



COMPARE is a multidisciplinary research network that is set up with the common vision to become the enabling analytical framework and globally linked data and information sharing platform system for the rapid identification, containment and mitigation of emerging infectious diseases and foodborne outbreaks. The system sets out to integrate state-of-the-art strategies, tools, technologies and methods for collecting, processing and analyzing sequence-based pathogen data in combination with associated (clinical, epidemiological and other) data, for the generation of actionable information to relevant authorities and other users in the human health, animal health and food safety domains.

*Next Generation Sequencing* (NGS) used for *Whole Genome Sequencing* (WGS) or *Whole Community Sequencing* (WCS or metagenomics) enables generating the complete genomic information from the isolate or sample independent of both the **sector** (public health, veterinary health, food safety), and **the type of pathogen** (viruses, bacteria, parasites). The outputs (sequence data) provide one common language that can be exchanged and compared **between laboratories and over time**, in combination with other associated data defined here as “**metadata**” including **contextual data** (e.g. data on sample type and process, clinical, microbiological, epidemiological and other data) **primary data** (raw sequence reads) and **derived data** (e.g., genomic alignments of reads, assemblies and functional annotation data sets). COMPARE aims to harness the rapid advances in these technologies to improve identification and mitigation of emerging infectious diseases and foodborne outbreaks.

To this purpose, COMPARE will establish a “One serves all” analytical framework – as depicted in the figure on the following page– showing the different components of the COMPARE Analytical Framework.

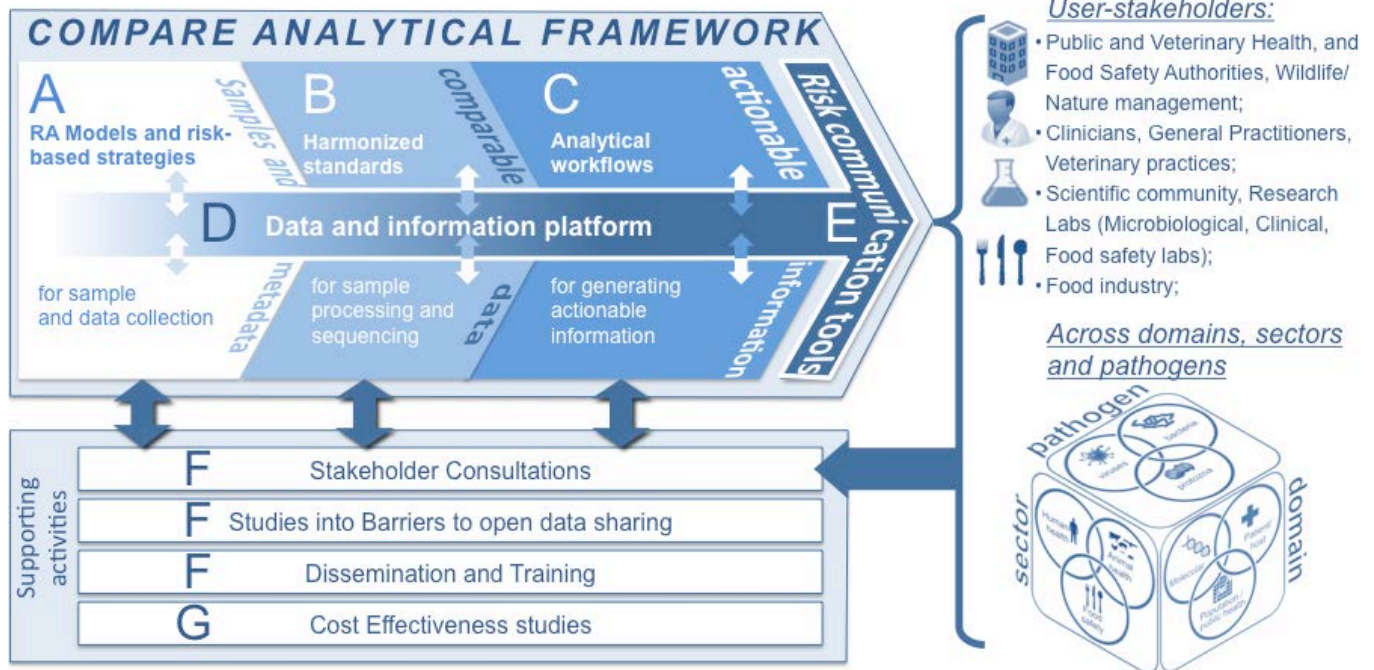
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The COMPARE consortium consists of the following members:

Technical University of Denmark	Universidad de Castilla- la Mancha
Erasmus University Medical Center	Artemis One Health Research bv
Statens Serum Institute	Aristotelio Panepistimio Thessalonikis
Friedrich Loeffler Institute	Tierärztliche Hochschule Hannover
Agence nationale de sécurité sanitaire de l’alimentation, de l’ environnement et du travail	Erasmus Universiteit Rotterdam
Robert Koch-Institut	Fondation Mérieux
Istituto Superiore di Sanita	Magyar Tudományos Akademia Wigner Fizikai Kutatokozpont
European Molecular Biology Laboratory	Institut Français de Recherche pour l’Exploitation de la Mer
Animal and Plant Health Agency/DEFRA	Responsible Technology
Rijksinstituut voor Volksgezondheid en Milieu	The Australian National University
Universitaetsklinikum Bonn	Leibniz Institut Deutsche Sammlung von Mikroorganismen und Zellkulturen
University of Edinburgh	Civic Consulting
Universiteit Antwerpen	University of Bologna
Academisch Medisch Centrum Universiteit van Amsterdam	Wellcome Trust Sanger Institute
University of Cambridge	



- A. Risk-assessment models and risk-based sampling and data collection strategies** that enhance our capacity to detect potential disease outbreaks;
- B. From samples and associated metadata to comparable data:** harmonised standards for sample processing and sequencing to obtain high quality and comparable sequence data from and metadata associated with a specimen;
- C. From comparable data to actionable information:** designing analytical workflows for turning *comparable data* into *actionable information* for addressing questions in frontline diagnostics, food-borne infections and (re-) emerging infections. “Actionable Information” is defined as information that enables users generating/receiving this information to take well-informed decisions and actions in pursuit of:
- *Pathogen identification and characterization:* Pathogen identification, genotyping and phenotyping, (e.g., detection of relevant antimicrobial resistance, virulence, epidemiological markers);
  - *Outbreak detection:* Detection of putative clusters by examining strain-specific clusters in time, place and host (person, animal and food);
  - *Outbreak investigation:* Rapid interrogation for given molecular strains to identify the potential origin of internationally distributed clones that may result in outbreaks; analysis tools to monitor extend of spread based on sequence diversity in relation to control measures;
  - *Outbreak prediction:* Automatic analyses for predicting risk of emergence of pathogens with outbreak potential.
- D. Designing and building a common data and information platform supporting rapid sharing, integration and analysis of sequence-based pathogen data in combination with other contextual metadata;** The system will be linked to existing and future complementary systems, networks and databases such as those used by ECDC, NCBI and EFSA.
- E. Risk communication tools** will be developed enabling authorities in the human and animal health and food safety sectors to effectively communicate the results obtained with the new analytical workflows;
- F.** The development of the analytical framework is underpinned by a set of supporting research, dissemination and communication activities promoting the acceptance of the system and its components. These activities encompass (i) **consultations with our stakeholders** serving on expert advisory panels throughout the project to maintain a prominent focus on user needs (ii) **studies on the barriers** (ethical, regulatory, administrative, logistical, political) to the implementation and widespread use of open-date sharing platforms, (iii) **dissemination and training activities;**
- G.** Finally COMPARE will include the development of a framework for estimating the **cost-effectiveness of the COMPARE system, including the value of safety.**