



CODE OF CONDUCT FOR PARTICIPATION IN WORKING GROUPS IN COMPARE NETWORK

Version May 2015

Definitions:

- Beneficiary: The legal entities that are signatories to the EC Grant Agreement and Consortium Agreement of COMPARE;
- Outside Users: Users of (parts of) the COMPARE system, that are not Beneficiaries;
- COMPARE: A multidisciplinary research network, funded by the European Commission (Contract number 643476).
- The COMPARE System: The COMPARE Data and Information Sharing Platform that provides and supports, as an open publicly available service, the combined application programmatic interfaces of the Registry, COMPARE Data Resource, Workflow Engine and portal;
- COMPARE Working Groups: Teams consisting of beneficiaries and outside users collaborating on a specific study question within the COMPARE project

The COMPARE system

COMPARE 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. See annex I for a summary of COMPARE.

At the core of COMPARE, an informatics infrastructure will be constructed in which a virtualized continuous data and computing environment will be provided, initially for the use of the Beneficiaries of the COMPARE contract, but - where considered relevant for the development of the COMPARE system - for Outside Users as well.

In order to develop the system, we defined specific projects that can help identify key questions and development needs for the COMPARE system. These projects are implemented by COMPARE Working Groups. They will be granted a cloud-based protected working space, provided by EBI, to allow pooling of data and comparative analyses, as specified in the workplan for each individual project. This agreement specifies the Code of Conduct for participating in such a Group when the submitting of data or the use of data is limited by (temporary) confidentiality.

Procedure for Outside Users gaining access to a cloud-based protected working space of the COMPARE project

Outside Users must sign this Code of Conduct prior to gaining access to one of the protected working spaces in the COMPARE project for the purpose of specific activities in the COMPARE Working Group. By signing this Code of Conduct, the Outside User agrees to the following:



- All data submitted to the COMPARE system, and not already available in the public domain, will be regarded as confidential and are owned by the submitting user. No such data will be used and/or published without the prior written consent from the owner.
- Data submitted to the database will become publicly available at a specified time, agreed to by the Working Group members, no later than 1 year after submission.
- Participants in a Working Group agree not to use data from the collaborative work without prior written consent from the owning party. Such consent will not be unreasonably withheld and provided within a reasonable time frame (2 weeks).
- The use of the COMPARE System is on a “give-and-take-basis”: participants agree to submit data as well as extract data for comparative analysis. Exceptions will be discussed among participants to reach a consensus.
- The persons receiving the data agree not to share the data with other institutions or persons not under his/her supervision.
- The provider of the data will not be held liable for the fitness to use, faults or errors in the data.
- In case of a cross border public health threat (e.g. international foodborne outbreak), it is, in accordance with their national law, the responsibility of the data providers to notify the relevant authorities. In case a Working Group participant becomes aware of a cross border health threat and the urgency of the situation is such that immediate action is required, the receiving participant might also be obliged by law to inform the relevant authorities of its country. In such a case data will be provided clearly marked confidential, and stating the source of the information as well as contact details of contributors. The latter situation will be handled in close communication with the COMPARE Coordinator or Deputy Coordinator. The COMPARE project is a work in progress. Legal and ethical conditions for the improvement of open source sharing of data are subject to change.
- Term of this agreement shall survive the COMPARE project by 5 years from the close of the project.

Access to the working space will be controlled through login names and passwords. Login names and passwords will be issued after completing and signing this Code of Conduct. We will send your (new) personal entry codes by e-mail. Please complete the agreement, sign and send to:

Jeffrey Skiby
compare@food.dtu.dk

Agreed:

Name: [name person signing on behalf of the organization]

On behalf of [name organization]

Signature:

Date:

Stamp of the organization:

ANNEX I: COMPARE SUMMARY

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 figure 1 – showing the different components of the COMPARE Analytical Framework.

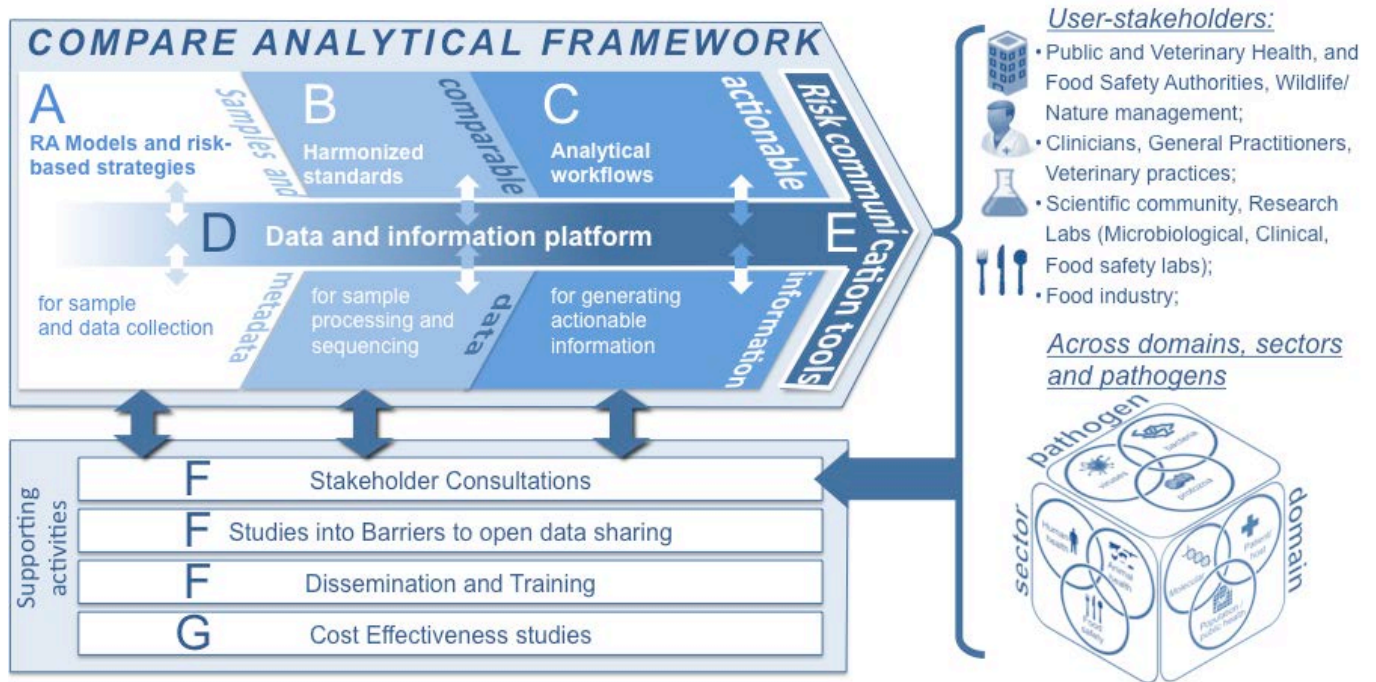


FIGURE 1: the COMPARE analytical framework and its main components from sample and data collection to generating actionable information to stakeholders in the human, animal and food sectors.



- 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:** harmonized 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, foodborne 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.**

COMPARE runs from 1 December 2014 to 30 November 2019. The consortium has been awarded EUR 20 million funding under the European Commission’s Horizon 2020 programme.

For more information about the project please contact:

- Prof. dr. Frank Aarestrup of DTU: fmaa@food.dtu.dk
- Prof. dr. Marion Koopmans of Erasmus MC: m.koopmans@erasmusmc.nl

The COMPARE consortium consists of:

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