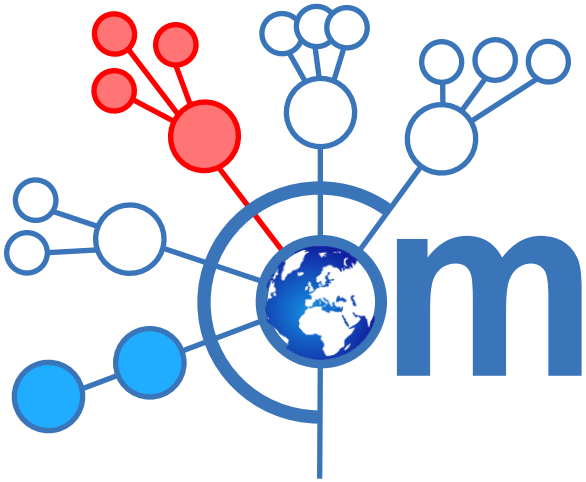

ompare

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.

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Current infectious disease situation

- Dynamics of common infectious diseases are changing
  - Demographic change, population density, anti vaccine, AMR, etc.
- New diseases / variants emerge frequently
  - Deforestation, population growth, health system inequalities, travel, trade, climate change
- Effects are difficult to predict due to complexity
  - Rapid flexible response
- Public health, diagnostic and 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

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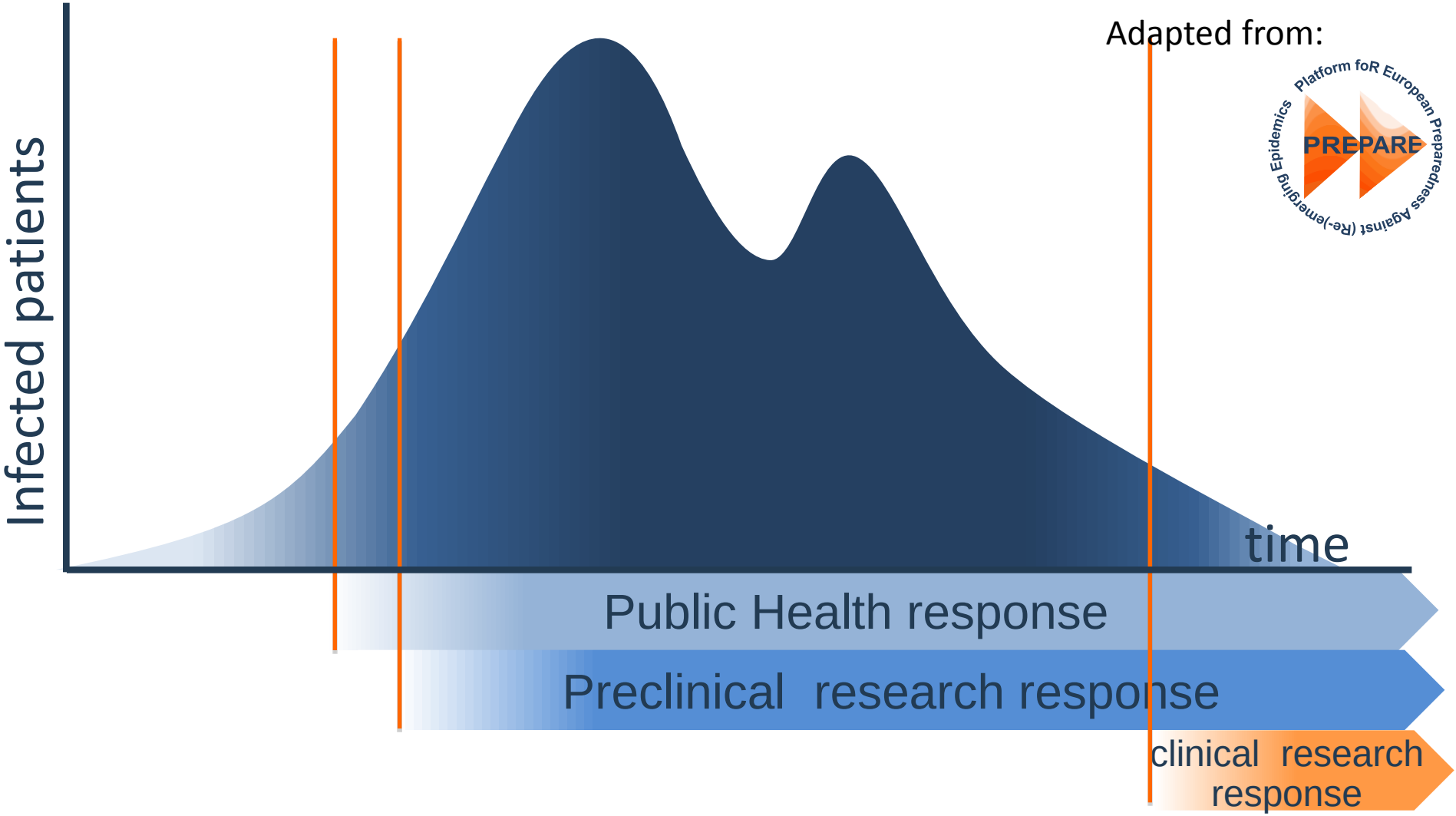
Response to ID outbreaks usually fragmented and late

Adapted from:



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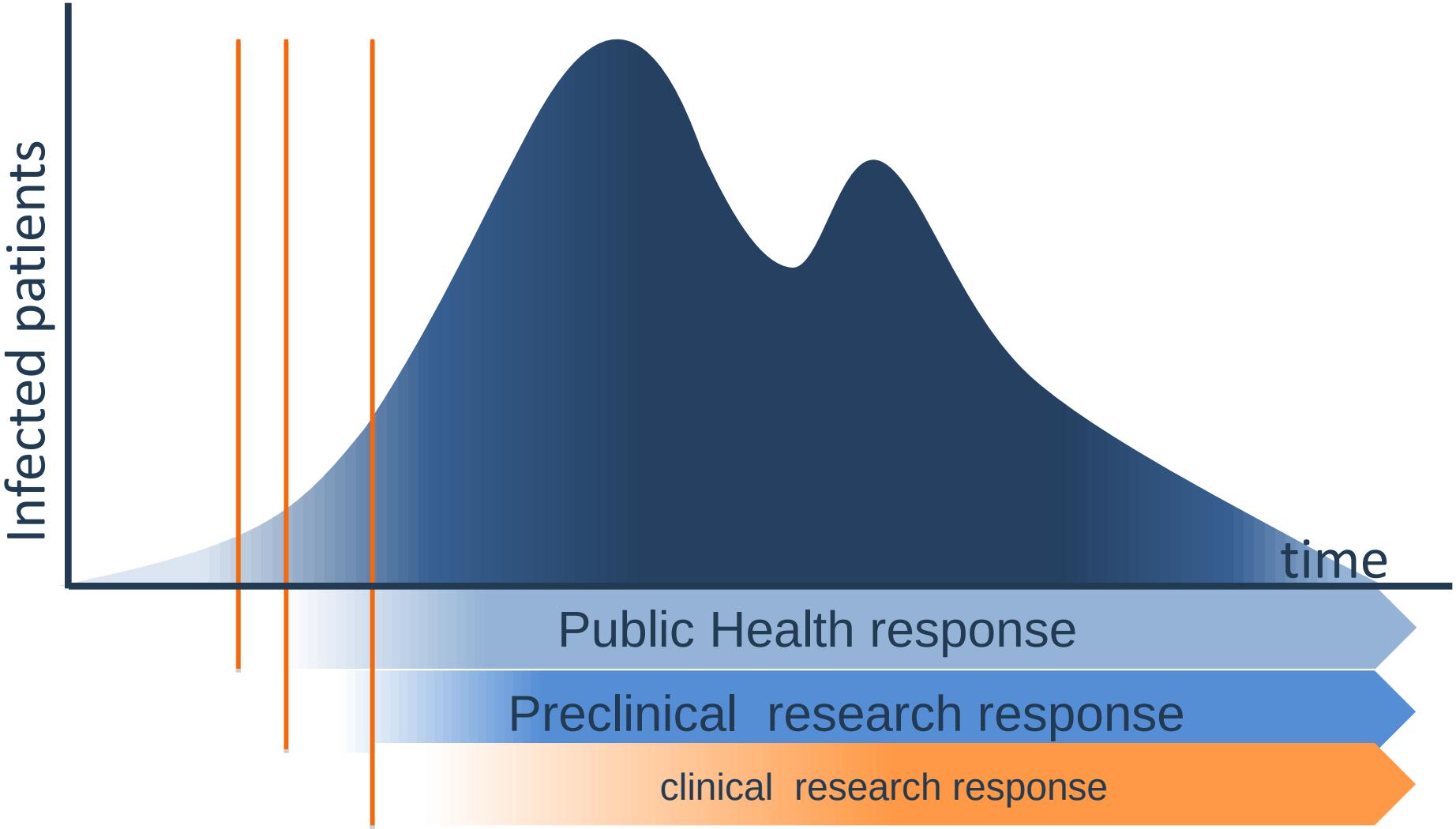
Response to ID outbreaks with improved detection and sharing of data



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What the world needs

- Real-time data on occurences 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 resistance
- Ability to rapidly compare between all types of data

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

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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
- Next generation sequencing capacity is developing fast, and costs are becoming competitive

- ➢ Capturing NGS developments may provide a universal language that can be harnessed for early detection and comparisons across disciplines and domains
- ➢ If the technology keeps developing, less equipped labs may leapfrog

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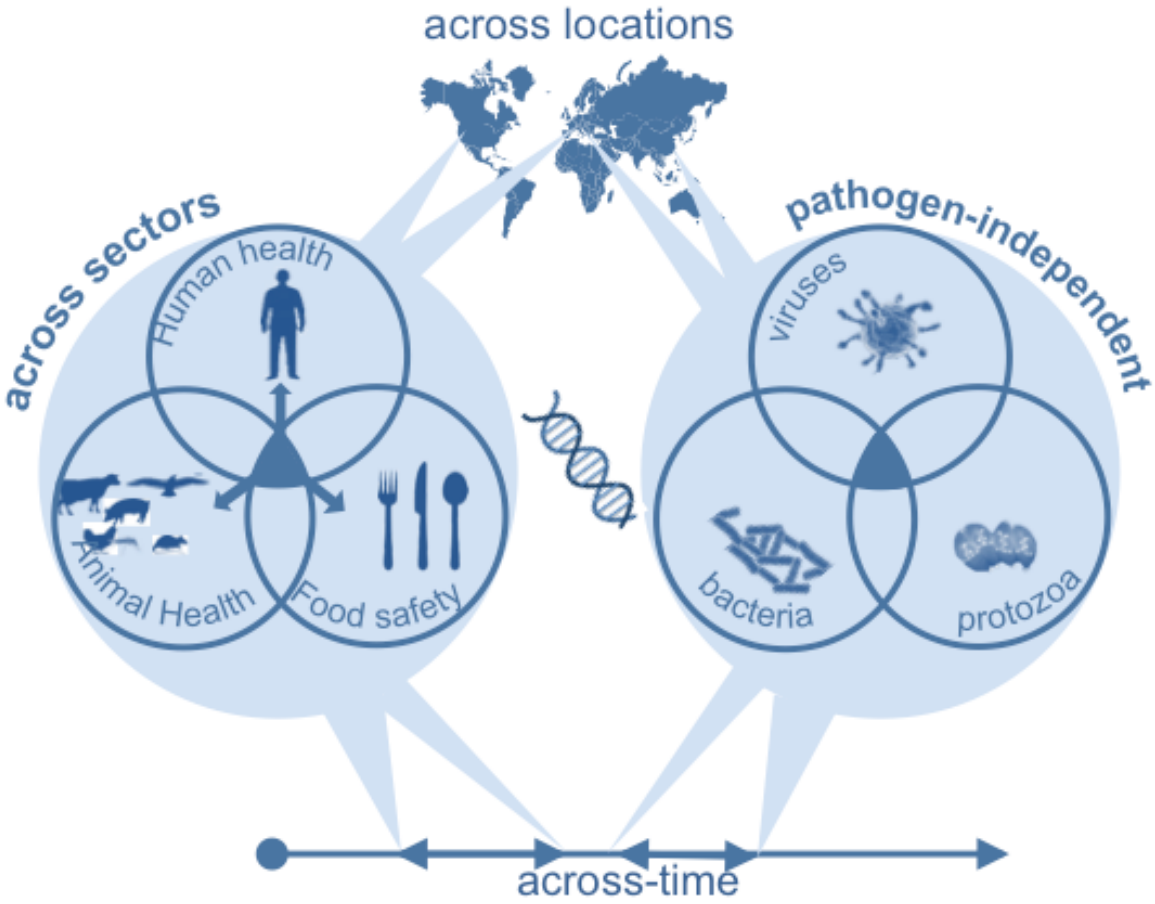
Our vision:

to build one system that serves all



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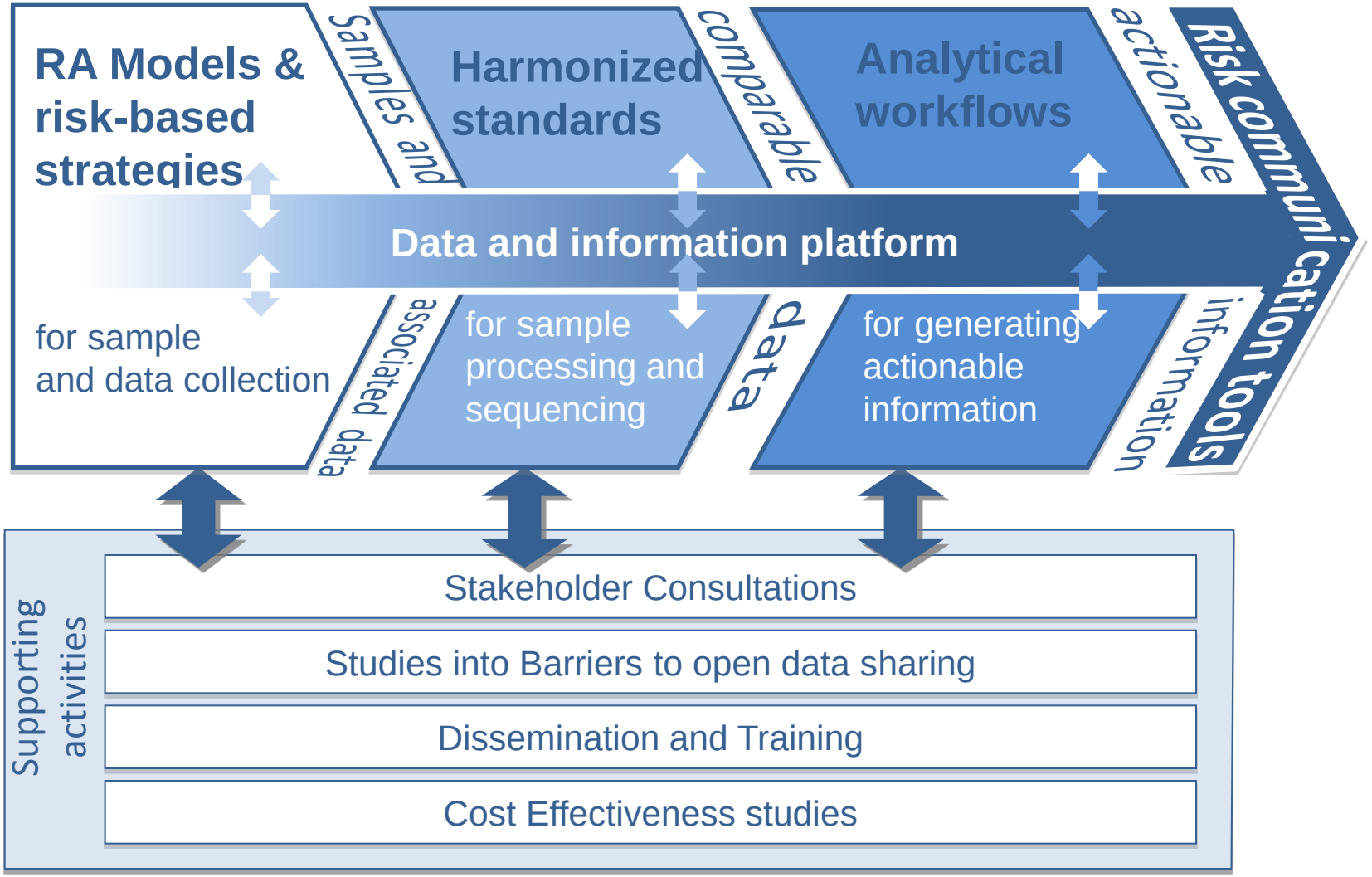
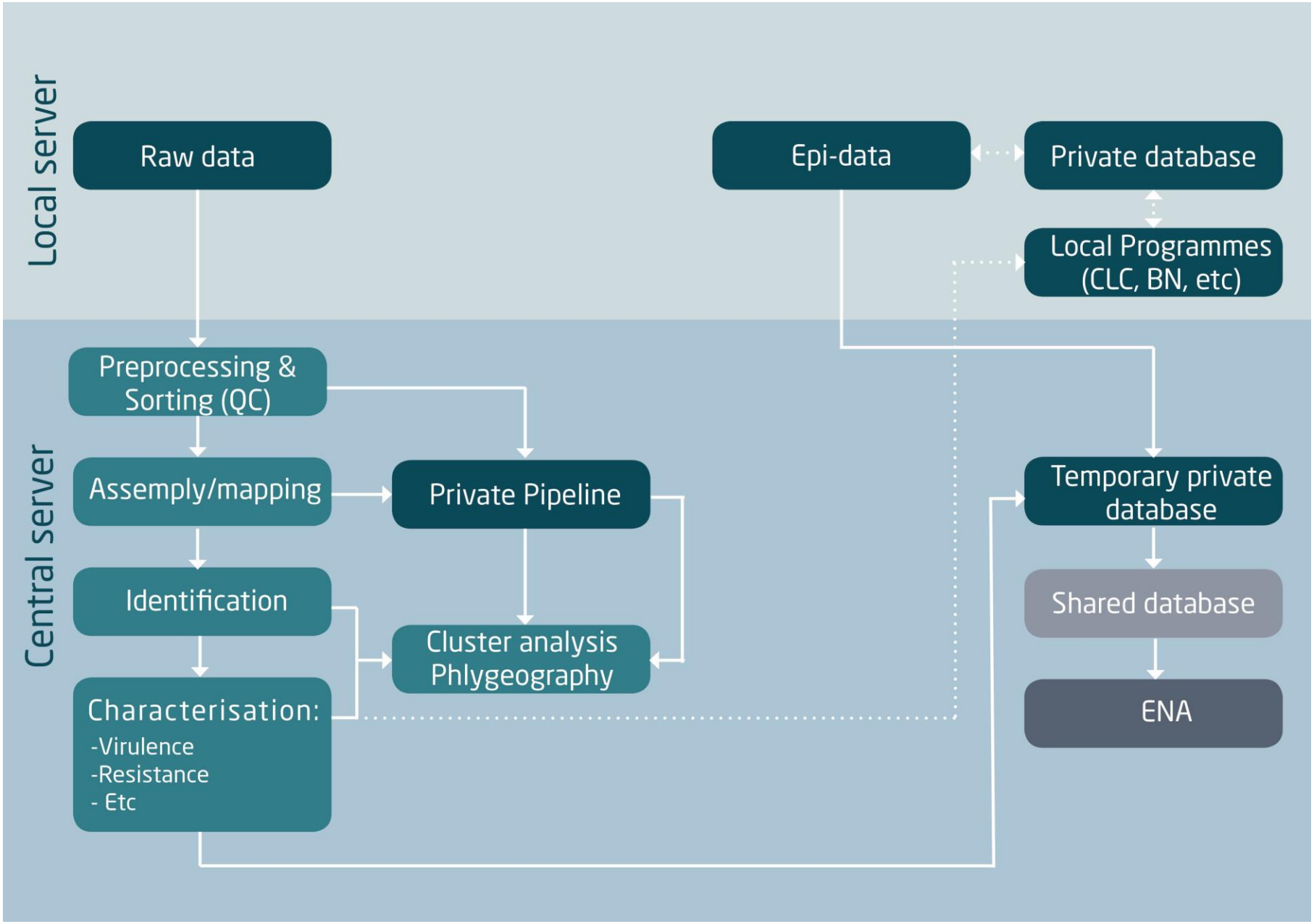
Project structure





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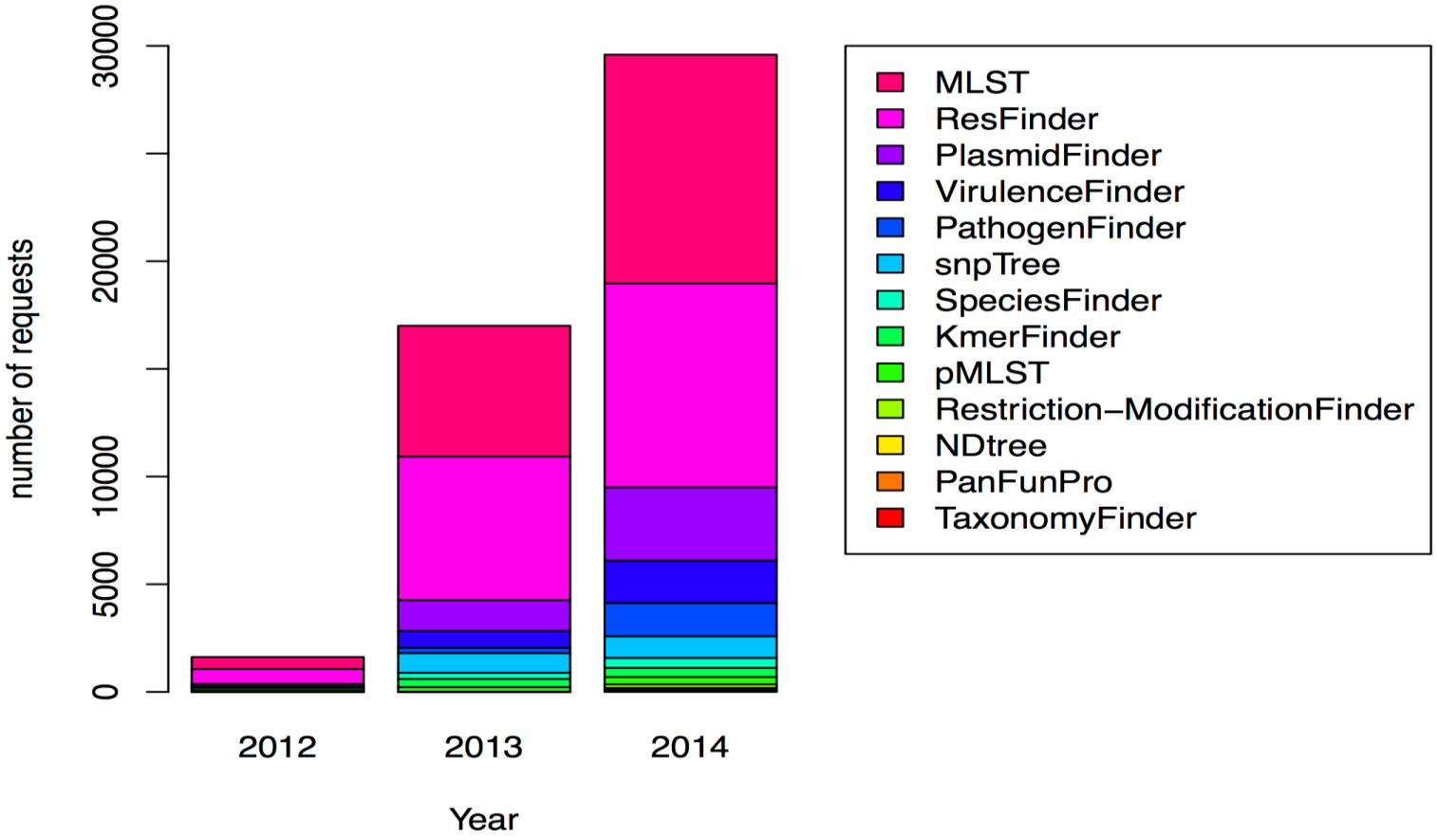
User Statistics



Until now: >600,000 submissions

Update

- Developed initial standards and studies for sampling, handling of samples, 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

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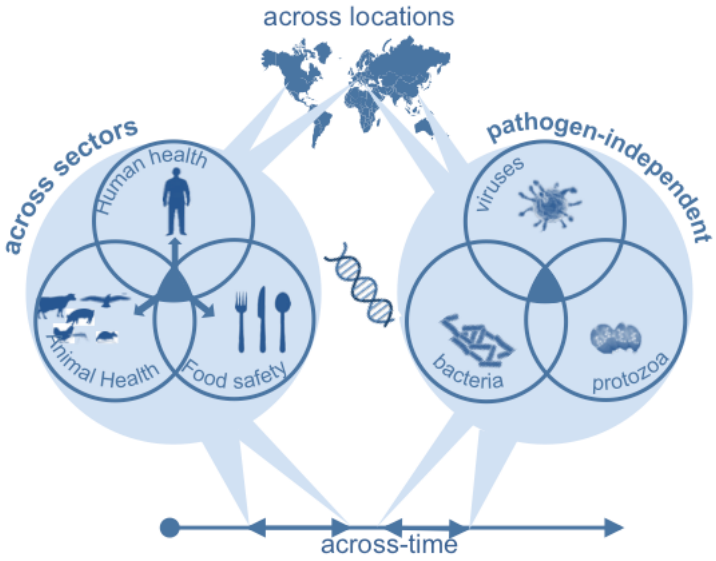
Our vision: one system serves all



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

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