

Towards a new (h)era: Preparedness for outbreak detection and response

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“The centralised and standardised approach for genomic-epidemiologic data opens opportunities for emergency preparedness against infectious diseases in Belgium”

INTRODUCTION

In response to the COVID-19 pandemic, the European Commission established the European Health Emergency Preparedness and Response Authority (HERA). Generally, it aims to strengthen the European Health Union by **improving preparedness and response to future national, cross-border, or pandemic outbreaks of infectious diseases**. The HERA-Incubator, funded by the European Centre for Disease Prevention and Control (ECDC), allows investments to upscale the national infrastructure for collecting Whole Genome Sequencing (WGS) data (Figure 1) to be linked with epidemiologic data as well as **building a sustainable infrastructure** that can be used more broadly in the context of outbreak preparedness and risk management (Figure 2). As a result, the current HERA-BE-Incubator project covers a **proof-of-principle** of a national genomic-epidemiologic eHealth framework for five national reference centers (NRCs) for human microbiology.

SARS-CoV-2



Influenza



Tuberculosis



Salmonella



Listeria

HIERARCHY OF PATHOGEN GENOMIC DATA SUBMISSION

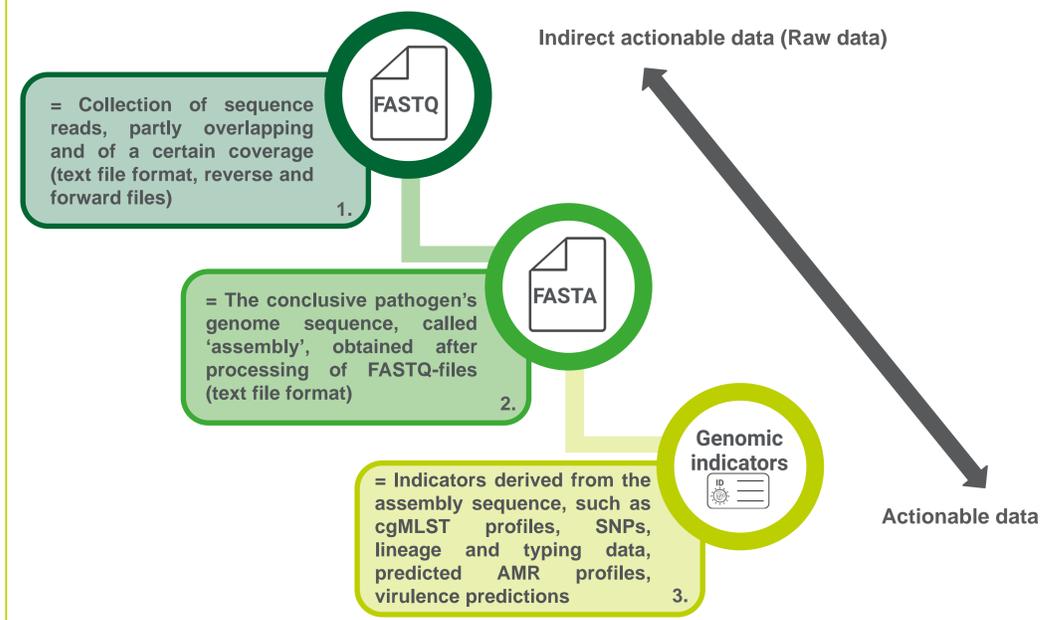


Figure 1: Hierarchy of genomic data submission. Different formats of genomic pathogen data are accepted for submission. Preference is given to FASTQ files, followed by FASTA files and genomic indicators. FASTQ files represent raw data in the form of sequencing reads, allowing for harmonised analysis through bioinformatics pipelines offered on a central bioIT platform. FASTA files contain consensus sequences and are derived from FASTQ files. Genomic indicators, such as predictions of antimicrobial resistance (AMR) or cgMLST profiles, represent interpretation results from bioinformatics processing of FASTQ or FASTA files. These indicators are actionable data that guide public health actions.

HIGH LEVEL DESIGN

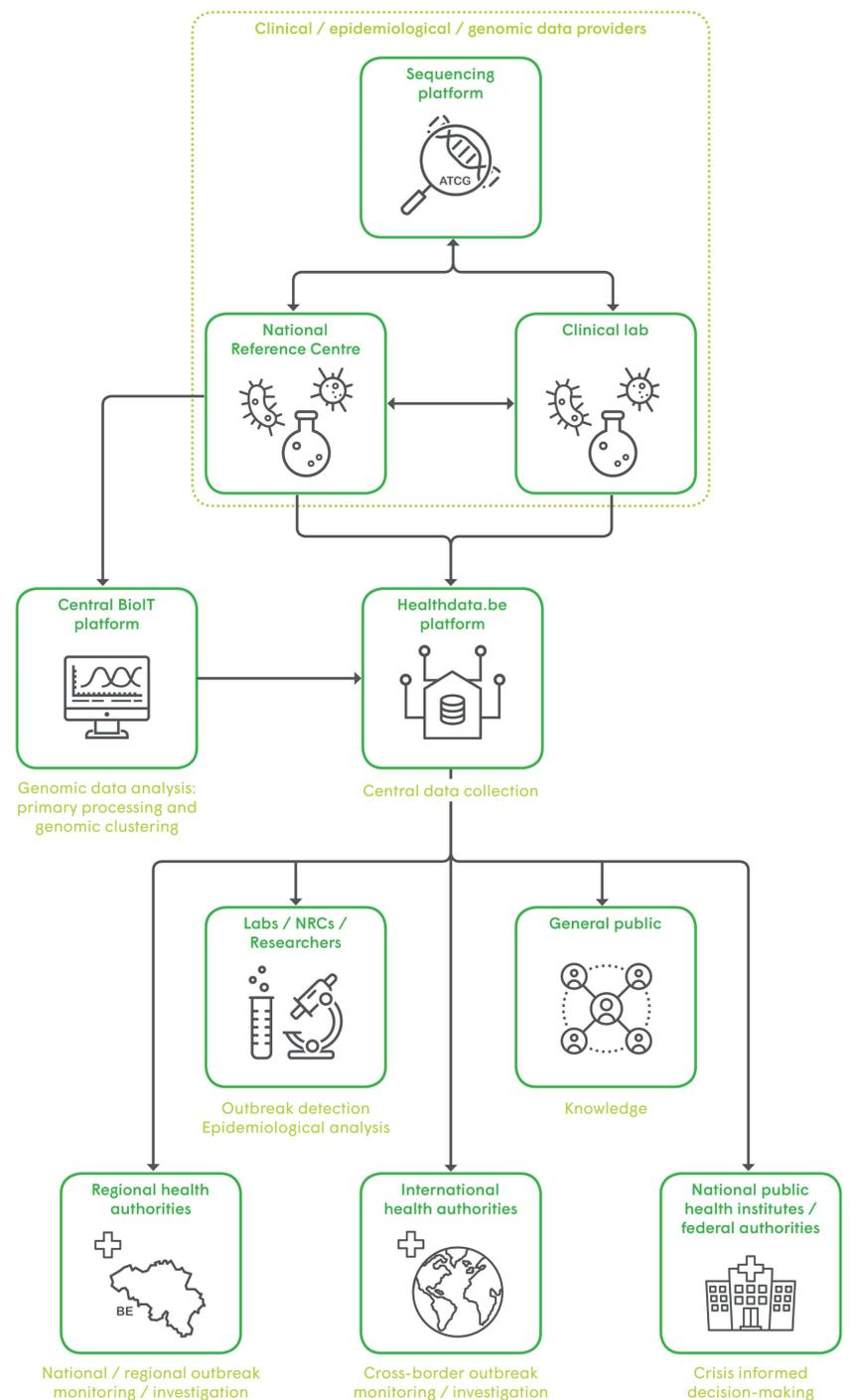


Figure 2: High level design of the national eHealth infrastructure for genomic-epidemiologic surveillance of infectious diseases. Epidemiologic and/or genomic data, originating from a national reference center or clinical laboratory, will be collected with a standardised variable set on a centralized platform. Raw genomic data will be dispatched immediately to a central bioIT-platform where an automated and harmonised bioinformatics analysis will be performed in the primary processing, through the consensus pipeline per pathogen. Resulting or uploaded FASTA files and genomic indicators will be stored on the healthdata.be-platform. From the centralized genomic-epidemiologic data platform, data will be distributed to various partners according to their needs for public health purposes in compliance with their mandates and data governance rules.

OPPORTUNITIES FOR PUBLIC HEALTH ACTORS

- Epidemiological and genomic data can be **linked** and analysed together
- Data is collected near **real-time**
- Timely and sensitive **variant/outbreak detection**
- **Improved outbreak management** and investigation by enhanced data availability
- Insights to **support surveillance** and public health actions.
- **Harmonised and automated** bioinformatics pipelines available for all involved labs
- Monitoring of **antimicrobial resistance profiles** predicted through genomics
- **Automated uploading** (system to system) and large data files possible
- Possibility to upload **FASTQ files to ENA** through the system