



**2nd Course on Bioinformatics Tools for
Next Generation Sequencing data mining:
use of bioinformatics tools for typing pathogenic *E. coli***

16-17 June, 2016

SIDBAE Training Room

(*Building 1, Floor B*)

Istituto Superiore di Sanità

Viale Regina Elena, 299 – Rome, Italy



Organized by:

- The EU Reference Laboratory for *E. coli*
- The ISS IT Service (SIDBAE)

Funded by the European Commission – DG SANTE

DIRECTOR OF THE COURSE

Stefano MORABITO

EU Reference Laboratory for *E. coli*

Dipartimento di Sanità Pubblica Veterinaria e Sicurezza Alimentare
Istituto Superiore di Sanità

SPEAKERS

EU Reference Laboratory for *E. coli*, ISS, Rome, Italy

Antonella MAUGLIANI

Valeria MICHELACCI

Rosangela TOZZOLI

IT Service (SIDBAE), ISS, Rome, Italy

Arnold KNIJN

Istituto Zooprofilattico Sperimentale Abruzzo e Molise, Teramo, Italy

Massimiliano ORSINI

European Food Safety Agency, Parma, Italy

Valentina RIZZI

European Center for Diseases Prevention and Control, Stockholm, Sweden

Saara KOTILA

TECHNICAL SECRETARIAT

Susan BABSA, Clarissa FERRERI

EU Reference Laboratory for *E. coli*

Department of Veterinary Public Health and Food Safety

Istituto Superiore di Sanità

Rome, Italy

Fabio GALATI, Arnold KNIJN

Servizio Informatico, documentazione, biblioteca ed attività editoriali (SIDBAE)

Istituto Superiore di Sanità

Rome, Italy

GENERAL INFORMATION

Venue: Istituto Superiore di Sanità, SIDBAE Training Room (Building 1, Floor B)

Viale Regina Elena 299, 00161 Rome

This event is part of the scientific and tutorial activities of the EU-RL VTEC, funded by the European Commission – DG SANTE

For any information regarding the event, please send an email to crl.vtec@iss.it

June 16th, Thursday

9.00	Registration	
9.15	Welcome, housekeeping, and general overview on the training course	Stefano Morabito
	Session 1	
9.30	Recent and on-going WGS initiatives and activities of EFSA	Valentina Rizzi
10.00	Recent and on-going WGS initiatives and activities of ECDC	Saara Kotila
10.30	Coffee break	
11.00	VTEC strains typing: from traditional methods to NGS	Rosangela Tozzoli
11.30	IT infrastructure and user interface: the Galaxy architecture and ARIES cluster	Arnold Knijn
12.00	Basic tools for NGS data mining: quality check, assembly, annotation, alignment and blast	Valeria Michelacci
12.30	Virulotyping and serotyping	Valeria Michelacci
13.00	Lunch	
14.00	Hands-on exercises: virulotyping and serotyping	Rosangela Tozzoli Valeria Michelacci Antonella Maugliani
15.00	Whole genome SNPs (wgSNPs) comparison: SNPtree, NDtree, CSI Phylogeny and kmer-based analysis	Valeria Michelacci
15.30	Hands on exercises: wgSNPs analysis	Valeria Michelacci Rosangela Tozzoli Antonella Maugliani
17.00	End of Session 1	

June 17th, Friday

Session 2

9.30	Hands on exercises: kmer-based wgSNPs analysis	Valeria Michelacci Rosangela Tozzoli Antonella Maugliani
10.15	Introduction to High Resolution Virulence Allelic Profiling (HReVAP)	Valeria Michelacci
10.45	Hands on exercises: HReVAP from melting temperatures	Valeria Michelacci Rosangela Tozzoli Antonella Maugliani
11.15	Coffee break	
11.45	Gene-by-gene approaches for typing through WGS: conventional MLST and <i>E. coli</i> accessory genome MLST (agMLST)	Massimiliano Orsini
12.15	Hands-on exercises: conventional MLST and agMLST	Valeria Michelacci Rosangela Tozzoli Antonella Maugliani Massimiliano Orsini
12.45	Concluding remarks	Stefano Morabito
13.00	Closure of the Course and Lunch	