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Towards a new (H)ERA: Developments to strengthen infectious diseases surveillance and pandemic preparedness

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Introduction

In order to achieve **pandemic preparedness**, a high capacity and interoperable infrastructure is crucial. Furthermore, the advent of Whole Genome Sequencing (**WGS**) in the field of microbiology allows for higher microbial subtyping. In combination with conventional testing and epidemiological data **integrated genomic-epidemiological analyses** can be performed. Therefore, we designed **Be-HERA as an overarching architecture** to strengthen the surveillance of infectious diseases.

Collecting data in a central way

Within the Be-HERA infrastructure, separate databases and platforms ensure **secure data gathering and processing**.

Central BioIT platform

- **A genomics processing environment** that takes in genomic data and technical metadata.

- **Automatic processing pipeline** for the relevant pathogens and database creation of **harmonized genomic indicators**.

- No collection of nominative or epidemiological data

Central NRC platform

- **Nominative data through restricted access** for each National Reference Centre (NRC)

- Use for NRC competencies and mandates such as **linkage of genomic data to metadata for cluster analysis and outbreak detection,** virulence and resistance profiles and vaccine escape

- **Expert validation** within the NRC platform.

Healthdata.be

- Developed and deployed a **secured** platform

- **Pseudonymized** and centralized data management and analysis platform (HD-DWH) providing clinical and epidemiological data combined with genomic indicator data. Non-nominative data through restricted access.

- **Facilitated reporting** on the epidemiological situation of infectious diseases to various stakeholders at a national and international level.
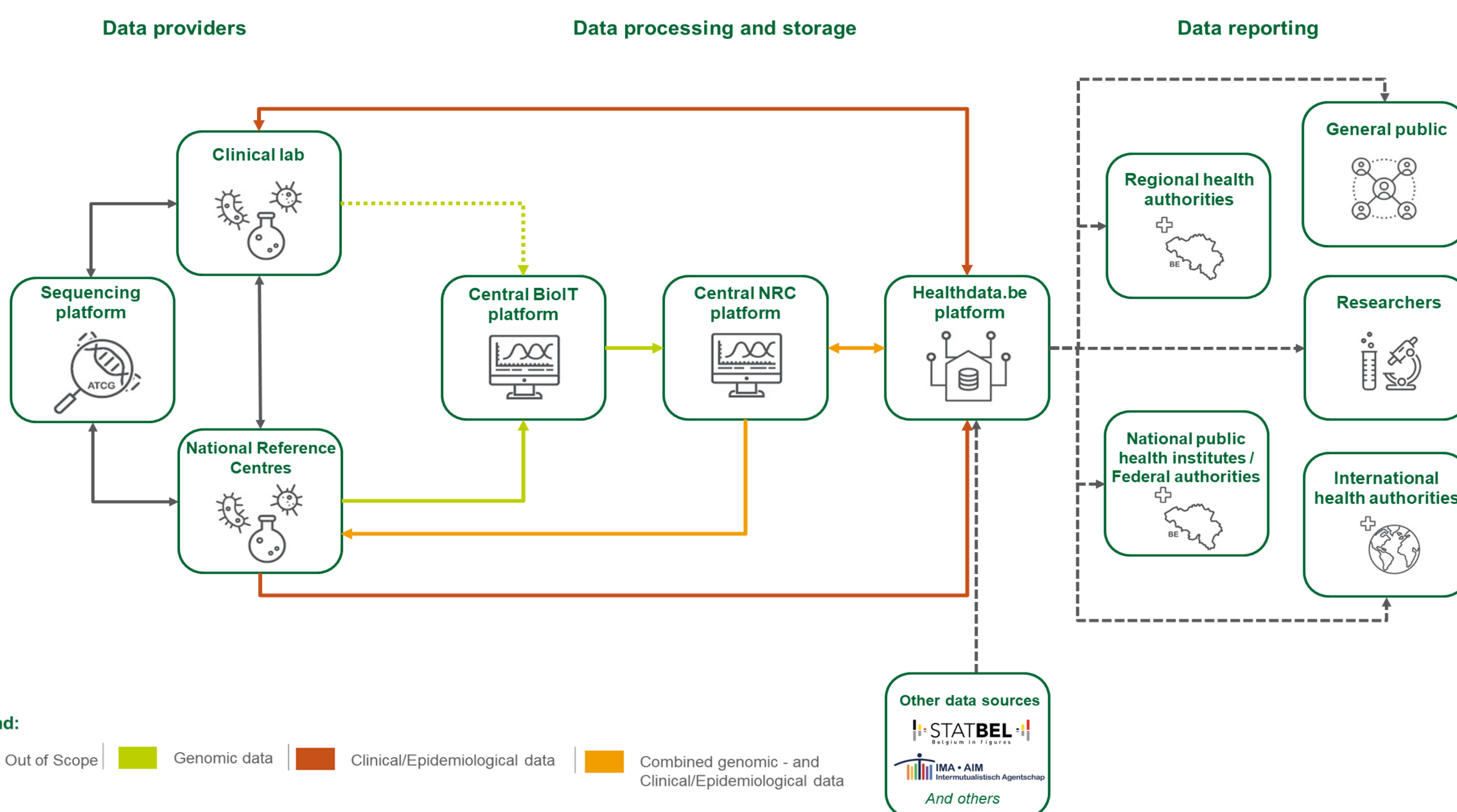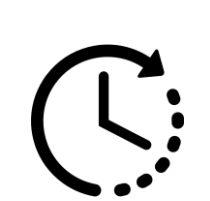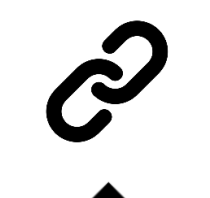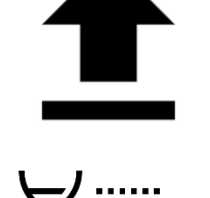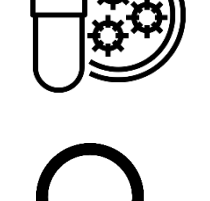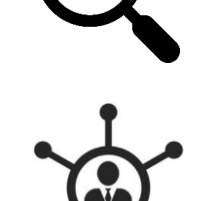
The Be-HERA infrastructure

Figure 1: An overview of the Be-HERA architecture with its different components.

Clinical and Epidemiological data is collected at the level of the **National Reference Centers (NRCs)** and sent to Healthdata.be.
Genomic data will be transferred to the **BioIT platform** where primary processing of the results will occur. From the central BioIT platform, genomic data are sent to the central **NRC platform** whereby a connectivity is in place with the Healthdata.be platform to combine clinical, epidemiological and the genomic data within the NRC platform according to their mandates.
The **Healthdata.be platform** covers the pseudonymized data warehouse that can be used for data reporting and research.

Advantages for public health actors

- Data is collected and distributed near real time
- Clinical/Epidemiological and Genomic data can be linked and analyzed together
- Automated uploading (system to system) and large data files possible
- Harmonized and automated bioinformatics pipelines available
- Monitoring of antimicrobial resistance profiles predicted through genomics
- Timely and sensitive variant/outbreak detection
- Improved outbreak management and investigation by enhanced data availability
- Possibility to upload FASTQ files to ENA through the system

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We would like to thank all the stakeholders for their commitment and contribution to build this infrastructure. Please consult the website for more information

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