

Declaration on linking
genomic databases across borders

1+MillionGenomes

"Towards access to 1 million Genomes
in the EU by 2022"

Angel Carracedo

**Fundación Pública Gallega de Medicina Genómica- SERGAS
CEGEN-Universidad de Santiago de Compostela**





Why a declaration of cooperation and what is the **scope**

- Coordinating secure access to data from **>1M genomes** that are **linked to health data**, as well as **pooling analytical capabilities**, in compliance with the **General Data Protection Regulation**, is **crucial** to advance the understanding of genetic associations that **cause or predispose diseases** **measures and to facilitate further development of personalised medicine.**
- **Citizens, researchers and health systems** in the Union can benefit from **the full potential of genomics** to advance targeted health care interventions leading **to better prevention, early diagnosis and treatment of diseases;**
- **Secure and authorised cross-border access to genomic and other health data** in the Union will **enable targeted research and innovation as well as efficient translation of that research into clinical settings and public health work**, which can lead to more effective therapies for individual patients and improved preventive measures.
- **Citizens needs are at the centre of data-driven healthcare ...;**

Member States of the European Union, the European Economic Area (EEA) and the European Free Trade Association (EFTA)



Aim of the initiative – MS commitment

- This cooperation, which will **build upon existing initiatives in genomics and personalised medicine**, will inter alia aim to:
- **Define a voluntary coordination mechanism of national, regional and local public authorities** to link ongoing genomic medicine initiatives and to **steer the activities** stemming from this declaration
- **Ensure distributed, authorised and secure access to national and regional banks of genetic and other relevant data** for the advancement of science and innovation, while taking appropriate measures to **protect the privacy** of individual data donors;
- **Support the development of technical specifications for secure access and cross-border exchange** of genomic datasets and **facilitate interoperability** of relevant registries and databases to support **research**; Promote the use of **open standards and data management systems** to ensure **interoperability** of **genomic and other health data**...;
- **Define a governance model** of cooperation, particularly concerning the terms and conditions for distributed access to genomic data



Aim of the initiative – Signatories invite Commission to:

- **Consider the shared vision** enshrined in this declaration and endorsed by the signatories **as it implements measures to support the digital transformation of health and care** further to the Digital Single Market mid-term review, notably aiming at "supporting data infrastructure to advance research, diseases prevention and personalised health and care";
- **Mobilise funds** from the Horizon 2020 and Connecting Europe Facility programmes **to support pilot actions**, pooling data and resources across the Union, and **demonstrate the benefits** in advancing genomic medicine. Consider further **support from future programmes**;
- Regularly **report on progress** achieved regarding the implementation of the commitments outlined above, including **updates on global developments** concerning genomic medicine.



- **Citizen's needs at the centre** of data-driven innovation as active agents in their own health journey;
- Citizens can benefit from **more precise and personalised treatments** as well as a more participatory healthcare experience
- **Researchers and health systems can benefit from the full potential of genomics** to advance targeted healthcare interventions
- The **union stays at the forefront** of genomic and personalised medicine, and improves its scientific capabilities and industrial competitiveness



Declaration on linking genomic databases across borders: **"Towards access to 1 million Genomes in the EU by 2022"**

- Signed on 10 April 2018 during Digital Day 2 by:
- Czech Republic, Cyprus, Estonia, Finland, Italy, Lithuania, Luxembourg, Malta, Portugal, Slovenia, Spain, Sweden and the UK
- A member states driven initiative supported by the European Commission



Digital Health and Care



TRANSFORMATION OF HEALTH AND CARE IN THE DIGITAL SINGLE MARKET - Harnessing the potential of data to empower citizens and build a healthier society

European health challenges

- ⊗ Ageing population and chronic diseases putting pressure on health budgets
- ⊗ Unequal quality and access to healthcare services
- ⊗ Shortage of health professionals

Potential of digital applications and data to improve health

- ✂ Efficient and integrated healthcare systems
- ✂ Personalised health research, diagnosis and treatment
- ✂ Prevention and citizen-centred health services

What EU citizens expect...

90% agree

To access their own health data (requiring interoperable and quality health data)

80% agree

To share their health data (if privacy and security are ensured)

80% agree

To provide feedback on quality of treatments

Support European Commission:

1

Secure access and exchange of health data



Ambition:

Citizens can securely access and share (e.g. with doctors or pharmacies) their health data anywhere in the EU.

Actions:

- eHealth Digital Service Infrastructure will deliver initial cross-border services (patient summaries and ePrescriptions) and cooperation between participating countries will be strengthened.
- Proposals to extend scope of eHealth cross-border services to additional cases, e.g. full electronic health records.
- Recommended exchange format for interoperability of existing electronic health records in Europe.



2

Health data pooled for research and personalised medicine



Ambition:

Shared health resources (data, infrastructure, expertise...) allowing targeted and faster research, diagnosis and treatment.

Actions:

- Voluntary collaboration mechanisms for health research and clinical practice (starting with "one million genomes by 2022" target).
- Specifications for secure access and exchange of health data.
- Pilot actions on rare diseases, infectious diseases and impact data.

3

Digital tools and data for citizen empowerment and person-centred healthcare



Ambition:

Citizens can monitor their health, adapt their lifestyle and interact with their doctors and carers (receiving and providing feedback).

Actions:

- Facilitate supply of innovative digital-based solutions for health, also by SMEs, with common principles and certification.
- Support demand uptake of innovative digital-based solutions for health, notably by healthcare authorities and providers, with exchange of practices and technical assistance.
- Mobilise more efficiently public funding for innovative digital-based solutions for health, including EU funding.





Declaration on linking genomic databases across borders: "Towards access to 1 million Genomes in the EU by 2022"

EU countries agreed to cooperate in linking genomic data across borders

**THEY
DID IT!**
& more will too



Signed by 20 EU Member States:
Austria, Bulgaria, Croatia, Cyprus, Czech Republic, Estonia, Finland, Greece, Hungary, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Portugal, Slovenia, Spain, Sweden and the UK.

9 Observers: *Belgium, Denmark, France, Germany, Hungary, Ireland, Norway, Poland and Switzerland.*



The 1+ Million Genome initiative

- Federated framework that would allow **secure** and **authorised** cross-border access to **genomic** and other **health data** across the EU, supporting **research, health care and prevention**.
- To allow users to search and access the data through a user-friendly and effective data governance structure **building on existing national and European initiatives**.
- To ensure that citizens, researchers and health systems in Europe can benefit from the full potential of genomics to **advance targeted health care interventions** leading to better **prevention, early diagnosis and treatment of diseases**

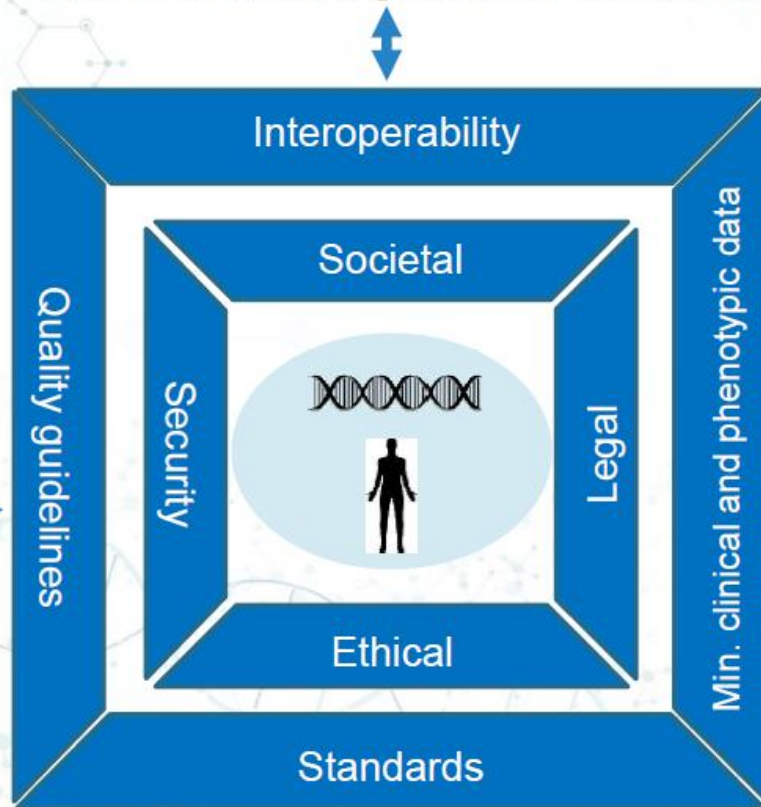
Member States of the European Union, the European Economic Area (EEA) and the European Free Trade Association (EFTA)





Join forces!

National clinical genomics initiatives



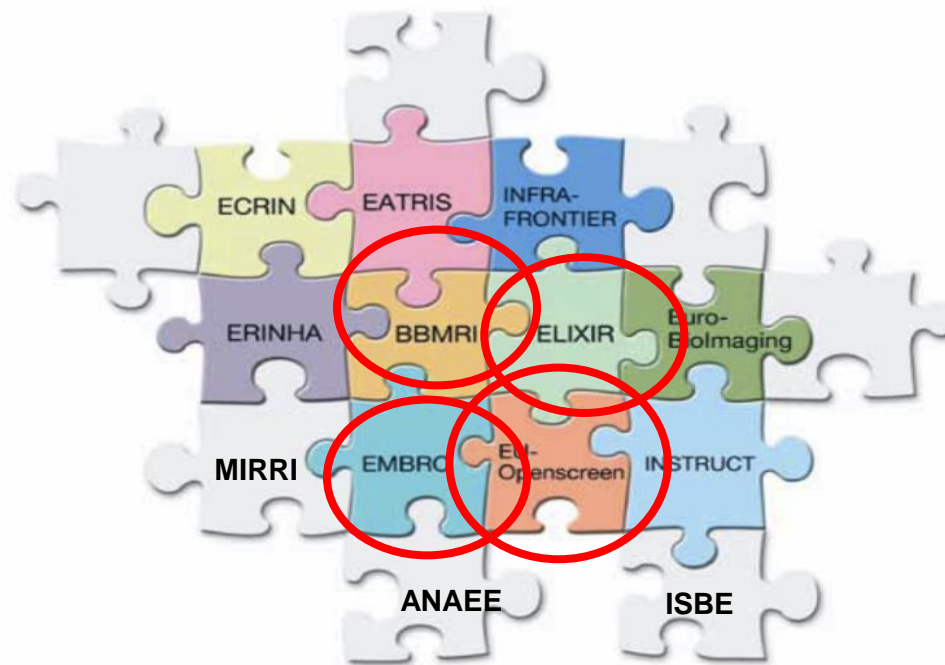
Canada-EC Joint Health Data Flagship Collaboration





European Research Infrastructure Consortium (ERIC)

- ERIC = **E**uropean **R**esearch **I**nfrastructure **C**onsortium
- Aimed at meeting long-term needs of Europe's research communities across scientific areas.
- ESFRI are facilities, resources or services of a unique nature to conduct top-level research activities in all fields.





BBMRI-ERIC is a research infrastructure of biobanks and biomolecular resources that provides expertise and services

in order to facilitate the use of European sample collections and data for the benefit of human health.

WE ARE

**MEMBERS OF
BBMRI-ERIC**

- Austria
- Belgium
- Bulgaria
- Czech Republic
- Estonia
- Finland
- France
- Germany
- Greece
- Italy
- Latvia
- Malta
- Netherlands
- Norway
- Poland
- Sweden
- United Kingdom



**OBSERVERS OF
BBMRI-ERIC**

- Switzerland
- Cyprus
- Turkey
- IARC

ELIXIR's mission is to operate a sustainable European infrastructure for biological information, supporting life-science research and its translation to society, the bio-industries, environment



ELIXIR connects national bioinformatics centres and EMBL-EBI into a sustainable European infrastructure for biological research data



ELIXIR Members



ELIXIR Observers



www.elixir-europe.org

 [@ELIXIREurope](https://twitter.com/ELIXIREurope)

 [/company/elixir-europe](https://www.linkedin.com/company/elixir-europe)





Genomics-based National Initiative projects across the ELIXIR Members



1. A-C-G-T Analysis of Czech Genomes for Theranostics (2018-ongoing)
2. FarGen (Denmark) (2011-ongoing)
3. France Médecine Génomique 2025 (2016-ongoing)
4. Genome Denmark (2012-ongoing)
5. Genome of the Netherlands (GoNL) / BBMRI-NL biobank 'omics' studies BIOS (2010-ongoing)
6. Genomics England (2013-ongoing)
7. FinnGen and the Sequencing Initiative Suomi, Finland (2015-ongoing)
8. Eesti biopangas: Estonian Genome Project (2000-ongoing)
9. The Scottish Genomes Partnership (2015-ongoing)
10. UK Biobank (2006-ongoing)
11. National Centre for Excellence in Research in Parkinson's Disease (Luxembourg) (2015-ongoing)
12. National Center for Medical Genomics - Czech national research infrastructure (2014-ongoing)
13. Genomic Medicine Sweden (2018-ongoing)
14. National contact point and network for rare diseases in Slovenia (2016-ongoing)
15. Swiss Personalised Health Network (SPHN) (2017-ongoing)
16. Welsh Genomics for Precision Medicine Strategy (2017-ongoing)
17. Northern Ireland Genomic Medicine Centre (2017-ongoing)
18. National Biomics Program, Hungary, (2018-ongoing)
19. National Oncology Program, Hungary, (2015-ongoing)

-  Public funding
-  Public-private funding





The European Genome-phenome Archive (EGA; <https://ega-archive.org/>)

- The EGA is a resource for the permanent archival and sharing of controlled-access genetic and phenotypic human data, resulting from biomedical research projects. The central EGA (operated from EMBL-EBI, UK and CRG, Spain) hosts over 1,700 studies consisting of more than 4,000 datasets from in excess of 900 data providers
- The EGA includes important reference data collections for human genetics research, such as EC RD-Connect, EC BLUEPRINT, UK10K, UK Biobank, The Human Induced Pluripotent Stem Cells Initiative (HipSci), Wellcome Trust Case Control Consortium, and EU as well as nationally funded International Cancer Genome Consortium (ICGC) studies.
- **The EGA is an ELIXIR Core Data Resource** and is the recommended ELIXIR deposition Database for access controlled human data

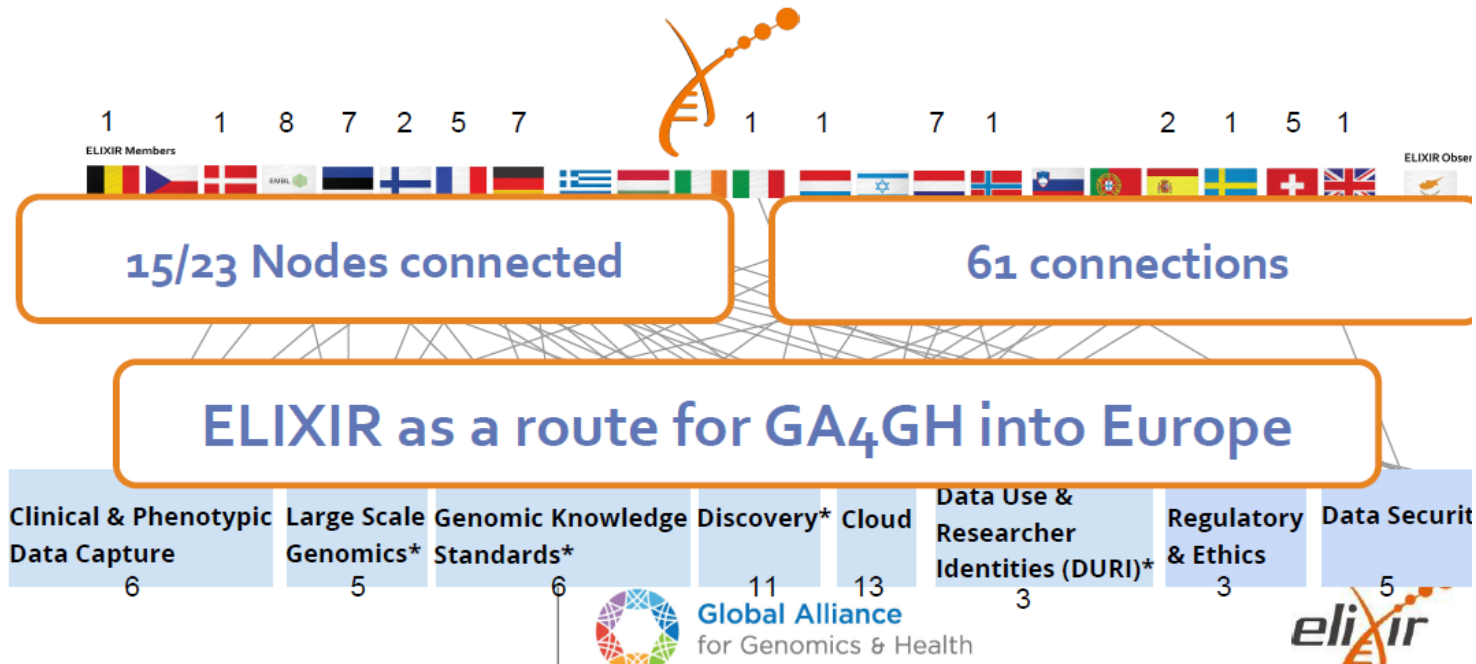


The GA4GH Mission

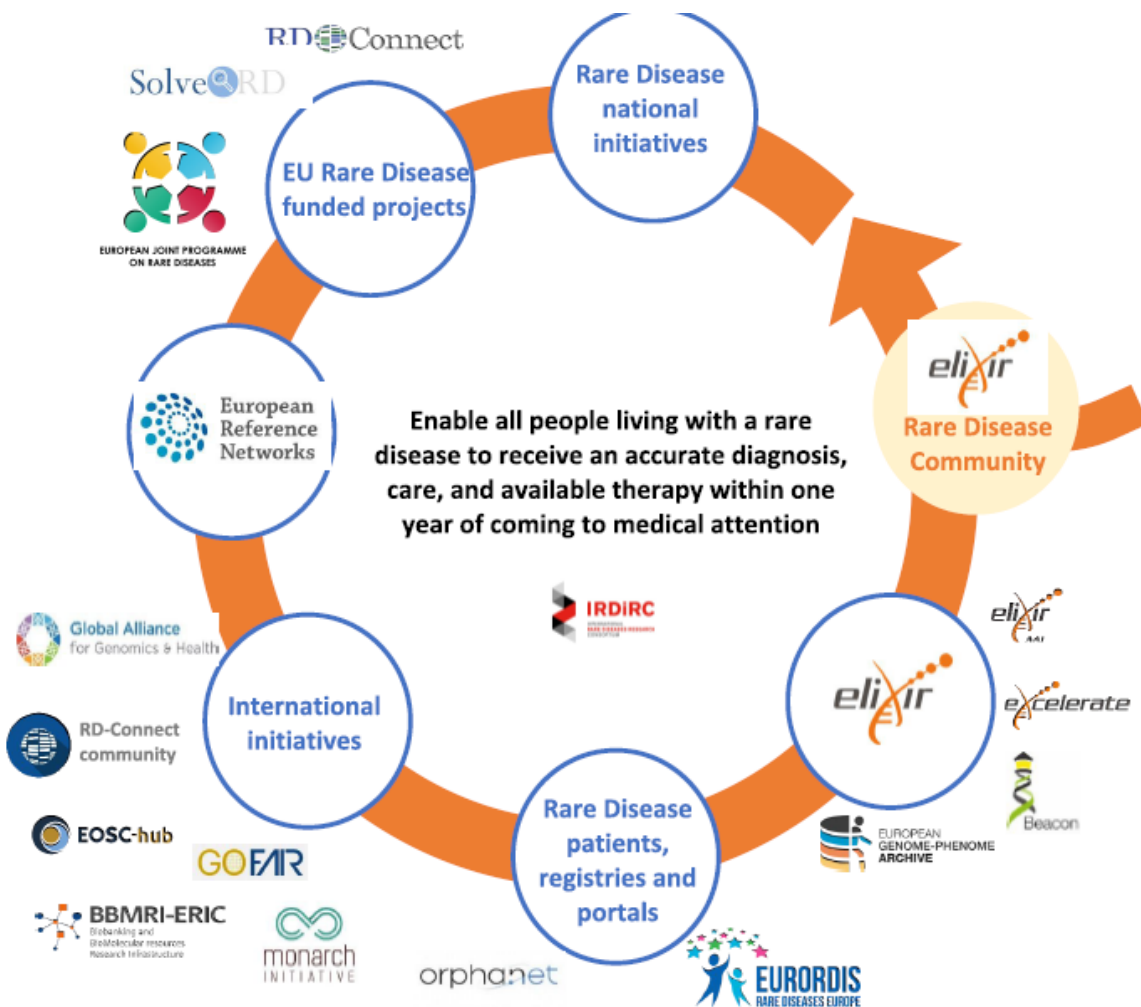


The Global Alliance for Genomics and Health aims to accelerate progress in genomic science and human health by developing standards and framing policy for responsible genomic and health-related data sharing

Mapping ELIXIR::GA4GH Interactions

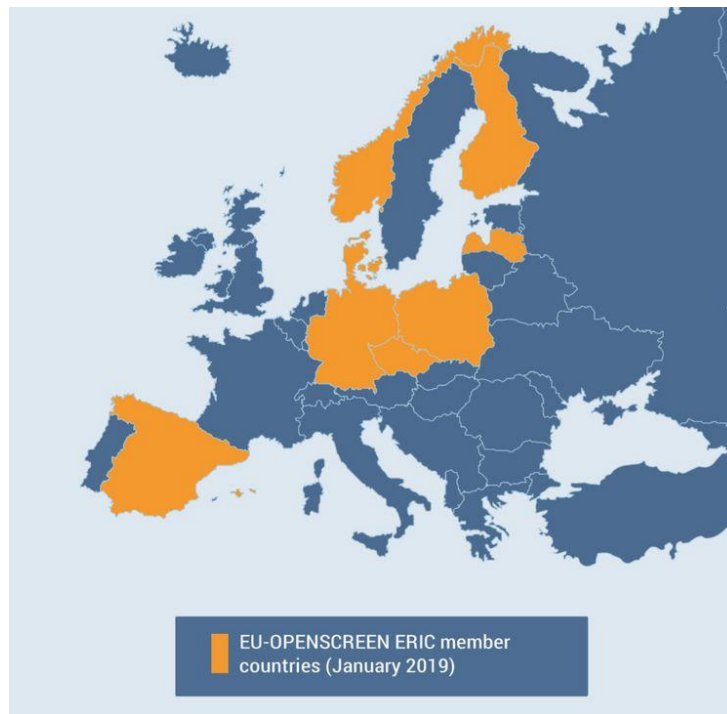


Rare disease community



- Infrastructure for RD research:
 - Registry of Rare Disease data resources and analysis tools (<https://rare-diseases.bio.tools>)
 - Data sharing and data discovery
- Interoperability of RD resources:
 - Standards and ontologies
 - FAIR data services
- Training

Biomedical ERICs & EU OPENSSCREEN



EU-OPENSSCREEN offers researchers from Europe and around the world open access to a uniquely broad range of high technologies and tools for the systematic screening of chemical substances for their biological effects. EU-OPENSSCREEN integrates high-capacity screening platforms throughout Europe, which jointly use a rationally selected compound collection, comprising up to 140.000 commercial and proprietary compounds collected from European chemists.



2018 Questionnaire to participants

- A number of **sequencing techniques** are commonly used (Illumina platforms)
- Data **quality** and quality of samples are measured via a mix of standard-based and in-house solutions
- **Standards in place** for sequencing, alignment, quality control and storage
- In most cases there are standards for interpretation of DNA sequences
- **Interoperability** standards often deployed for data exchange
- **Requirements to use specific methodologies** apply to several activities (licensing of institutions, certification of professionals, external quality assessment)
- **Phenotype data** is collected via medical doctors, Human Phenotype Ontology (HPO) and clinical care teams
- Sequenced genomes, are **linked to clinical** and other types of data (e.g. proteomics and biobanks) by around 80% of respondents.
- **Measuring benefits** of WGS seem to still be in early phases of development
- Cost-effectiveness/sustainability studies of genomics in 50% of respondents

Current activities

- 10 working groups – link up to expertise/projects/initiatives identify gaps/needs/activities
 - 3 use cases
 - Mapping of current and future genomic initiatives and data
 - Interim governance structure – national mirror groups
- Road map

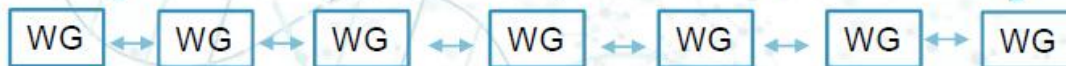
Interim governance

Steering Committee/Board – signatory MS

Acting as the governing body made up of representatives from MS

Coordinating group

National mirror group



WG-lead/co-lead
Members
Experts
European infrastructures
Groups/initiatives/projects



Creation of working groups

- WG1 Scope, stakeholders and governance
- WG2 Ethical, Legal, and Societal Issues (ELSI)
- WG3 Common standards and min. dataset for clinical and phenotypic data
- WG4 Good sequencing practice
- WG5 Federated, secure, interoperable and privacy-respecting framework and access governance
- WG6 Health economics and outcome research
- WG7 Involvement of the private sector
- WG8 Use case - Rare diseases
- WG9 Use case - Cancer
- WG10 Use case - Populations, Precision prevention, Pharmacogenomics



WG1 Scope, stakeholders and governance



- Chair: Malin Eklund (Swedish Research Council, SE)

- Scope

- Formulate goal and benefits of the initiative
- Suggest governance structure
- Identify opportunities for support from EU initiatives e.g. Horizon 2020, Structural Funds, initiatives for digital health
- Suggest model of contribution from each participating MS
- Examples/pilot studies for added value of genome sharing
- Need for generating a collection of new data (genomic, phenotypic, exposomics)
- Stakeholder engagement





WG2 Ethical, Legal, and Societal Issues (ELSI) – Regina Becker (LUX)

Protecting genomic and clinical data

Harmonization of consent forms

How to store your data securely

How to anonymize your data

How to share data with all legal and ethical requirements

Application of European and local data protection regulations





WG3 Standards for capturing clinical and phenotypic data requirements

- Chair: Vacant

- Scope

- Define the clinical and phenotypic data requirements necessary in order to make genetic data useful in each clinical use case
- Mapping of available services and structures working on standards for structured clinical and phenotypic data collection
- Provide guidelines for collection of clinical and phenotypic data
- Bring forward best practise examples showing the added value of additional clinical information (including exposome data, life style data etc) linked to genetic data



WG4 Good sequencing practice

- Chair: Ivo Gut (CNAG-CRG, ES)

- Scope

- Publish guidelines for Good Genomics Practice, covering sample management, data generation and data analysis for the different use cases
- Suggest a model for maintaining the guidelines - ensure engagement of ongoing initiatives
- Propose a meta data structure detailing the sample processing, sequencing and analysis work carried out
- Define quality metrics for sequencing data and minimal thresholds





WG5 Interoperability, data transfers, federated systems and data access governance

- Chair: Tommi Nyrönen / Ilkka Lappalainen (CSC, FI)
- Scope
 - Outline the infrastructure resource components needed to establish the framework that allows identification, selection, and access to the genetic data, and how these components shall interoperate
 - Access for all three key stakeholders need to be considered: healthcare, universities and commercial entities
 - Identify and formulate benefits and rules of access for private stakeholders that will safeguard data protection rules and intellectual property rights
 - Suggest resources needed in order to establish the framework in time to make 1 million whole genomes accessible by 2022



WG6 Health economics and outcome research

- Chair: Ilse Custers (ZonMW, NL)
- Scope
 - Based on health economic analysis: benefits of sharing genomic data that are linked to clinical data in order to more effectively prevent and treat diseases.
 - Benefits of longitudinal real time data
 - Contribution to sustainability challenge
 - Cost efficiency (gains in efficiency vs cost of sequencing and analysing) if possible in the context for the three use cases



WG7 Involvement of the private sector

- Chair: *vacant*

- Scope

- Examples of on-going initiatives and models for IP, contribution and access.
- Analyse purpose, benefits and challenges and suggest a process/structure/model on how the initiative can work together with the private sector
- Summarize ongoing similar initiatives where industry is involved. Describe the collaboration model used including IP rights





WG8-10 “Rare diseases”, “Cancer” & “Populations, Precision prevention, Pharmacogenomics”

- Chair WG8: Bruno Dallapiccola (Ospedale Bambino Gesù, IT)
- Chair WG9: Ruggero de Maria (Alleanza Contro il Cancro, IT)
Dimitris Thanos (Biomedical Research Foundation Academy of Athens, GR)
- Chair WG10: Andres Metspalu (Estonian Genome Center, EE)
- Scope
 - Identify ongoing national/European pilot projects
 - Propose pilot projects / EU tool/database
 - Describe the value of European level data sharing;
 - Describe how shared data can be used within the specific disease area
 - Consider the needs of both end-users/patients, research, health care and industry including disease gene discovery, mechanism study, diagnostics, therapy, prevention and knowledge building





Proposal on “Good Genomics Practice” (currently being discussed)

I. Gut&Bale

- Patient or research subjects should give consent for genomic analysis that allows for linkage to health (phenotypic) data, ideally this would also include longitudinal data linkage and re-contact and/or return of pertinent and additional looked-for findings.
- Sample acquisition should be consistent, documented and appropriate for a clinical, research or dual-use pipeline. Samples should ideally be stored in an easily retrievable facility such as a Biobank or Biosample Centre or a Biobank network.
- DNA extraction and preparation should be done using standardised and validated methods to ensure samples meet standards for integrity, quality, yield and volume.



- Whole genome sequencing should be carried out in an accredited facility – clinical or research – with appropriate quality metrics. Ideally, the minimum standard of 30x read depth across 95% of the genome. Quality metrics should include measures of evenness of sequencing across genome, percentage of genome that reaches a minimum threshold for reliably calling variants, and the ratio of edits between paired reads.
- For tumour genomes, the read depth should be a minimum of 75X across 95% of the genome along with an appropriate quality germline sample. In addition, quality metrics for tumour genomes should include measures of callability of somatic mutations across the genome and paired-reads mapping to different chromosomes.



- WGS data should be analysed using a [standardised] validated, benchmarked and documented pipeline with – as far as possible - tools and file formats that are common and open-source;
 - WGS should be aligned to the latest reference genome standard, currently GRCh38 (but consideration given to cost-effective means of re-aligning certain older datasets)
 - Genome data should use formats compatible with BAM or VCF or that where possible conform to standards



- Sequence variation annotation should use standardised and documented methods. Where appropriate this should specify how the variants are called from the reference genome, and the method of variant annotation.
- Variant interpretation should use standardised guidelines (for both germline and somatic variation) in order to allow consistency in interpretation and data sharing. Specified relevant publicly available or shared variant databases (such as ClinVar) and gene-disease validity databases (such as PanelApp) should be utilised to aid interpretation. Publicly available variant databases, such as [ClinVar, HMGD plus others like the Human Variome Project



- Genome data should be stored in secure facilities. It is not necessary that raw data is made available across the EU 1 Million Genomes Initiative partnership.
- Variants together with phenotypes should be made available across the 1 M genome initiative in a federated system that allows two-sided queries, match making and integrative analyses.
- The tools and materials should be available in the languages used in national healthcare as well as opportunities use to make materials available in multiple languages – for example the approach uses in HPO.



Spanish initiative

Representatives

Luis Serrano CRG

Angel Carracedo FPGMX-USC

WG1 Scope, stakeholders and governance – **Raquel Yotti**, Gonzalo Arévalo

WG2 Ethical, Legal, and Societal Issues (ELSI) – **Carmen Ayuso, Pilar Nicolas Jimenez**

WG3 Common standards for capturing clinical and phenotypic data requirements –
Alfonso Valencia

WG4 Good Genomic Practice / development of standards for sequencing, annotation and clinical interpretation – **Ivo Gut**

WG5 Interoperability, transfer between countries, local/federated system incl. systems development and deployment and data access governance – **Ximo Dopazo**

WG6 Health economics and outcome research- **Alvaro Hidalgo**

WG7 Involvement of the private sector: Not appointed

WG8 Use case Rare Diseases – **Pablo Lapunzina**

WG9 Use case Cancer – **Nuria Lopez-Bigas**

WG10 Use case, Common, Complex Diseases – **Angel Carracedo, Marina Pollánç**

National Mirror WGs being built



Matrix Genomics State of Play



Rare Diseases							
Name of project/initiative/infrastructure etc.*	Generated on what level: national, regional, local	Main purpose of data (research, clinical, both)	Linked clinical data (please describe)	WGS, WES or other (specify)	No of seq. available	Storage location (where those sequences are stored)**	Could be made accessible/searchable
300 EXOMES TO ELUCIDATE RARE DISEASES - CNAG	National	Research	Brugada Syndrome	WES	30	FPGMX	
300 EXOMES TO ELUCIDATE RARE DISEASES - CNAG	National	Research	CMMR-D syndrome	WES		FPGMX	
300 EXOMES TO ELUCIDATE RARE DISEASES - CNAG	National	Research	spinocerebellar ataxia and spastic paraparesis	WES		FPGMX	
300 EXOMES TO ELUCIDATE RARE DISEASES - CNAG	National	Research	cerebral microangiopathy	WES		FPGMX	
ASC	International	both	TDAH/DI/TEA/TOC trios	WES	2.100	FPGMX	As soon as it was published
AES2016. PI1601057	National	Research	colorectal cancer	WES	120	FPGMX	As soon as it was published

Cancer							
Name of project/initiative/infrastructure etc.*	Generated on what level: national, regional, local	Main purpose of data (research, clinical, both)	Linked clinical data (please describe)	WGS, WES or other (specify)	No of seq. available	Storage location (where those sequences are stored)**	Could be made accessible/searchable

Common, complex diseases (P4 - Populations, Precision prevention, Pharmacogenomics)							
Name of project/initiative/infrastructure etc.*	Generated on what level: national, regional, local	Main purpose of data (research, clinical, both)	Linked clinical data (please describe)	WGS, WES or other (specify)	No of seq. available	Storage location (where those sequences are stored)**	Could be made accessible/searchable



cnag

centre nacional d'anàlisi genòmica
centro nacional de análisis genómico



Institution Meet our Team Resources Contact us Research News & Events Jobs Find us



Powerful genomics solutions with the NovaSeq 6000 sequencing system



Current CNAG capacity 5.000 human genomes at 30x coverage.
Planned a second NovaSeq by the end of this year which would double the capacity to 10.000.

FPGMX planning a NovaSeq by the end of this year

Intergation of the private sector (NIMGenetics ...)

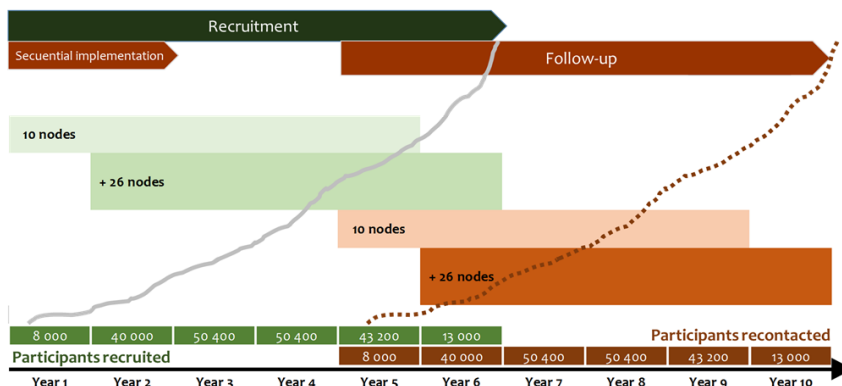


“CONAMIGOS” PROJECT
 (COHORTE NACIONAL ABIERTA MULTIPROPÓSITO
 DE INVESTIGACIÓN E INNOVACIÓN GLOBAL
 PARA EL OBJETIVO SALUD)

A highway for biomedical research in Spain
 A Proposal for a Large National Cohort of Adults Residing in Spain

PROGRAM TIMELINE AND ENROLLMENT	
Timeline	<ul style="list-style-type: none"> Progressive implementation (see diagram). Follow-up (a minimum of 10 years after end of recruitment): <ul style="list-style-type: none"> Continuous updates through repeated participant engagement and sharing of participants' electronic health records (EHRs). Updating health exposure information and physical examination every 4 years Repeated gathering of biological samples every 4 years
Recruitment centers	<p>36 primary health care centers, covering all Autonomous Communities.</p> <p>36 recruitment nodes</p> <p>*population (in millions) *number of nodes</p>
Participant selection	<p>Adults (30-70 years) randomly selected from the population covered by the primary health recruitment centers + a sub-cohort of vulnerable populations (separate protocol amendments will be developed for this purpose) (Selection of the whole family? TBD: pros and cons)</p>

ConAmigos TIMELINE (First & second rounds)



Marina Pollán
Centro Nacional de
Epidemiología



Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations

Amit V. Khera^{1,2,3,4,5}, Mark Chaffin^{4,5}, Krishna G. Aragam^{1,2,3,4}, Mary E. Haas⁴, Carolina Roselli⁴, Seung Hoan Choi⁴, Pradeep Natarajan^{2,3,4}, Eric S. Lander⁴, Steven A. Lubitz^{2,3,4}, Patrick T. Ellinor^{2,3,4} and Sekar Kathiresan^{1,2,3,4*}

WG10 Precision prevention

1% population analyzed for individual risk assesment for common traits

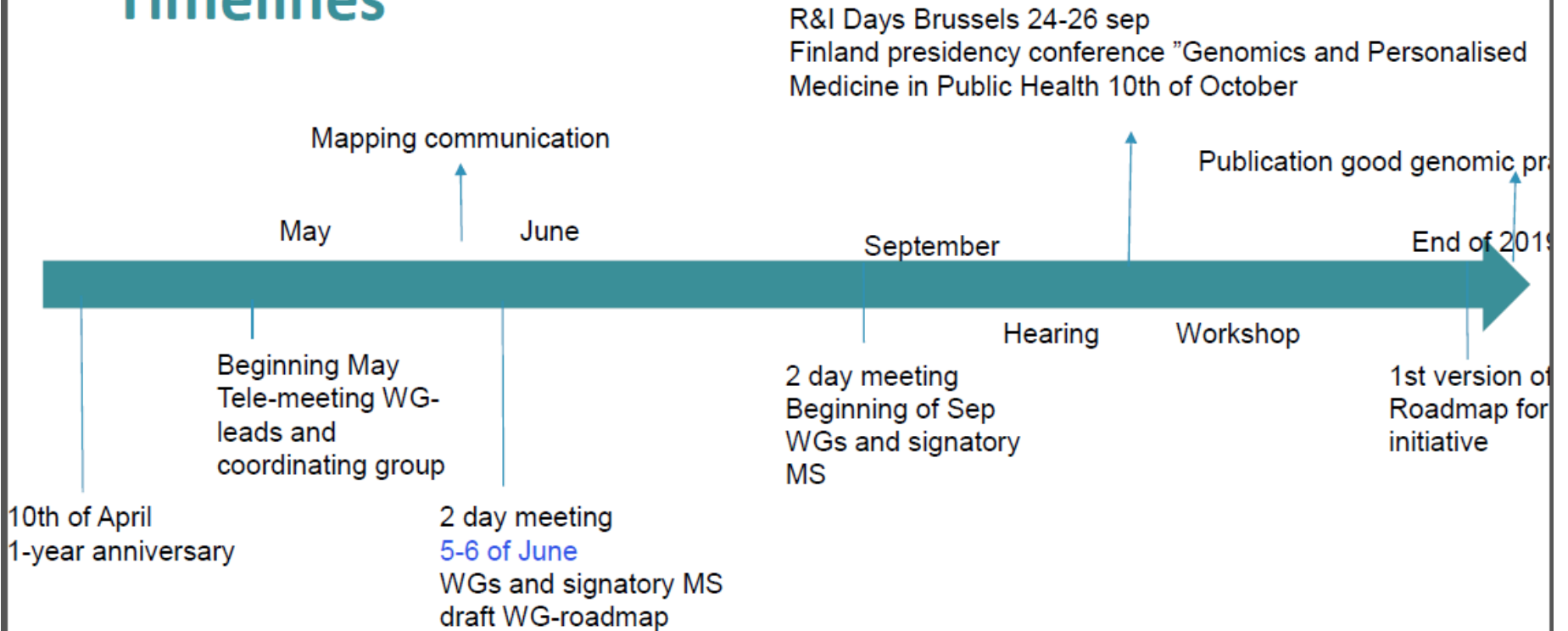
Combine WGS and genotyping data

Current genotyping capacity (40,000 GWAs/year)





Timelines



R&I Days Brussels 24-26 sep
Finland presidency conference "Genomics and Personalised
Medicine in Public Health 10th of October

- Analysis of mapping exercise
- Identify current projects/initiatives/groups relevant for the topic
- Suggest process for how to connect and collaborate with relevant expertise
- *Report on national/regional priorities for structural funds*

- WGs: Formulate a suggestion for a road map on what need to be addressed and when for ex. road map for setting up interoperability framework and requirements to join
- → September meeting 1st draft - roadmap for the initiative



