analysis tools, to construct phylogenetic trees and grasp microbial population genetic diversity. Using simple datasets from foodborne pathogens, they will interpret population structure, pathogen evolution, and transmission dynamics from obtained trees.

By course end, participants will proficiently interpret phylogenetic trees, enhancing their ability to investigate transmission patterns in epidemiological studies.