

USE CASES GENOMICS DATASHARING

Marc Van den Bulcke, Kankercentrum, Sciensano
Brussel, 8 mei, 2023



Topics

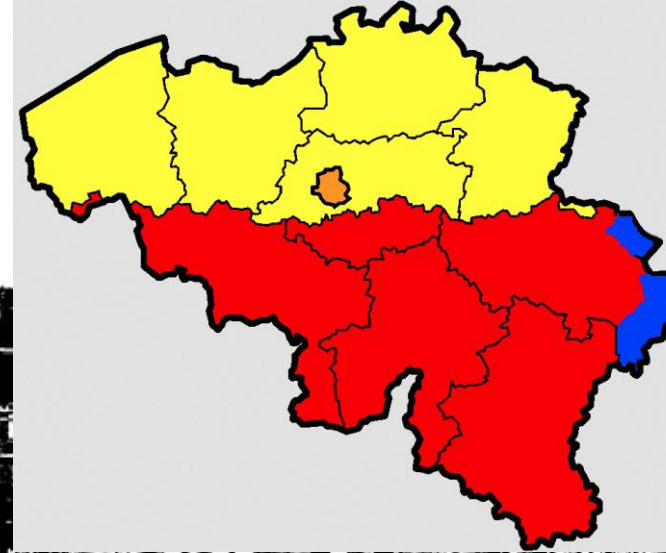
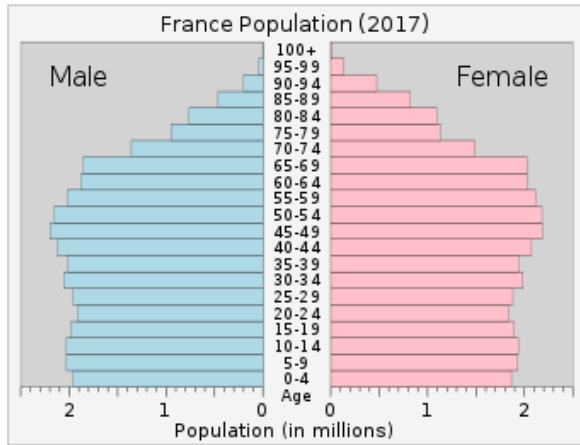


General framework

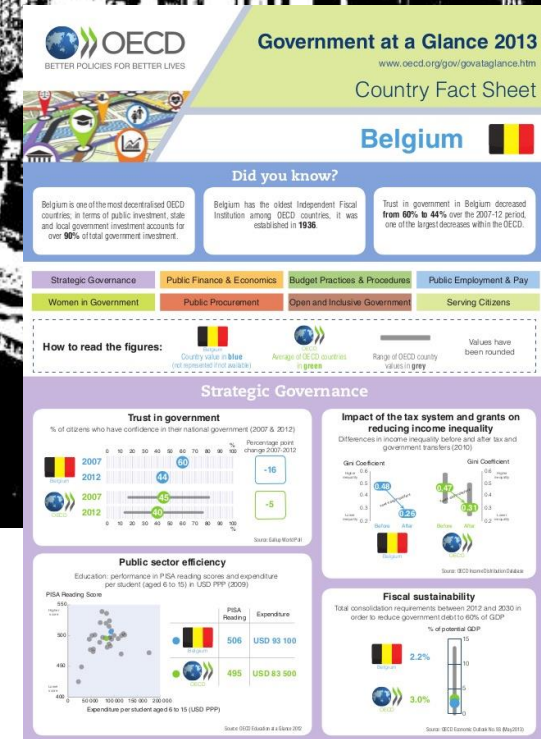
Usecase 1: genetic variability of Belgian population

Usecase 2: Population health – predisposition of cancer

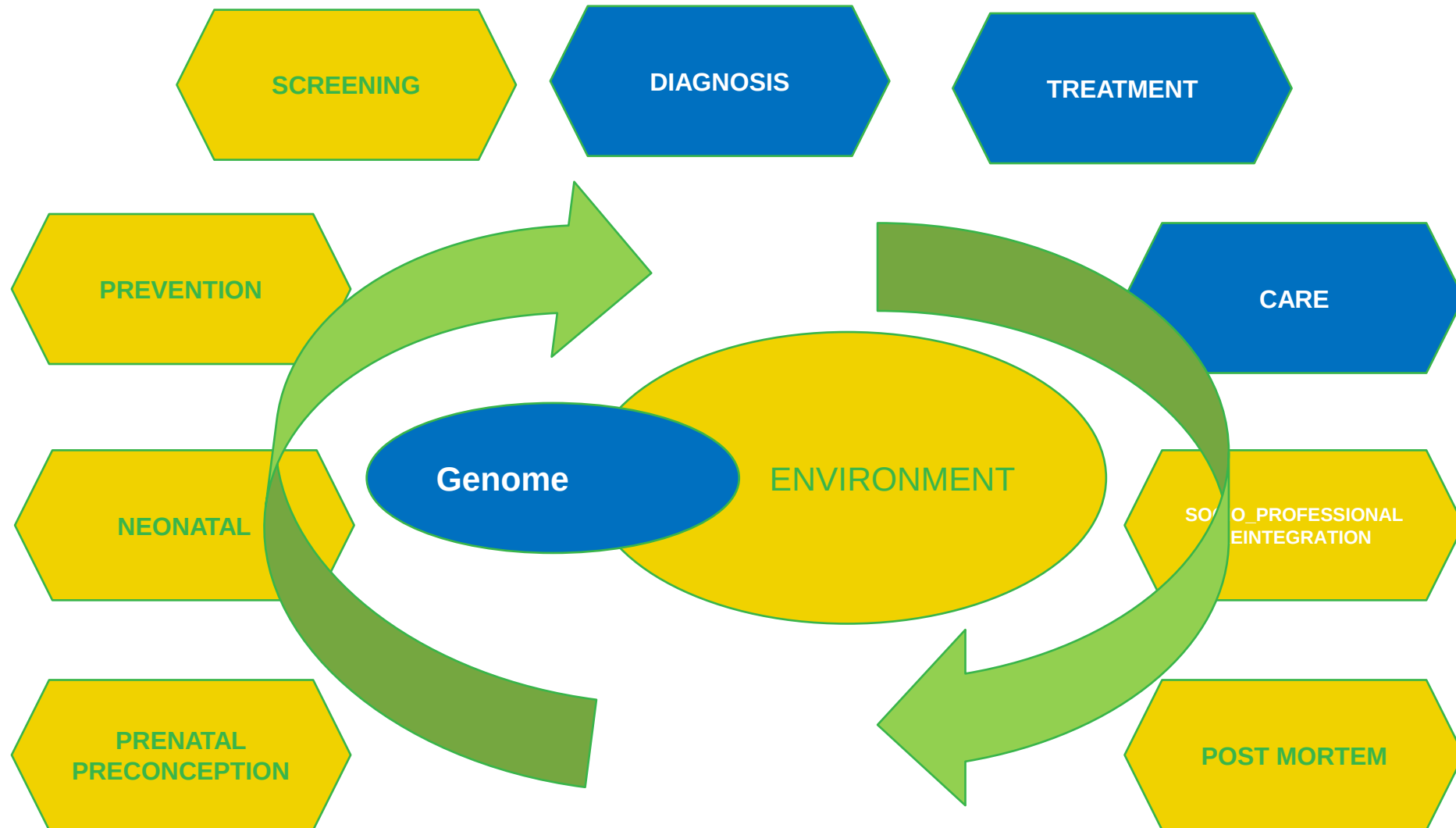
Usecase 3: medical application – data-driven/patient-matching in oncology



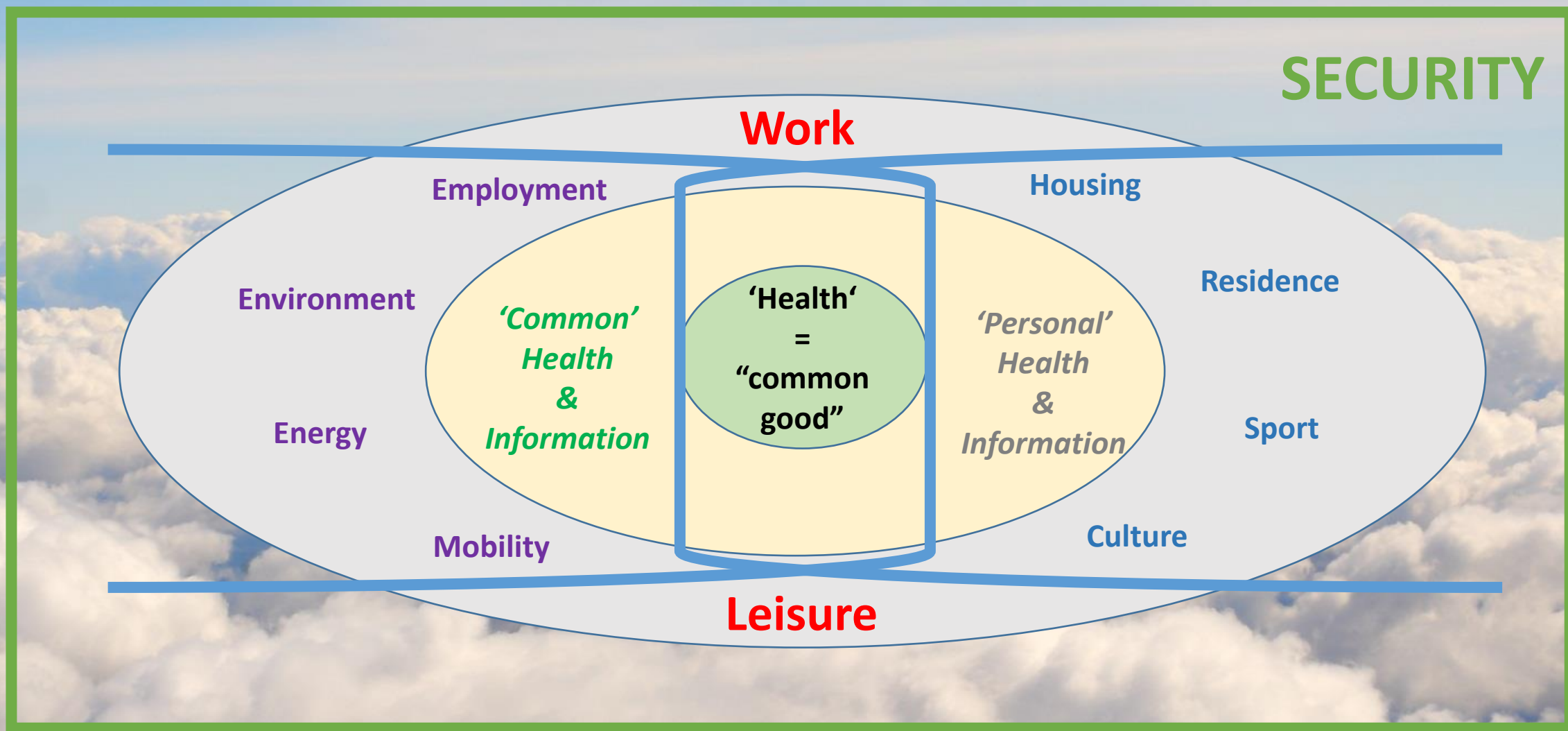
DEMOGRAPHICS
SOCIO-ECONOMICS
POLITICAL
GEOGRAPHICAL
CULTURAL



Life course perspective - SCIENSANO



PRECISION HEALTH AND HEALTHCARE



USECASE 1: GENETIC VARIABILITY of Belgian population

Van den Eynden et al. *Human Genomics* (2018) 12:6
DOI 10.1186/s40246-018-0136-8

Human Genomics

PRIMARY RESEARCH

Open Access

The genetic structure of the Belgian population



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Abstract

Background: National and international efforts like the 1000 Genomes Project are leading to increasing insights in the genetic structure of populations worldwide. Variation between different populations necessitates access to population-based genetic reference datasets. These data, which are important not only in clinical settings but also to potentiate future transitions towards a more personalized public health approach, are currently not available for the Belgian population.

Results: To obtain a representative genetic dataset of the Belgian population, participants in the 2013 National Health Interview Survey (NHIS) were invited to donate saliva samples for DNA analysis. DNA was isolated and single nucleotide polymorphisms (SNPs) were determined using a genome-wide SNP array of around 300,000 sites, resulting in a high-quality dataset of 189 samples that was used for further analysis. A principal component analysis demonstrated the typical European genetic constitution of the Belgian population, as compared to other continents. Within Europe, the Belgian population could be clearly distinguished from other European populations. Furthermore, obvious signs from recent migration were found, mainly from Southern Europe and Africa, corresponding with migration trends from the past decades. Within Belgium, a small north-west to south-east gradient in genetic variability was noted, with differences between Flanders and Wallonia.

Conclusions: This is the first study on the genetic structure of the Belgian population and its regional variation. The Belgian genetic structure mirrors its geographic location in Europe with regional differences and clear signs of recent migration.

Keywords: Genetic variability, Population genomics, Public health genomics

Background

After the completion of the Human Genome Project in 2003, international efforts were initiated to map human genetic variation between populations. This variation has been described for 26 populations worldwide via the 1000 Genomes Project [1, 2]. While this is a valuable resource for studying global genetic variation, both the number of samples per population and the total number of populations studied are relatively low. To gain sufficient statistical power and avoid false positives/negatives due to unmatched control populations in genotype-phenotype association

studies, population-based genetic reference data are required from more specific and extended populations [3]. To address this, population-based whole genome sequencing initiatives have been performed at the national level throughout Europe [4–7]. From these genetic population studies, it has become clear that there is a strong correlation between the geographical location and the genetic structure of different populations [8, 9], also at the more regional level (e.g., along a north-south axis in the Netherlands) [6, 7, 9, 10]. Currently, this genetic information is not available for the Belgian population.

Therefore, a population-based cross-sectional study, called BelPHG-21 (Belgian Public Health Genomics in the twenty-first century), was organized that aims at describing the genetic variability in the Belgian population and relating

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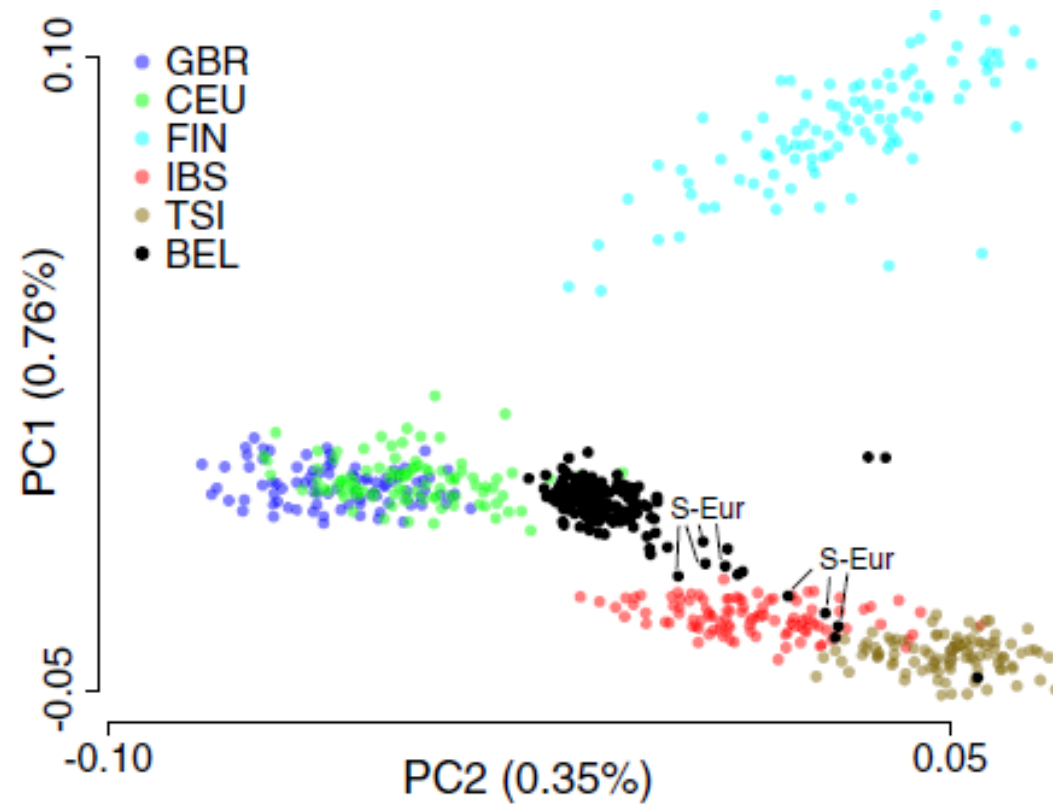
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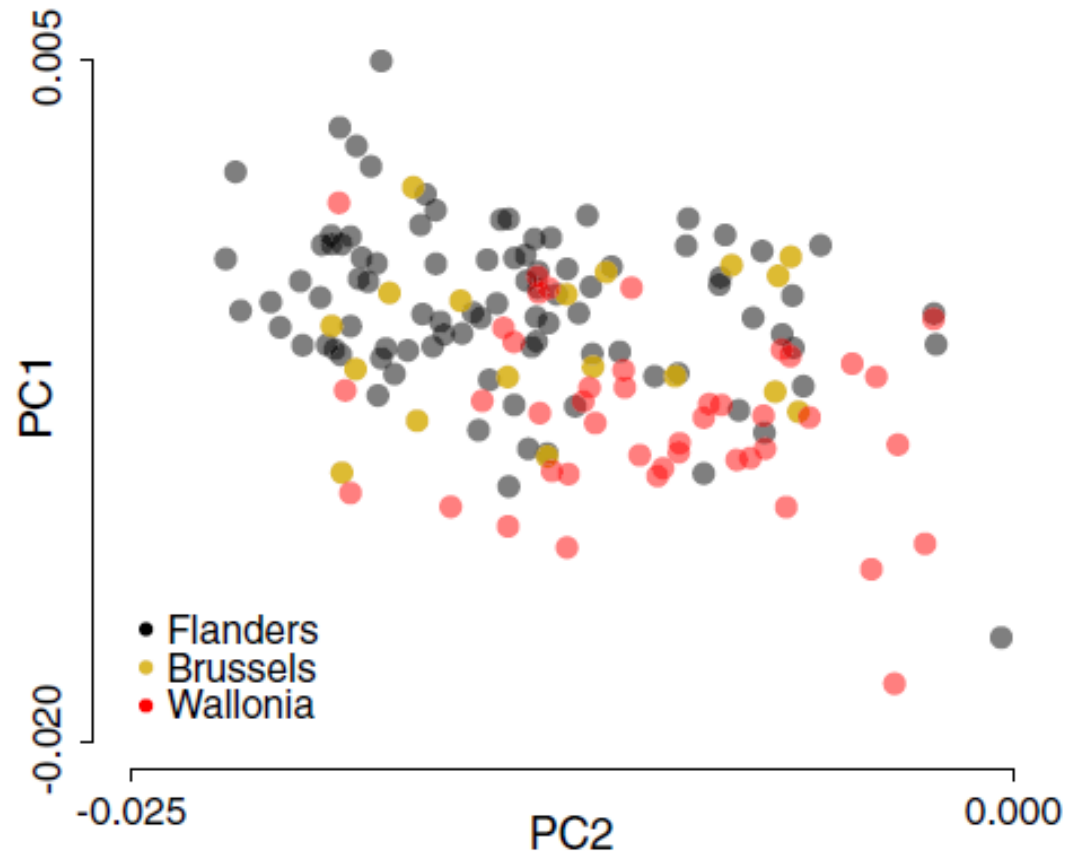


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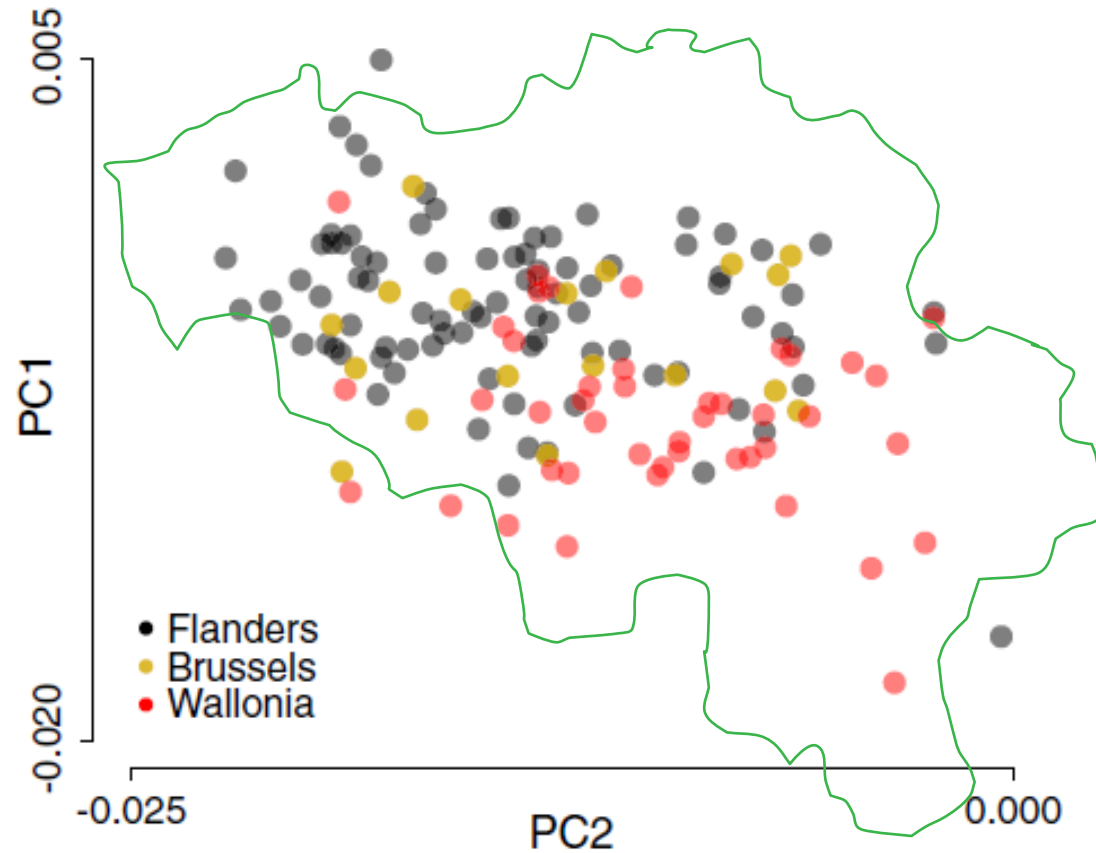
GENETIC VARIABILITY: Belgian vs. European



GENETIC VARIABILITY: Within Belgium



GENETIC VARIABILITY: Within Belgium



GENOME OF EUROPE

EC Call on “**Genome of Europe**” has been published

<https://ec.europa.eu/info/funding-tenders/opportunities/portal/screen/opportunities/topic-details/digital-2023-cloud-ai-04-genome>

Expected Outcome:

- Joint or coordinated sequencing (WGS).
- New WGS data for a large number of representative European citizens generated in accordance with the guidance, specifications and standards agreed within 1+MG (1+MG Trust Framework).
- Integration of eligible population-based WGS data generated independently of the GoE and made available to the project.
- The Genome of Europe federated reference database established and accessible through the federated European genomic data infrastructure and the European Health Data Space (EHDS) infrastructure for secondary use of health data (HealthData@EU).

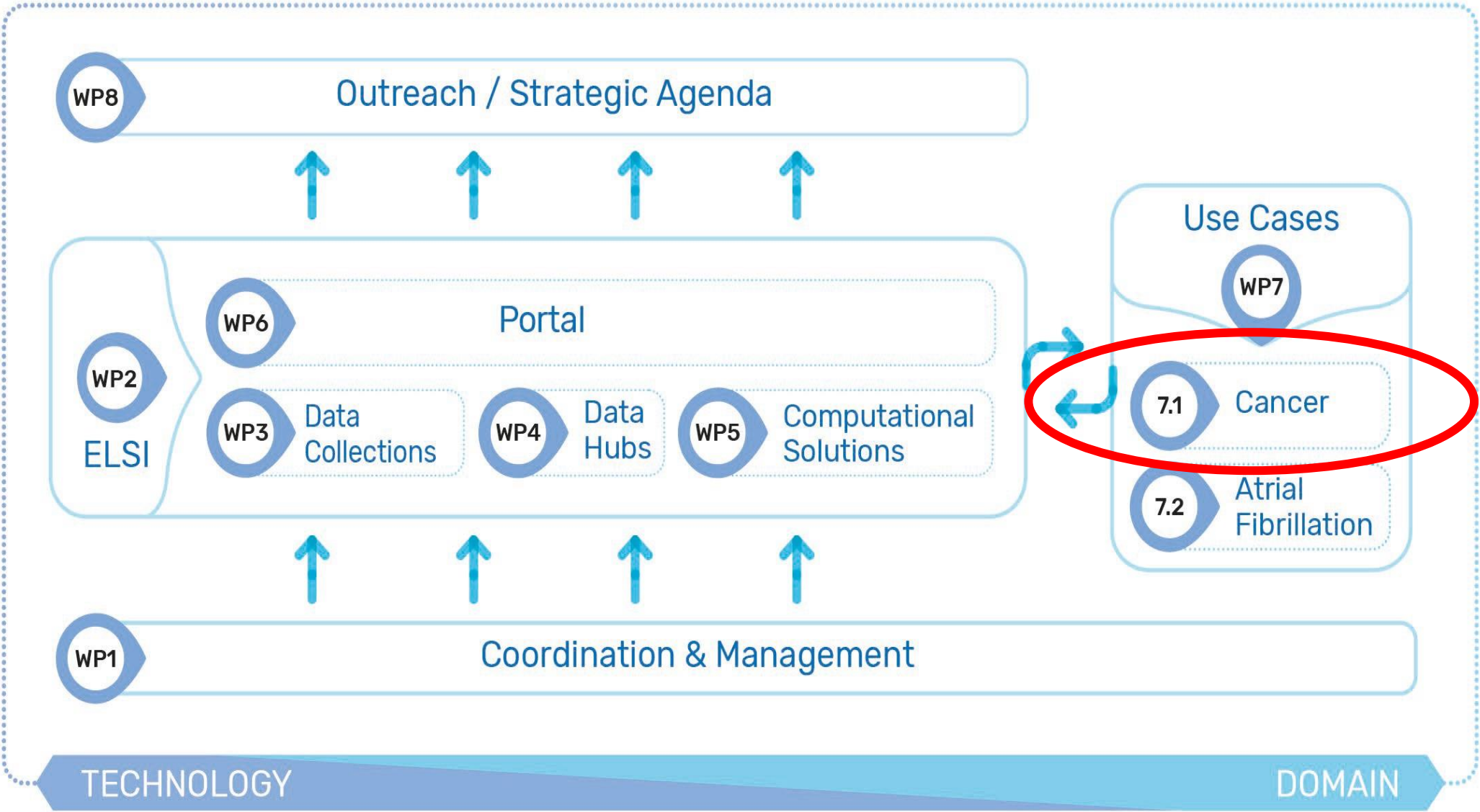
USECASE 2: Population health – predisposition of cancer

“We need to make the most of the potential of e-health to provide high-quality healthcare and reduce inequalities. I want you to work on the creation of a **European Health Data Space** to promote health-data exchange and support research on new preventive strategies, as well as on treatments, medicines, medical devices and outcomes. As part of this, you should ensure citizens have control over their own personal data.” **Ursula von der Leyen, EC President**

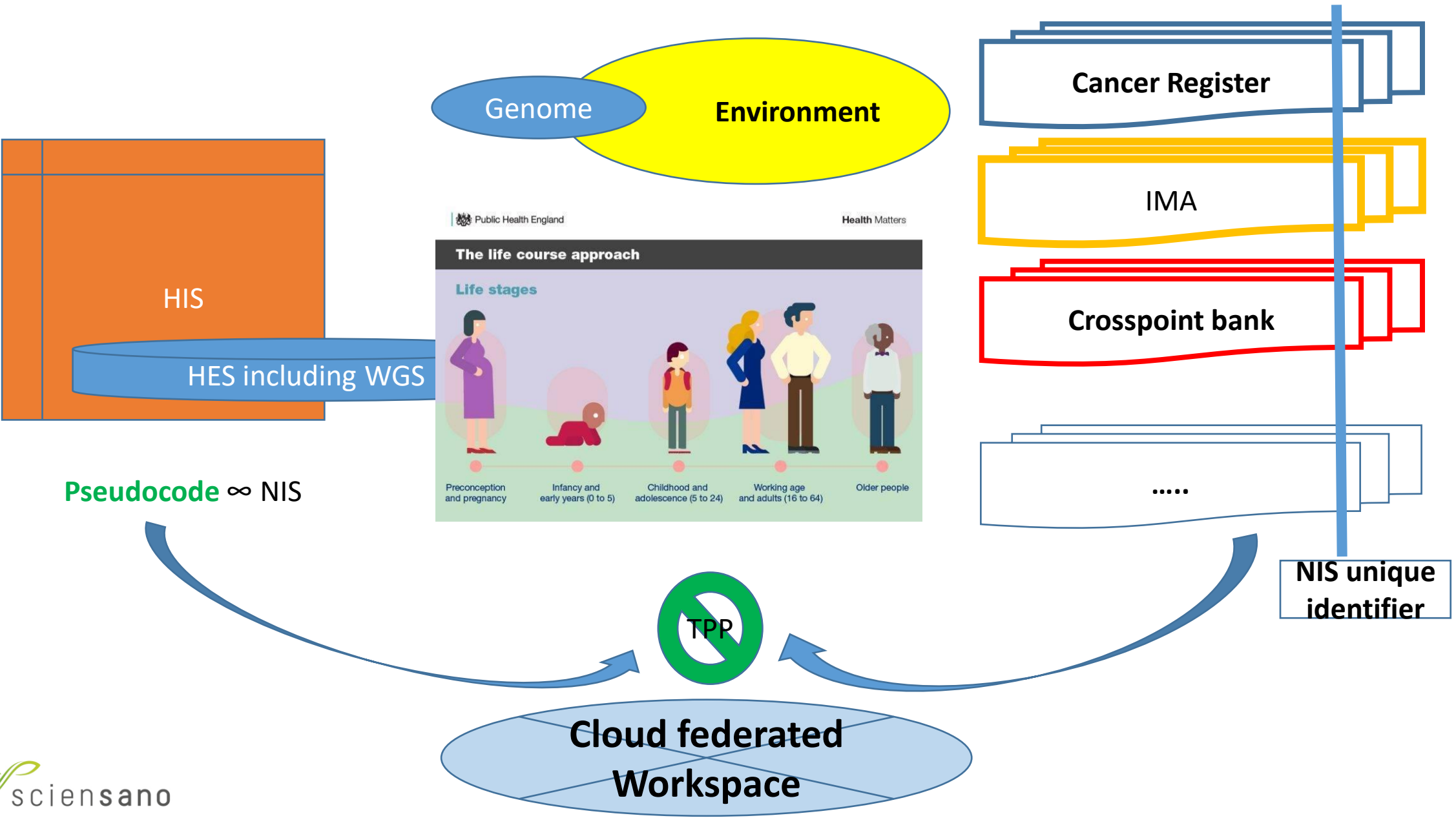
The aim in the above use case is to **assess how genomic information gathered at the population level can contribute to developing high-risk profiling for the major risk factors for cancer**, e.g. tobacco, alcohol, obesity, sun-exposure, and other factors such as family history, socio-economic status or health literacy. In addition, alignment will be set up with the activities under the 1M genomes initiative(s) coordinated by the European Commission.

Special attention will be given to integrating technical and analytical issues into common protocols in the cancer and environment use-cases.

CSA HealthyCloud Project Structure



CSA-HRIC: cancer use-case



USECASE 3: Medical application – data-driven/patient-matching in oncology

- NGS in clinical oncology
- Data-driven/patient-matching in oncology

FR NL EN
ComPerMed

NGS GUIDELINES
ALGORITHMES
PROJECTS
ORGANISATION
CONTACT

Actuellement, le profilage de l'ADN par Next Generation Sequencing (NGS) fait partie intégrante du diagnostic clinique en oncologie. Il permet de **personnaliser le traitement et d'optimiser la prise en charge** des patients (cancéreux).

La Commission de Médecine Personnalisée (Compermed) est un comité qui **rassemble l'expertise scientifique belge** en oncologie et en hématologie-oncologie.

Sa mission initiale est de **déterminer l'utilité clinique des mutations somatiques** en (hémato)-oncologie.

Les **principaux objectifs** du Compermed sont :

- élaborer des "guidelines" techniques permettant d'assurer la qualité des tests moléculaires utilisés en oncologie et hématologie-oncologie et plus particulièrement des tests NGS ciblés;
- de définir quels gènes au minimum doivent être analysés pour une tumeur donnée (solide et hémat). Le choix de ces gènes est basé sur les évidences scientifiques (des) utilisées (cliniques) spécifiques pour la tumeur en question;
- de mettre à jour les "guidelines" cliniques en (hémato)-oncologie au niveau des tests NGS de diagnostic moléculaire;
- évaluer les nouvelles technologies "omique" dans le cadre d'une utilisation en clinique en (hémato)-oncologie.

Compermed est un des objectifs fixés par le roadmap NGS d'octobre 2015. Face à l'évolution rapide et la complexité technique de ces analyses, la Commission de Médecine Personnalisée (Compermed) a été mise en place fin 2015 par le Centre du Cancer.

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healthy all life long

HEALTHDATA

Central data registration

NGS register

PITTER

Precision register

Belgian Cancer Registry

OVERALL DNA

EEN LEVEN VOL DNA

ELSI

BJMO
PRACTICE GUIDELINES
57

The Belgian next generation sequencing guidelines for haematology-oncology

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GOVERNANCE

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Case studies
Tumeurs solides
2019/1

BiomarkerMS benchmarking track FR

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RZIV

activities platform CDx:
linked reimbursement procedure

TO BE:

Medicines + molecular CDx tests: chapter VIII + annex

CRM
Minister
MD

6 months + suspensions

Molecular CDx tests

first: WG Clinical Biology

TMC
Medico-mut
Minister
RD

6 months

Concept:

article 33ter:

new "generic" nomenclature codes for tests linked to a drug

3 levels of complexity and reimbursement

published by royal decree

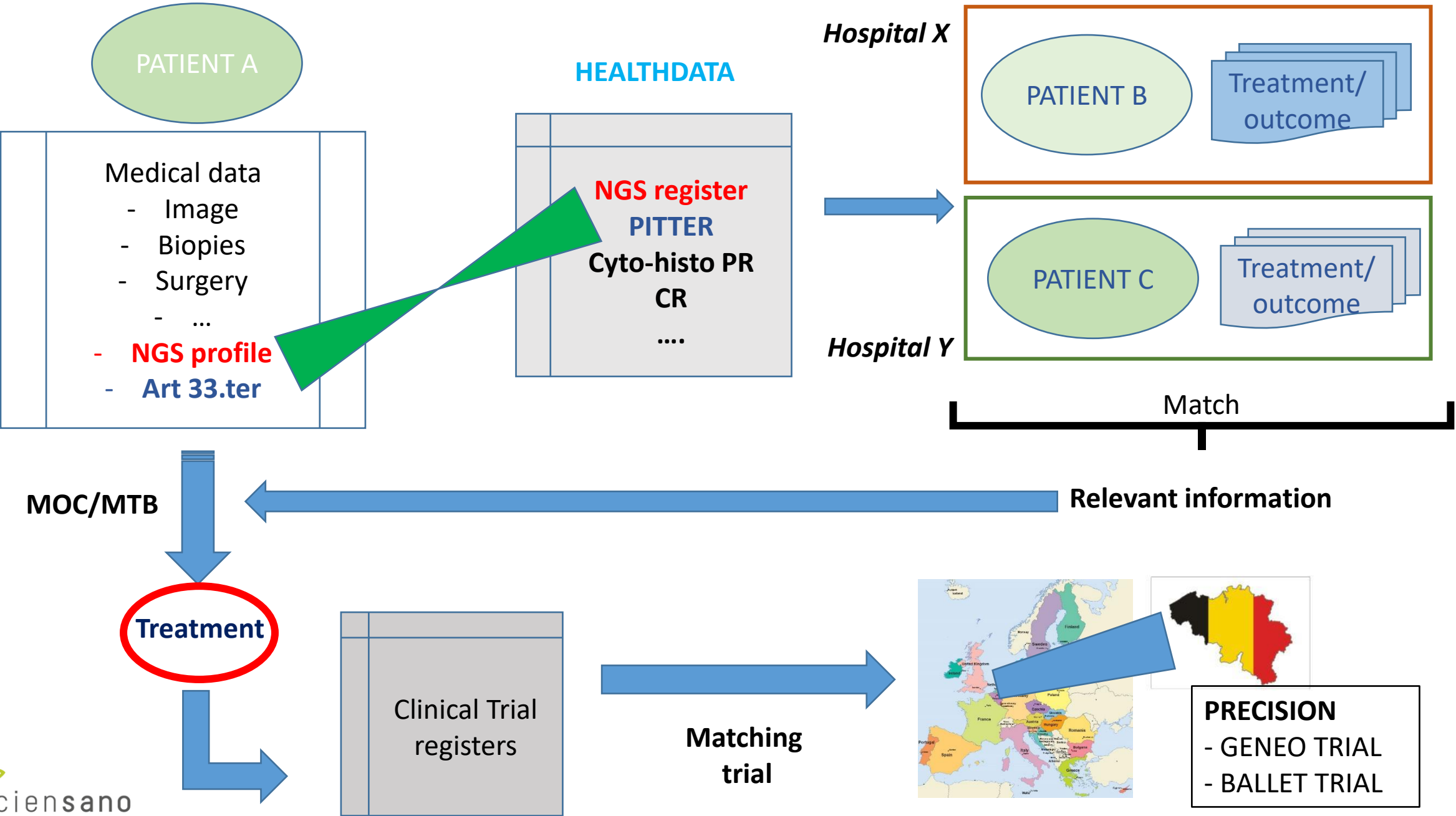
chapter "VIII":

"personalised" drugs

+ annex with "companion" tests

HTA: if the Minister decides to reimburse the drug, the marker will be added to the list by the same Ministerial Decree

PATIENT-MATCHING FRAMEWORK



THANKS