

Preparedness towards the use of NGS for characterization and typing of pathogenic *E. coli*

Valeria Michelacci

11th Annual Workshop of the National Reference
Laboratories for *E. coli* in the EU

Rome, November 10th 2016



Istituto Superiore di Sanità, Dep. of Veterinary Public Health and Food Safety
European Union and National Reference Laboratory for *E. coli*, Rome, Italy



Typing methods for *E. coli*: pros & cons

	PFGE	MLST	MLVA	wgSNP
Discriminatory level	Strain typing	Phylogenetic analysis	O157 and O26 strain typing Work in progress for the others	Ref-based strain typing pipeline for O157 and O26 Work in progress for the others
Possibility to automate	No	Yes (especially if NGS-based)	Yes	Yes
Standardization	Yes	Yes	Yes for O157	Not yet

Next Generation Sequencing applied to *E. coli*

Characterization and typing of isolates in short time and at low costs

Lack of standardization

Difficult assembly due to many repetitive regions

Difficult choice of reference sequences



Participation in national and international scientific activities on WGS

National **Committee for Genomics** in Veterinary Public Health

Promoters: ISS (Stefano Morabito), IZS-VE (Antonia Ricci) and IZSA-AM (Massimiliano Orsini)



- NGS in Veterinary Public Health, technology and applications – Bologna, May 2016
- Metagenomics and veterinary public health – Palermo, October 2016

European initiatives:

- **GMI** meetings & Ring Trial
- **Public Health WGS** group meetings (A discussion on methods and challenges of using WGS for surveillance of food-borne pathogens) at the Statens Serum Institut in 2015 and 2016 & Ring Trial
- Observers at **ENGAGE** first workshop in Warsaw



EURL participation in national and international activities on WGS

EFSA Scientific Colloquium n° 20: “Use of Whole Genome Sequencing (WGS) of food-borne pathogens for public health protection”, 2014

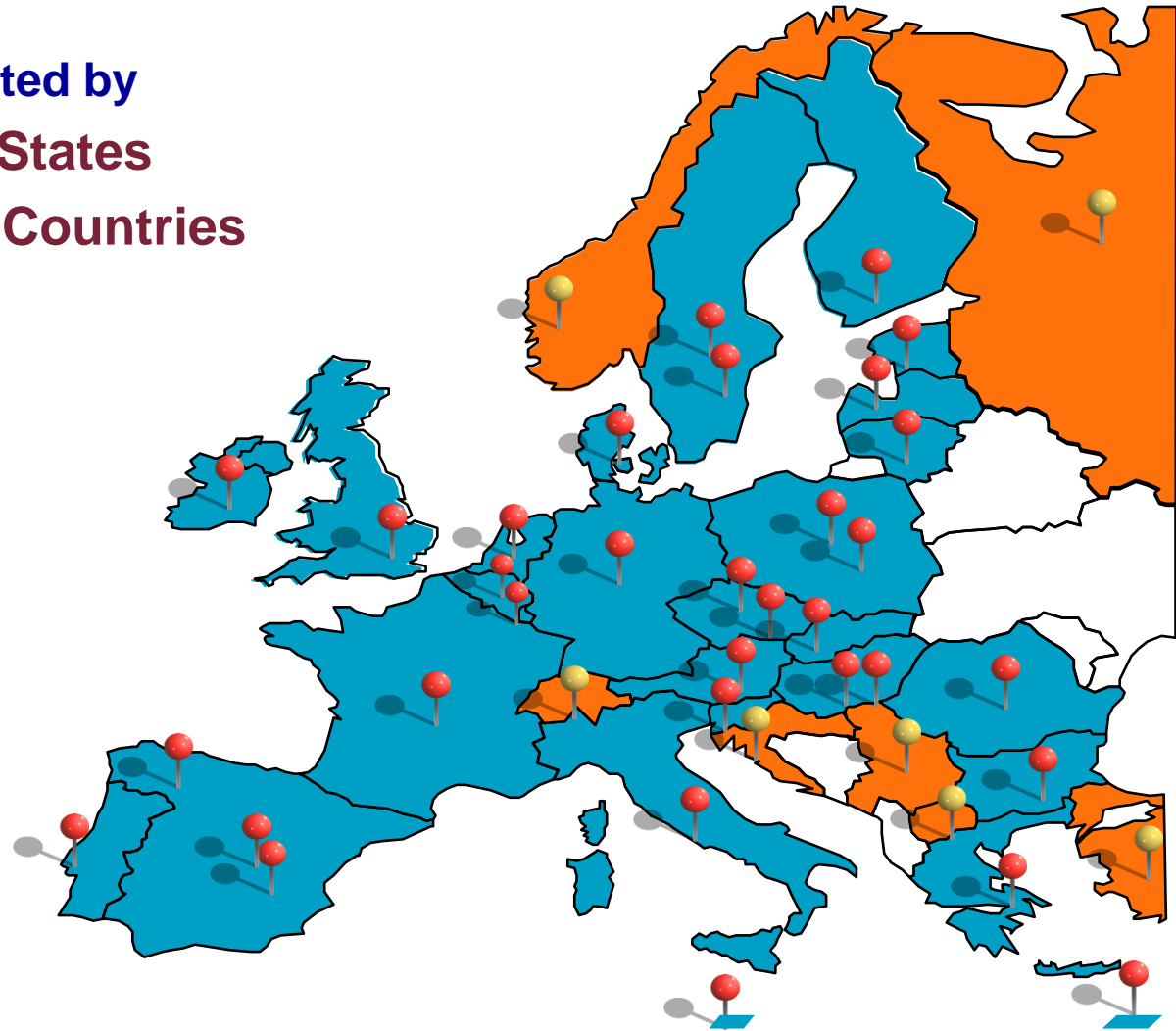


FWD-ECDC NEXT Expert group for the production of the SCIENTIFIC ADVICE: “Expert Opinion on the introduction of next-generation typing methods for food- and waterborne diseases in the EU and EEA”, 2015



NGS in the network of NRLs for *Escherichia coli*

41 NRLs designated by
27 EU Member States
+ 7 other European Countries



E. coli network and NGS: State of the Art

In 2014 all the NRLs expressed the need for education in genomics data analysis by replying to a questionnaire

8 NRLs already access to benchtop sequencers

8 NRLs plan to outsource NGS data production



Many others are following...



May 2015

WGS has already replaced existing methods	WGS complements existing methods	WGS will complement existing methods in the next year or two	No plans to apply WGS-based methods	Not Known
1	9	8	12	3

STEC
Public
Health labs

The European Commission has just carried out an inventory on the preparedness on the use of NGS



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Training at the EU RL for *E. coli* on NGS data analysis



EU Reference Laboratory for *E. coli*
Department of Veterinary Public Health and Food Safety
Unit of Foodborne Zoonoses
Istituto Superiore di Sanità



EU Reference Laboratory for *E. coli*
Department of Veterinary Public Health and Food Safety
Unit of Foodborne Zoonoses
Istituto Superiore di Sanità



Basic Course on Bioinformatics tools for Next Generation Sequencing data mining

11-12 June, 2015

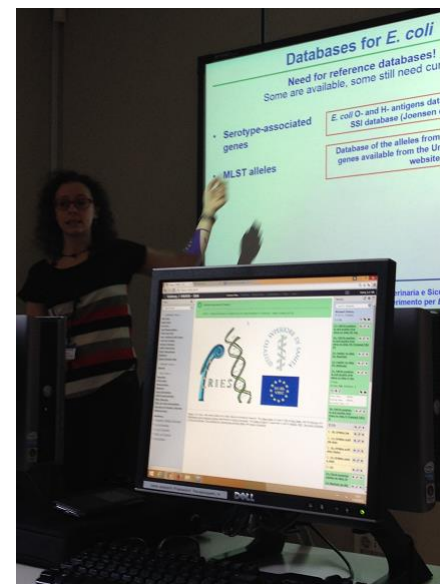
SIDBAE Training Room



2nd Course on Bioinformatics for Next Generation Sequencing Data Mining: Use of Tools for Typing Pathogenic *E. coli*

16-17 June, 2016

Istituto Superiore di Sanità, SIDBAE Training Room



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European Union and National Reference Laboratory for *E. coli*, Rome, Italy**



Basic course in 2015



22 attendees

14 participants

7 from NRLs

supported by DG-SANTE

2 from NRL Italy

5 from Italian Official Labs

8 observers

2 from NRL Italy

3 Italian Official Labs

2 from other ISS labs

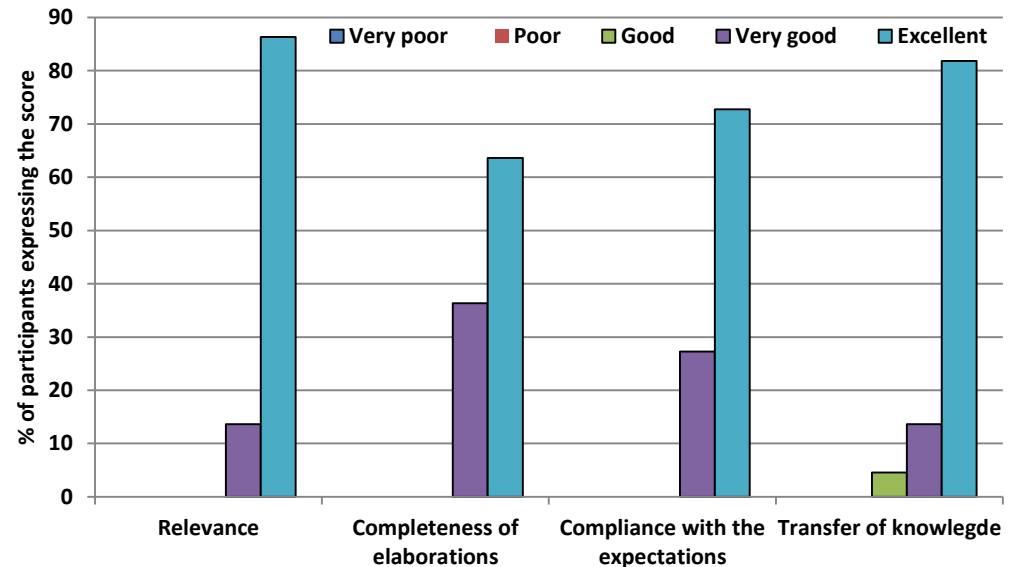
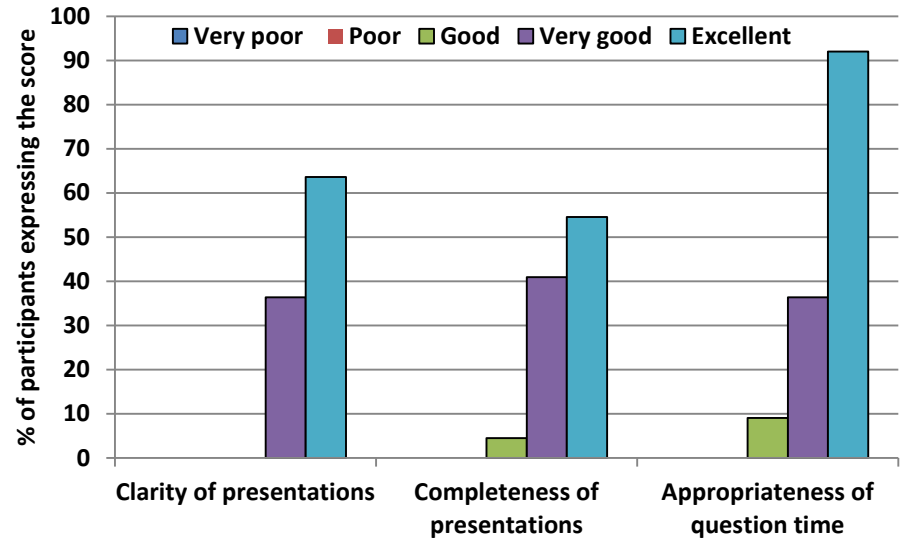
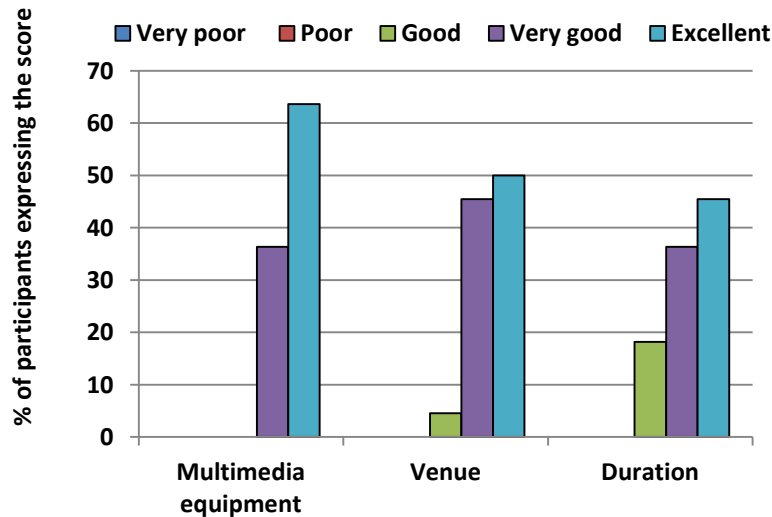
1 EFSA observer

NGS course 2015 – topics and satisfaction survey

Data formats

Basic tools: assembly, mapping

Blast, annotation, virulotyping, serotyping, MLST, wgSNPs



2nd course on NGS tools for *E. coli* typing in 2016

22 attendees



14 participants

6 from NRLs
supported by DG-SANTE

2 Italian Official Labs

4 from NRL Italy

1 EFSA

1 ECDC

8 observers

1 from EURL

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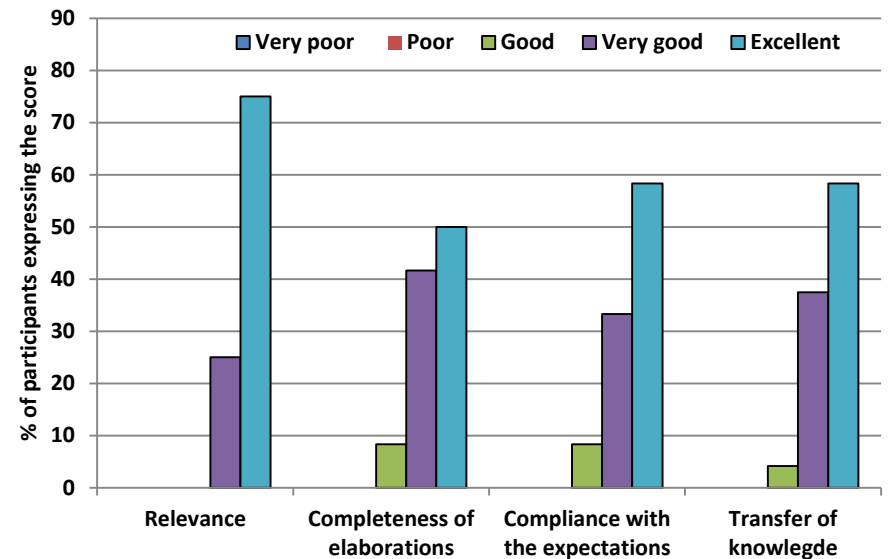
NGS course 2016 – topics and satisfaction survey

Virulotyping, serotyping

wgSNPs: ref-based and kmer-based

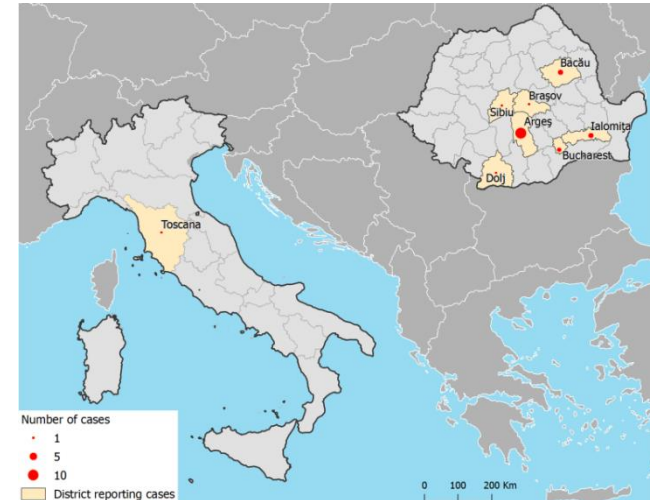
HReVAP

agMLST



Assistance to Member States during outbreak investigation

Multicountry (Romania-Italy) outbreak of STEC O26



Two scientists from Cantacuzino Institute and National Centre for Communicable Disease Surveillance and Control for Health (RO) were funded by the FWD EXPERT EXCHANGE PROGRAMME (FWDEEP) to visit the EU-RL to be assisted in analysing whole genome sequencing data for supporting outbreak investigation

ARIES: A Galaxy-based workspace for intensive data analyses

Galaxy / ARIES - ISS

Analyze Data Workflow Shared Data Visualization Help User

Using 8.0 GB

Istituto Superiore di Sanità

ARIES - Advanced Research Infrastructure for Experimentation in Genomics - Galaxy Instance at ISS

ARIES

ISTITUTO SUPERIORE DI SANITÀ

EU-RL VTEC

History

- metagenomics biosolids
19 shown, 55 deleted
6.7 GB
- 74: Krona chart on data 73
- 73: species assigned to Mobio_15 trimmed
- 70: blastx FASTQ to FASTA on data 55 vs Viral proteins Database_31052015
- 65: FASTQ to FASTA on data 55
- 63: FastQC on data 55: RawData
- 62: FastQC on data 55: Webpage
- 56: FASTQ positional and quality trimming on data 1: log
- 55: Mobio15-trimmed FASTQ
- 45: viral_1.1.genomic.fna
- 44: Viral proteins Database_31052015
- 43: viral_1.protein.faa
- 36: viral.nonredundant_protein_1.protein.faa
- 26: protein BLAST database from data 25
- 25: viral.nonredundant_protein_1.protein.faa
- 19: Species assigned to megablast FASTQ to FASTA Mobio15 vs 16S_20150128
- 4: Mobio15 FASTA vs Viruses_DB
- 3: Mobio15 FASTA E.coli virulence genes
- 2: FASTQ to FASTA Mobio15
- 1: Mobio15_05052015.fasta

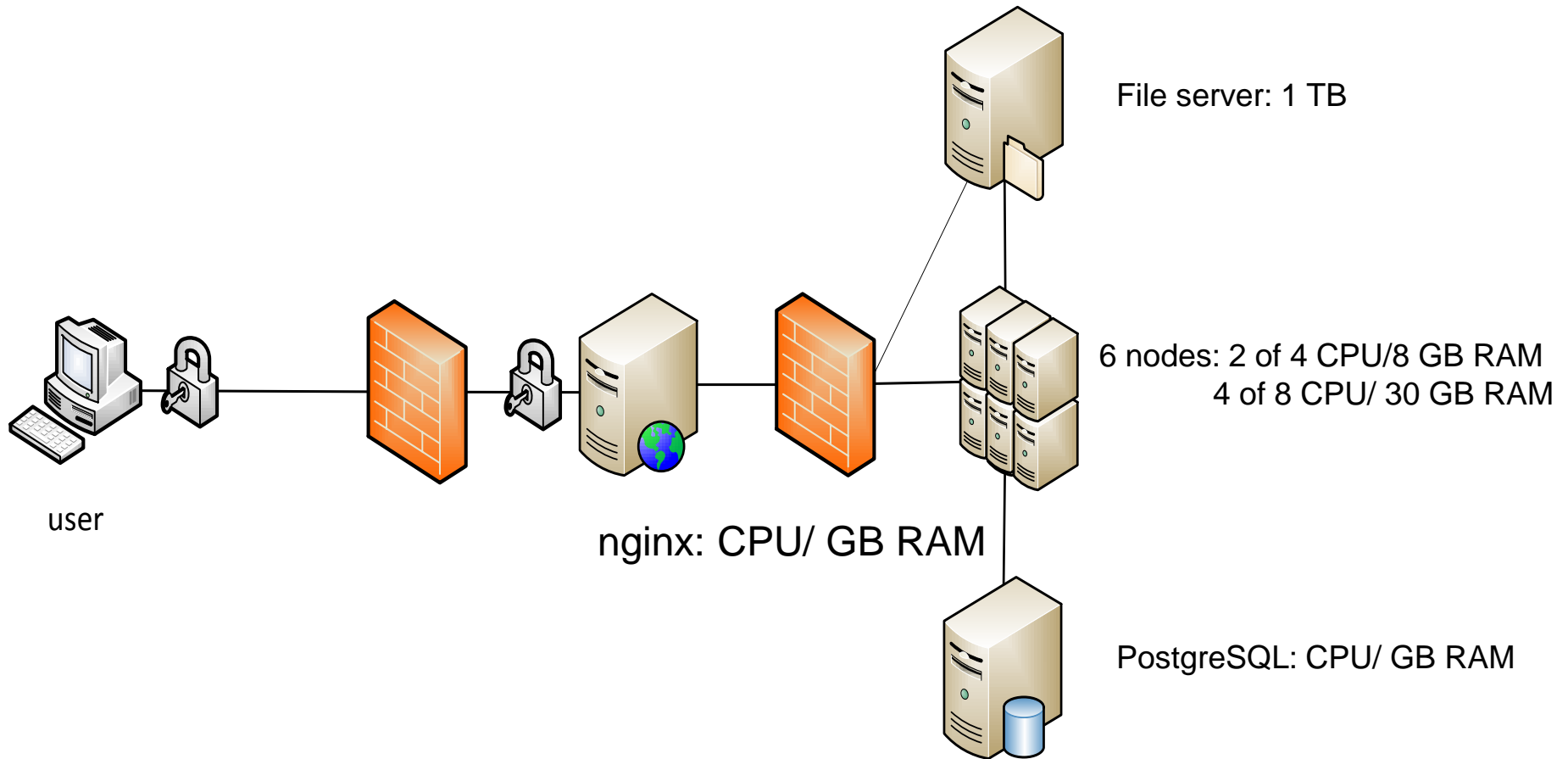
Galaxy is an open, web-based platform for data intensive biomedical research. The Galaxy team is a part of BX at Penn State, and the Biology and Mathematics and Computer Science departments at Emory University. The Galaxy Project is supported in part by NHGRI, NSF, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Emory University.



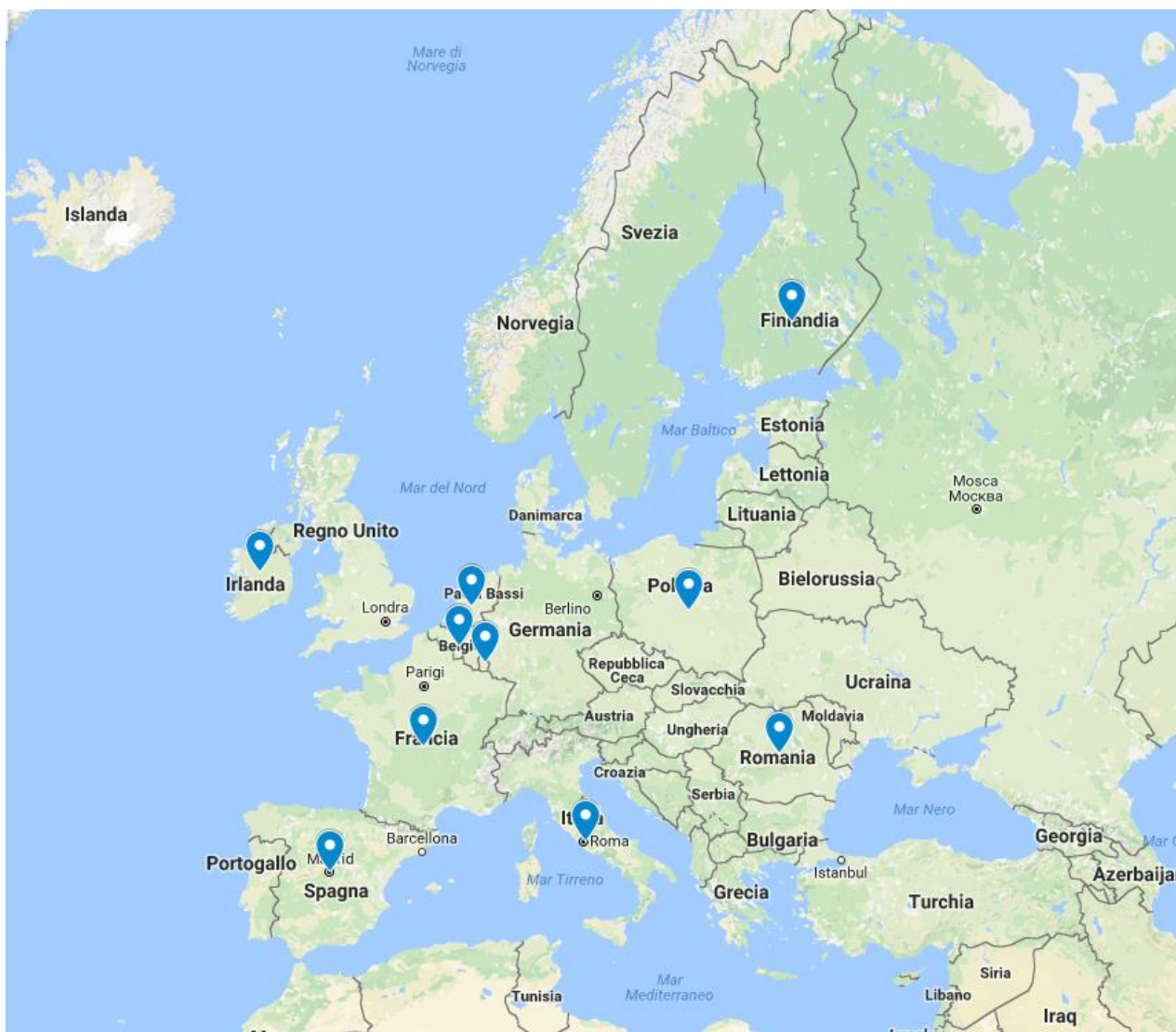
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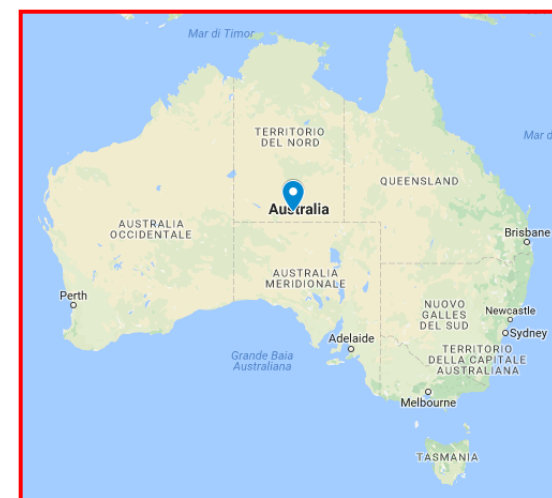
ARIES Under the hood



ARIES geographic spread



**Total:
50 users**



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Tools

--- COMMON TOOLS ---

[Get Data](#)[Send Data](#)[Lift-Over](#)[Text Manipulation](#)[Filter and Sort](#)[Join, Subtract and Group](#)[Convert Formats](#)[Extract Features](#)[Fetch Sequences](#)[Fetch Alignments](#)[Statistics](#)[Graph/Display Data](#)[GraPhAn](#)

---HREVAP TOOLS---

[HReVAP](#)

---NGS TOOLS---

[In Silico PCR](#)[E coli typing](#)[NGS: Assembly](#)[NCBI Blast](#)[Manipulation](#)[Gene Annotation](#)[FASTA/FASTQ manipulation](#)[NGS: Mapping](#)[NGS: SAM Tools](#)[NGS: BED Tools](#)[NGS: QC and manipulation](#)[Operate on Genomic Intervals](#)

---METAGENOMICS TOOLS---

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ARIES - Advanced Research Infrastructure for Experi



Please read our [disclaimer](#) before using ARIES.

QC

Assembly de novo

Mapping

Microbial genome annotation

NCBI Databases

Databases shared with
CGE/SSIs

Custom Databases

***E. coli* typing:**

Virulotyping

Serotyping

Clermont phylogrouping

HReVAP

MLST

ksnp3 for ref-free wgSNPs

agMLST

Perspectives

- **Guidelines** for ARIES use and/or web-based training modules
- Activation of **EURL-visiting training programs** for NGS data analysis
- Further **collaboration with EFSA and ECDC** to implement NGS for surveillance and outbreak investigation – discussion on Nomenclature in ECDC NEXT Group in association with PulseNet International

