


Collaborative Management Platform for
detection and Analyses of (Re-) emerging
and foodborne outbreaks in Europe

A global platform for the sequence-based rapid identification of pathogens

Prof. Frank M. Aarestrup, coordinator (Technical University of Denmark)

Prof. Marion Koopmans, deputy coordinator (Erasmus Medical Center, the
Netherlands)



This project has received funding from the *European Union's Horizon 2020*
research and innovation programme under grant agreement No 643476. 
research and innovation programme under grant agreement No 643



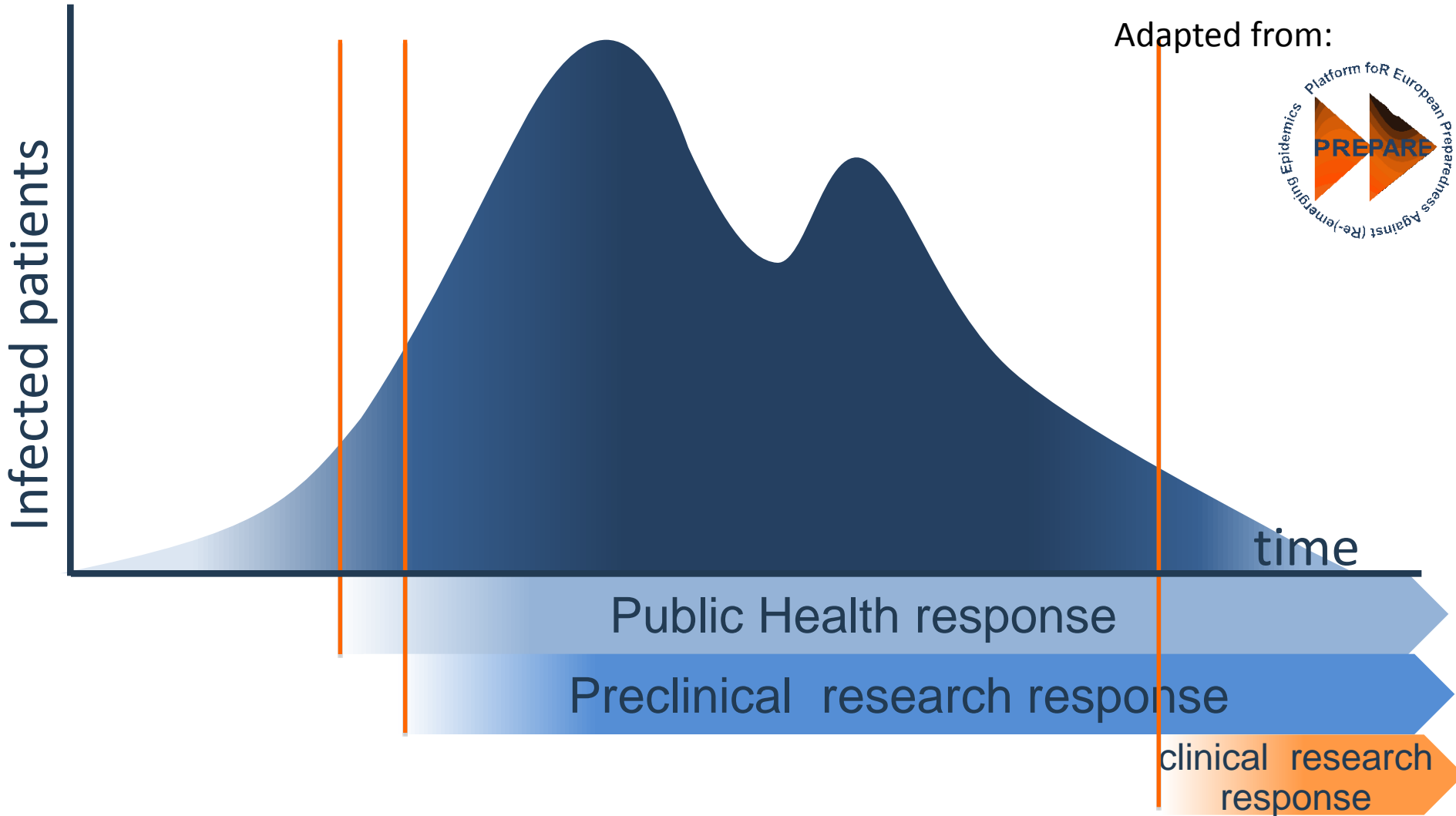
Current infectious disease situation



- Dynamics of common infectious diseases are changing
 - Demographic change, population density, anti vaccine, AMR, etc.
- New diseases / variants emerge frequently
 - Population growth, travel, trade, climate change
- Effects are difficult to predict due to complexity
 - Rapid flexible response
- Public health, diagnostic / vaccine development and clinical response depend on global capacity for disease surveillance
 - Rapid sharing, comparison and analysis of data from multiple sources and using multiple methodologies



Response to ID outbreaks usually fragmented and late



Adapted from:

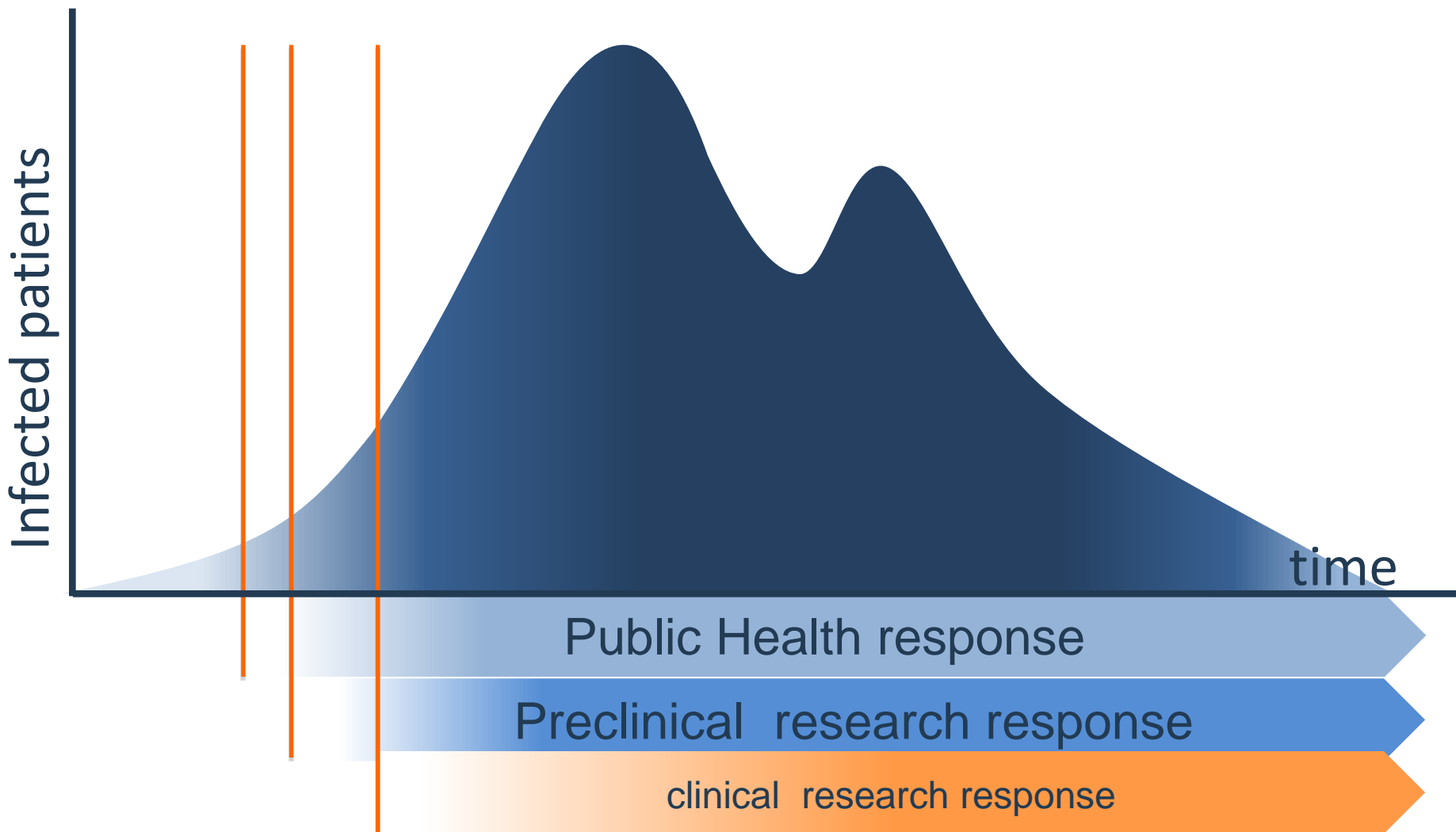
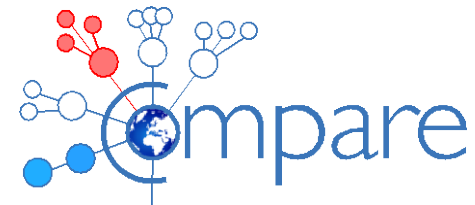


Courtesy Frank Deege

This project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 643476.



Response to ID outbreaks with improved detection and sharing of data

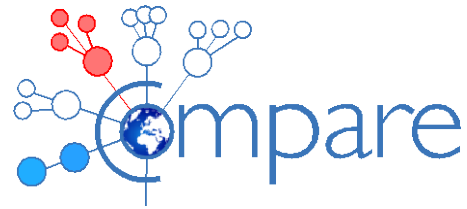


Courtesy Frank Deege

This project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 643476.



What the world needs



- Real-time data on occurrences of all infectious agents
- (Automatic) detection of related clusters in time and space
- Possibility to observe trends in clones and species as well as virulence and AMR
- Ability to rapidly compare between all types of data

There can be no real-time surveillance without real-time data sharing



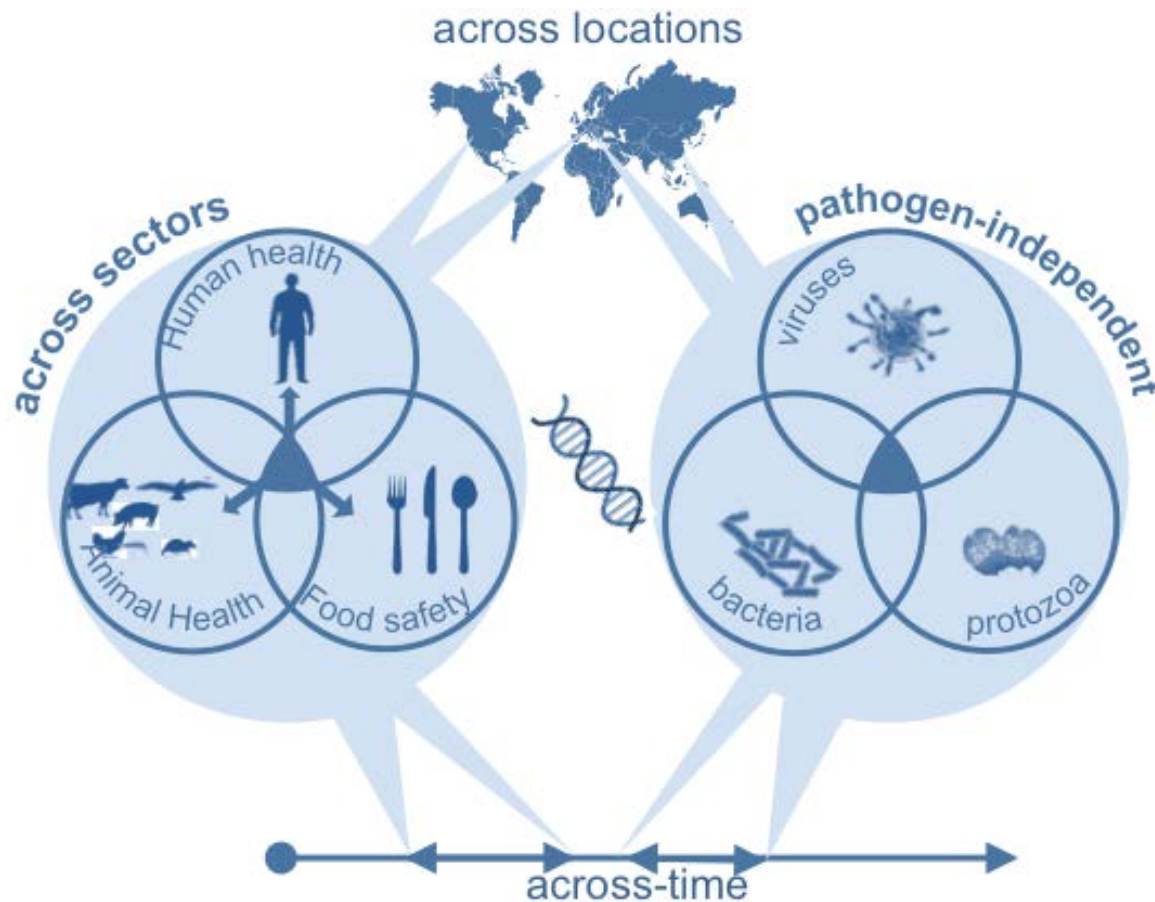
NGS advantages



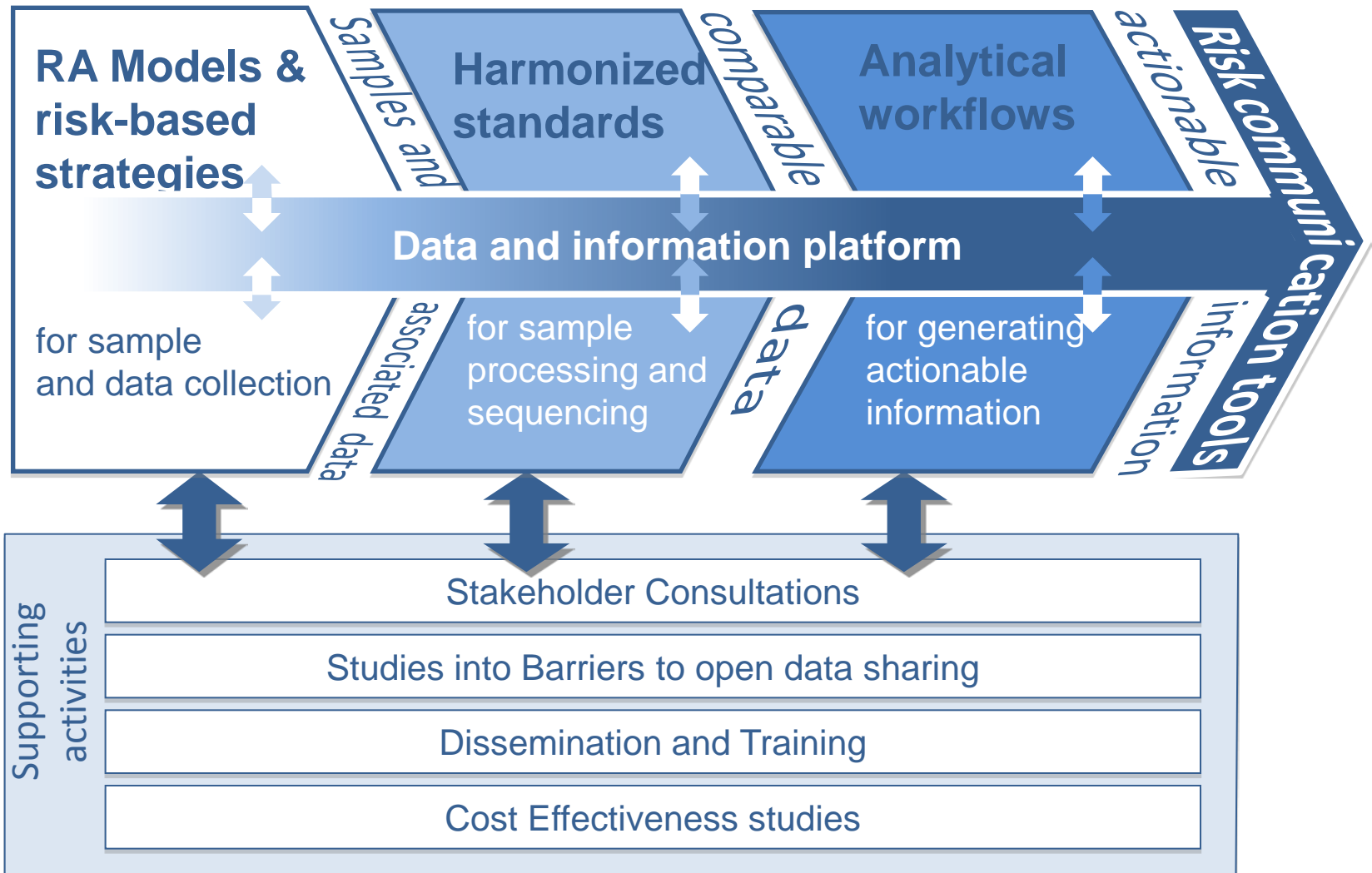
- Laboratory diagnostics increasingly rely on (pathogen) genomic information
 - RNA / DNA are common across pathogens, therefore, methods to analyse pathogen genomes are potentially universal
 - NGS capacity is developing fast, and costs are becoming competitive
-
- NGS may provide a universal language that can be harnessed for early detection and comparisons across disciplines and domains
 - Easy to learn and implement, less equipped labs may leapfrog
 - Lack of local bioinformatics and IT solutions



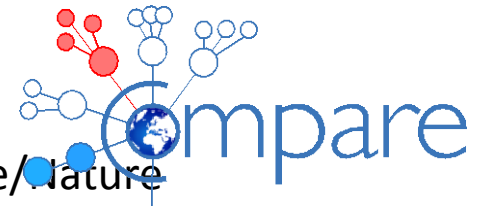
Our vision: to build one system that serves all



Project structure



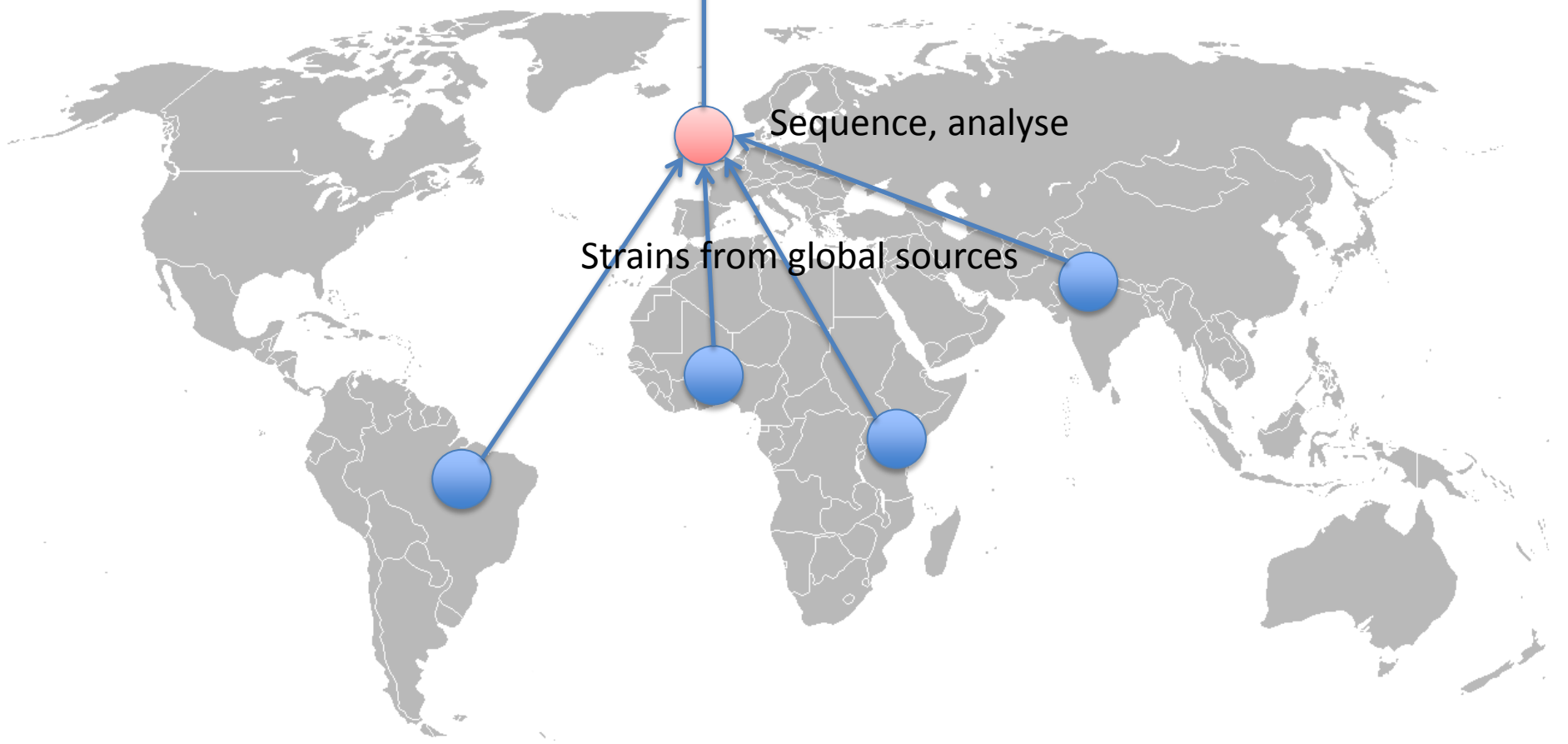
Traditional way



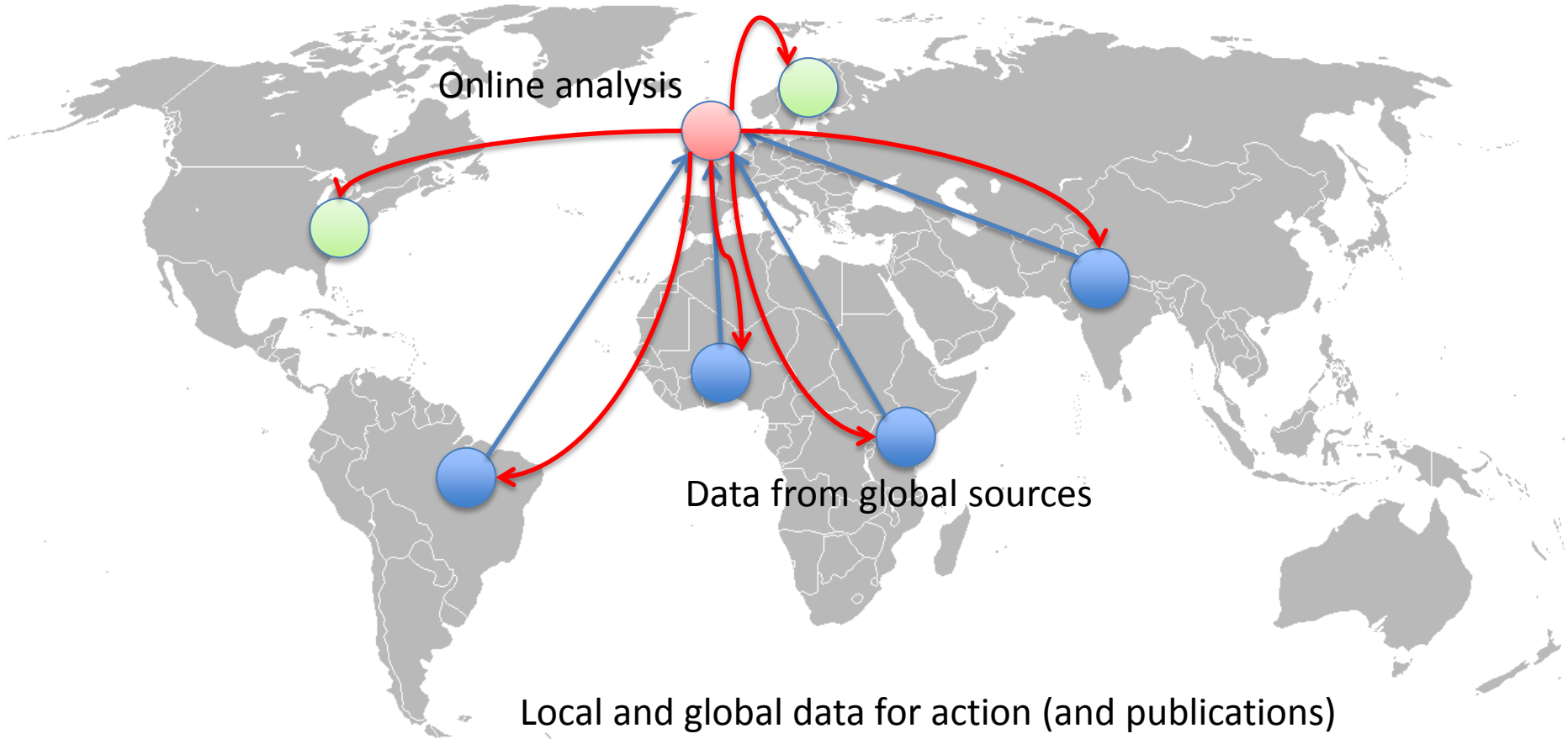
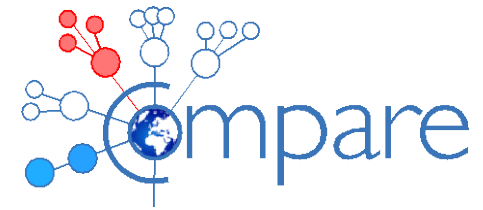
Publish in Science/Nature

Sequence, analyse

Strains from global sources



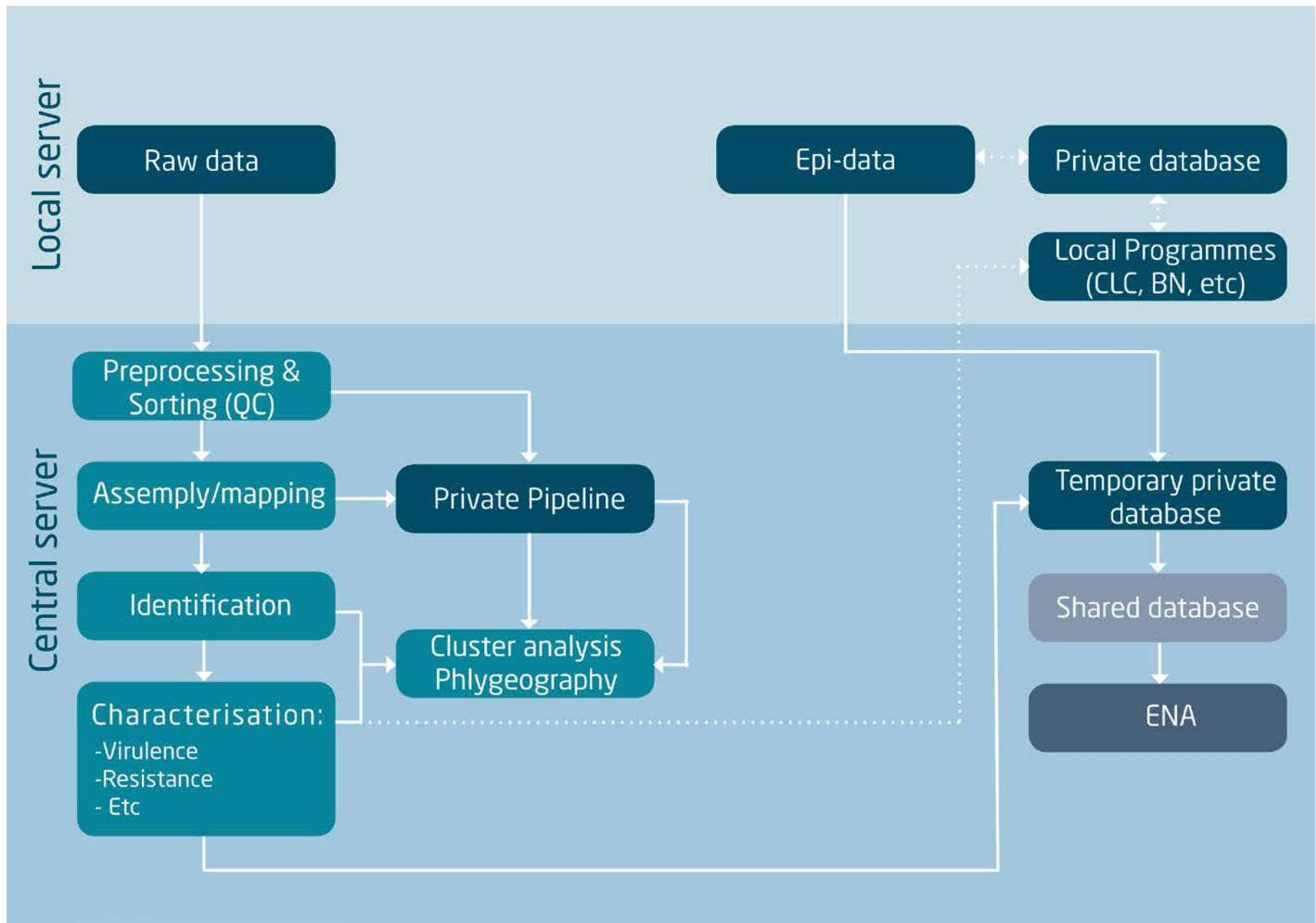
Our way



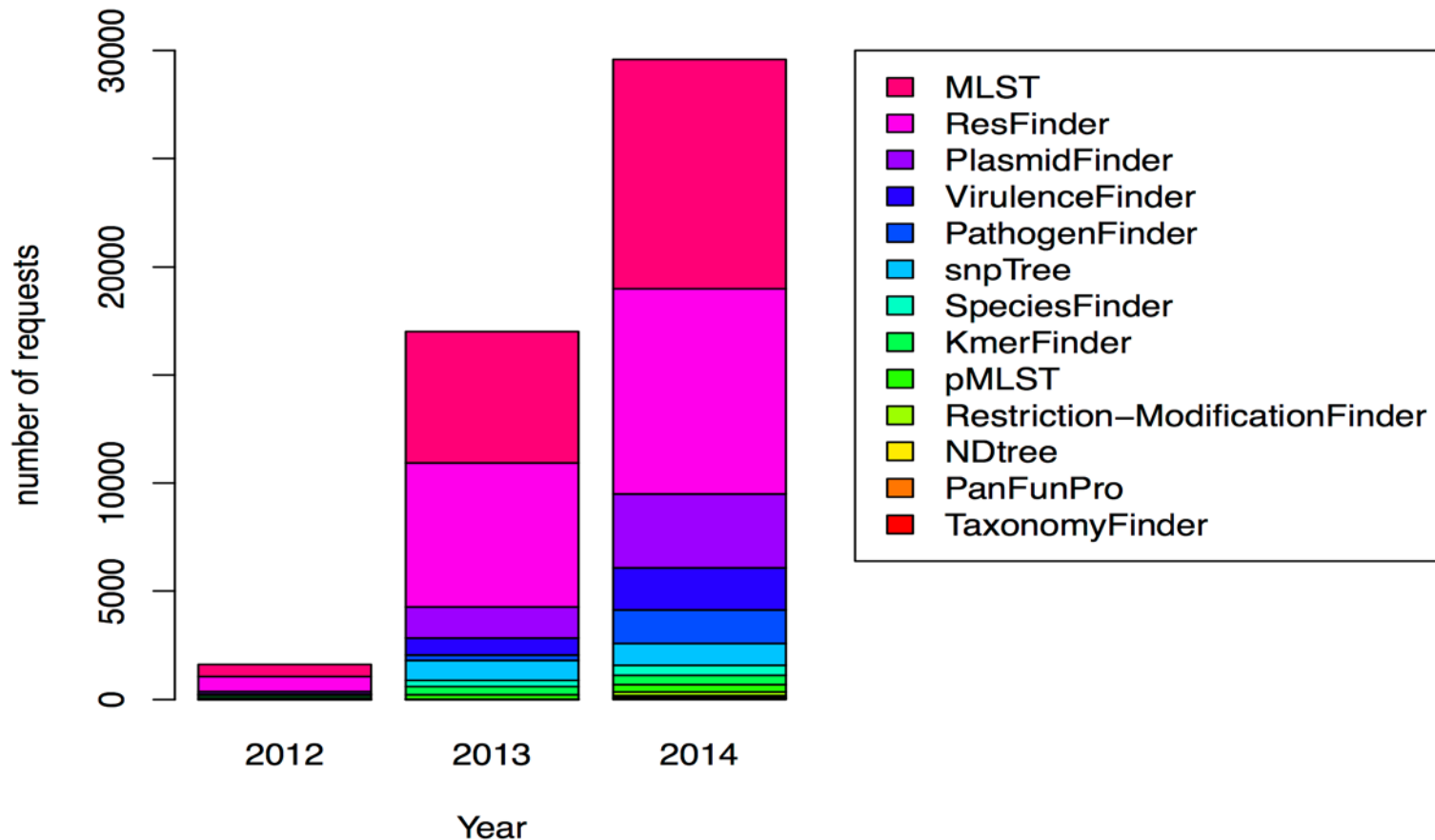
Online analysis

Data from global sources

Local and global data for action (and publications)



User Statistics



Until now: >600,000 submissions from 12,000 IP-
addresses in +100 countries

Update

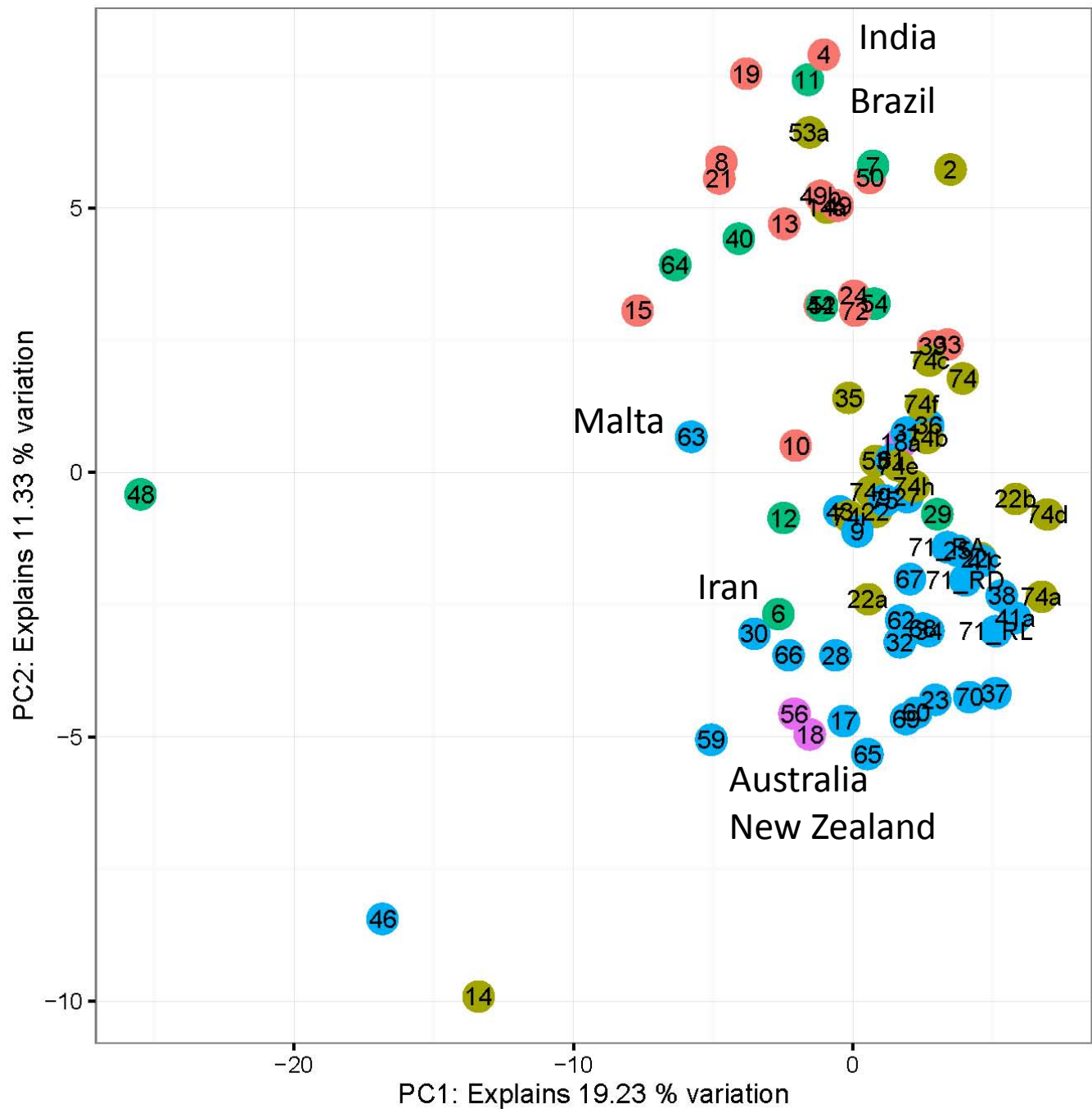


- Developed initial standards and studies for sampling, handling, sample preparation, sequencing and bioinformatics and conducted ring trials.
- Workflows / needs for clinical diagnostic, food safety and emerging diseases developed and pilot projects started.
- Web-accessible sites for sharing of sequence data have been created (data hubs), the first comparisons of analytic pipelines in beta testing.
 - AI/H5N8, ebola, salmonella, AMR and global metagenomic surveillance and real-time sharing

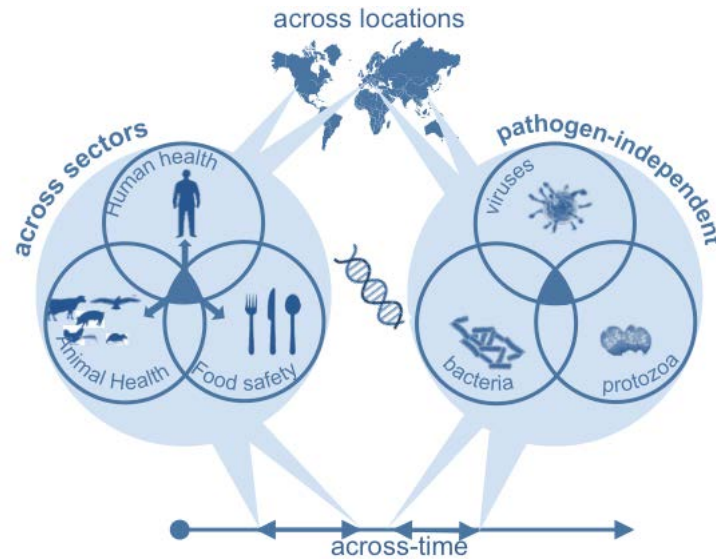


Glol

are



Our vision: one system serves all



Guiding principles:

- Cross sector, cross domain, open source (not commercial)
- Interaction with the rest of the world (all inclusive)
- Data for action (actionable outputs)
- Central repository (ENA, DDJ, NCBI) (bring the tools to the data)

There can be no real-time disease detection & surveillance without real-time data sharing