Spain National Tripartite Event Open Science in Data Intensive Scientific Communities: Genomics

Salvador Capella-Gutierrez





UNIÓN EUROPEA "Una manera de hacer Europa"



MINISTERIO DE CIENCIA E INNOVACIÓN











European Health Data Space European Cancer Mission

European

meosc



International



Global Alliance for Genomics & Health

Collaborate. Innovate. Accelerate.

Cancer Genome Consortium

International Cancer Genome Consortium

International

Spanish

ΪМРаСТ







ELIXIR – a distributed infrastructure for life sciences

The goal of ELIXIR is to coordinate life science resources from across Europe so they form a single infrastructure.

This makes it easier for scientists to:

- Find and share data
- Exchange expertise
- Agree on best practices in scientific research
- Find resources (e.g. databases, software tools, training)

Each node is committed to financially sustain the

infrastructure. ELIXIR Members

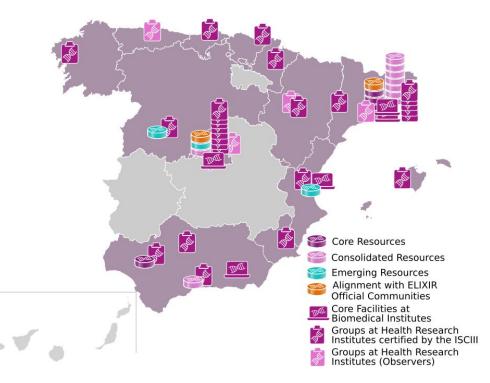


INB - Spanish National Bioinformatics Institute

The **INB**, created in 2003, became one of the technological platforms of ISCIII (2018 - 2021) with two overarching objectives:

- 1. Maintain and increase the alignment of the INB with **ELIXIR** looking for deeper synergies.
- Increase the translational capacity of the INB towards the Spanish National Health System (SNS).

INB is nowadays part of **IMPaCT-Data**







(Some relevant) Projects

Conceptual



European



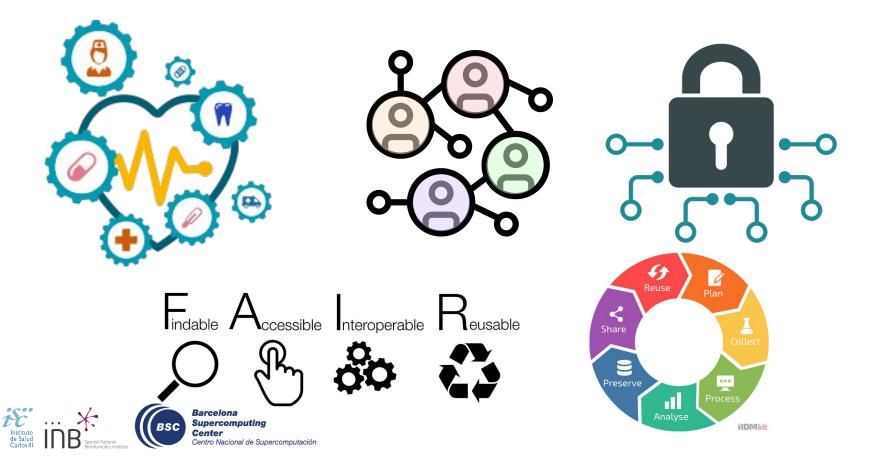
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BSC Barcelona Supercomputing Center Centro Nacional de Supercomputación **ÏMPaCT** Data



Keep concepts on Research Health (Genomics) Data





Aspects to consider in the implementation of the FAIR Principles

To be Findable:

- F1. (meta)data are assigned a <u>globally unique</u> and eternally persistent identifier.
- F2. data are described with <u>rich metadata</u>.
- F3. (meta)data are <u>registered or indexed in a</u> <u>searchable resource</u>.
- F4. metadata <u>specify</u> the data identifier.

To be Accessible:

- A1 (meta)data are <u>retrievable by their identifier</u> using <u>a standardized communications protocol</u>.
 - A1.1 the <u>protocol</u> is open, free, and universally implementable.
 - A1.2 the <u>protocol</u> allows for an authentication and authorization procedure, where necessary.
- A2 <u>metadata are accessible</u>, even when the data are no longer available.



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To be Interoperable:

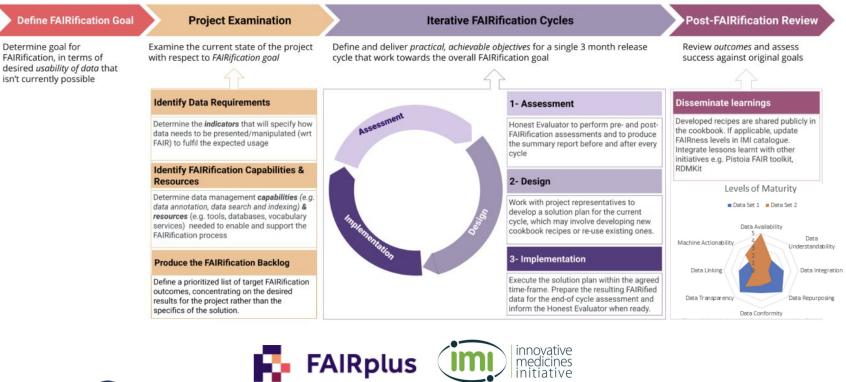
- I1. (meta)data use a <u>formal, accessible, shared,</u> <u>and broadly applicable language</u> for knowledge representation.
- I2. (meta)data use <u>vocabularies that follow FAIR</u> principles.
- I3. (meta)data include <u>qualified references</u> to other (meta)data.

To be Re-usable:

- R1. meta(data) have a <u>plurality of accurate and</u> <u>relevant attributes</u>.
 - R1.1. (meta)data are released with a <u>clear and accessible data usage license</u>.
 - R1.2. (meta)data are associated with their <u>provenance</u>.
 - R1.3. (meta)data <u>meet domain-relevant</u> <u>community standards</u>.



Practical experience on the FAIRification of research data





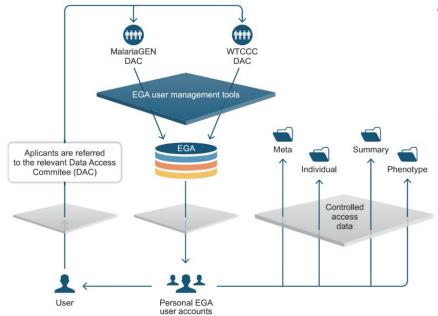








European Genome-phenome Archive (EGA)



The EGA is a resource for permanent secure archiving and sharing of all types of potentially identifiable bio-molecular and phenotypic data resulting from **biomedical research** projects. EGA contributes and follows international standards.

- Data is provided by **research centers** and **health care institutions**.
- Access is controlled by Data Access Committees.
- Data requesters are researchers from other research or health care institutions.





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https://ega-archive.org





The EGA allows going from data to therapy all around the world

Housto

Published: 27 October 2010

The patterns and dynamics of genomic instability in metastatic pancreatic cancer

Peter J. Campbell, Shinichi Yachida, Laura J. Mudie, Philip J. Stephens, Erin D. Pleasance, Lucy A. Stebbings, Laura A. Morsberger, Calli Latimer, Stuart McLaren, Meng-Lay Lin, David J. McBride, Ignacio Varela, Serena A. Nik-Zainal, Catherine Leroy, Mingming Jia, Andrew Menzies, Adam P. Butler, Jon W. Teague, Constance A. Griffin, John Burton, Harold Swerdlow, Michael A. Quail, Michael P. Christine Iacobuzio-Donahue & P. Andrew Futreal C. Cambridge, UK

 Nature
 467, 1109–1113(2010)
 Cite this article

 3186
 Accesses
 885
 Citations
 29
 Altmetric
 Metrics

- (1) Study deposited EGAS000000064
 - The paper has over 700 citations
- ★ Datasets re-used many, many times

Yap1 Activation Enables Bypass of Oncogenic Kras Addiction in Pancreatic Cancer

Avriah Kapoon,^{1,10} Waxtong Yao, ^{1,10,11} Hacogiang Ying, ^{1,10,11} Salani Hau, ¹ Alison Laween,¹ Oayan Tiang, ¹ Yi Dong, ¹ Chang-Juai Wu, ¹ Angong Sadamadan, ^{1,1} Baol Hu, ¹ Oang Chang, ¹ Oard C, Chun, ¹ Hamey Ai-Khail, ¹ Bhan Jang, ¹ Honga Ku, ¹ Berl Pietcher-Sanankone, ¹ Caral Lun, ¹ Oillian L Horeltz, ¹ Aortes Vale, ^{1,1} Pietogiang Pritizzon, ^{1,1} Nos Sanchez, ¹ Huanni Wang, ¹ Askan Pontopoor, ¹ Janka Daug, ¹ Timothy Hellmann, ¹ Rady L Jacheno,¹ Lynda Chin, 14 Y, Alan Wang, ² Giulio Draetta, 434 and Ronald A. DePinho artiment of Cancer Biology nortment of Genomic Medicin partment of Molecular and Cellular Oncolor tute for Applied Cancer Science examined of Patholicov chemistry and Molecular Biology sensity of Taxas MD Anderson Carrier Center, 1915 Melonates Baulevent Muster, TX 72000, URA Institute of Cancer Research, 15 Cotewold Road, Betmont, Sutton, Surrey SM2 SNG, UK asserve (EPFL) Station 18. such deliberty. The Social Enderty leads to of Taartment of Pathology, Brigham and Wo net Boston MA DOT15, USA Co-fini autor Comespondence: hy

(2) Molecular mechanism identified

KRAS DRIVEN TUMORS

KRAS ON

YAP DRIVEN TUMOR

OFF

(3) New therapeutic strategy shaped

> Cancer Lett. 2017 Aug 28;402:61-70. doi: 10.1016/j.canlet.2017.05.015. Epub 2017 May 30.

A combinatorial strategy using YAP and pan-RAF inhibitors for treating KRAS-mutant pancreatic cancer

Xiao Zhao ¹, Xiuchao Wang ², Lijun Fang ³, Chungen Lan ², Xiaowei Zheng ², Yongwei Wang ¹, Yinlong Zhang ⁴, Xuexiang Han ¹, Shaoli Liu ⁴, Keman Cheng ¹, Ying Zhao ¹, Jian Shi ¹, Jiayi Guo ¹, Jihui Hao ², He Ren ⁵, Guangjun Nie ⁶

Affiliations + expand PMID: 28576749 DOI: 10.1016/j.canlet.2017.05.015

Beijing, China





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Federated EGA

The Federated EGA is envisioned as a network fostering reuse of human biomedical data for research purposes in a federated context. Several ELIXIR nodes have engaged in establishing the federation together with the current EGA core institutions (CRG and EMBL-EBI)



El almacén invisible que guarda datos genómicos de un millón de personas

El Archivo Europeo de Genomas y Fenomas, que dispone de 16 petabytes de datos de salud muy sensibles para investigación científica, está custodiado en el superordenador MareNostrum de Barcelona y en Cambridge



HACIA LA MEDICINA PERSONALIZADA

Barcelona lidera un proyecto científico internacional para investigar enfermedades con datos de un millón de genomas







European institutes commit to data access across borders

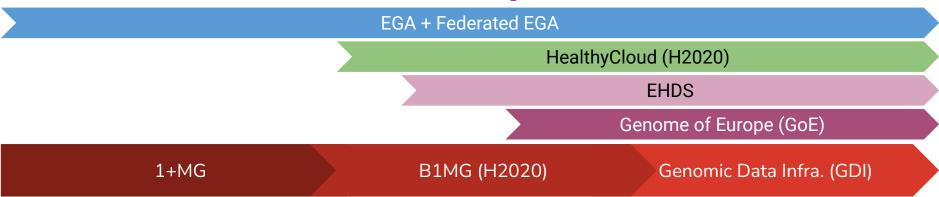
Research institutes from five European countries have committed to improving the way researchers discover and access sensitive human data across national borders to enable more efficient health research.



Credit: Karen Arnott/EMBL



Genomics Data at European scale



1+ Million Genomes

... X

22 EU countries, the UK and Norway have signed the Declaration 'Towards access to at least 1 million sequenced genomes in the EU by 2022'.

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Beyond 1 Million Genomes

B1MG will go 'beyond' the 1+M genome target and 'beyond' the signatory countries, collaborating with an array of international initiatives and consult a range of stakeholders to support the creation of a pan-European genome-based health data infrastructure.

GDI

Will support the 1+MG Initiative to fulfil the goal to provide a cross-border federated network of national genome collections associated with other relevant data for advancing data-driven health and care solutions to benefit citizens of Europe.



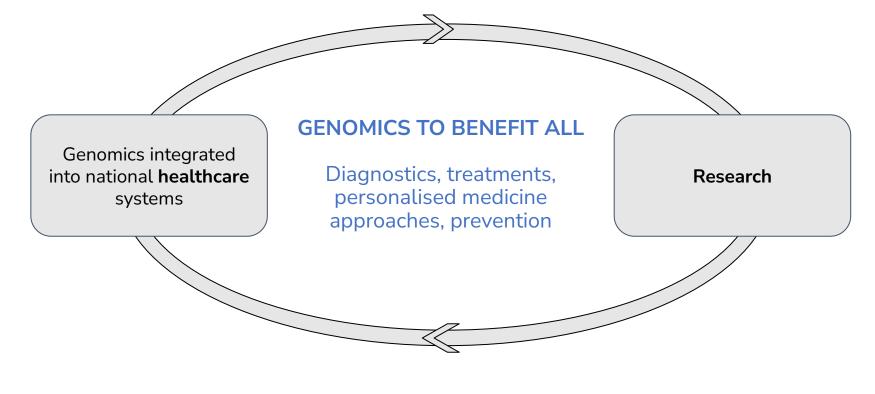
Overall ambition

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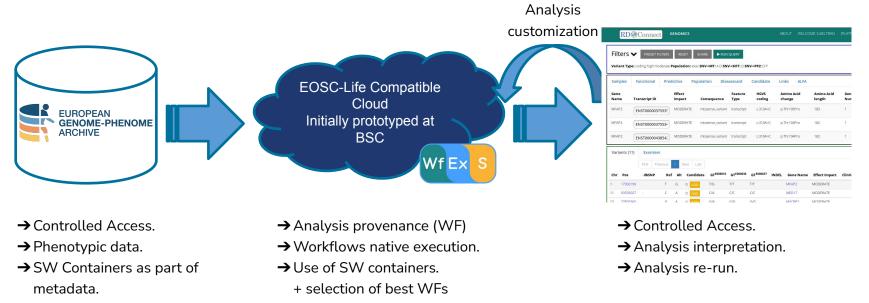




Using access-controlled FAIR data for research



Demonstrator #7. An **integrative analysis pipeline** of genomic and transcriptomic human data for disentangling the genetic origin of a rare-disease in the context of the European Open Science Cloud.







Health data at different scales

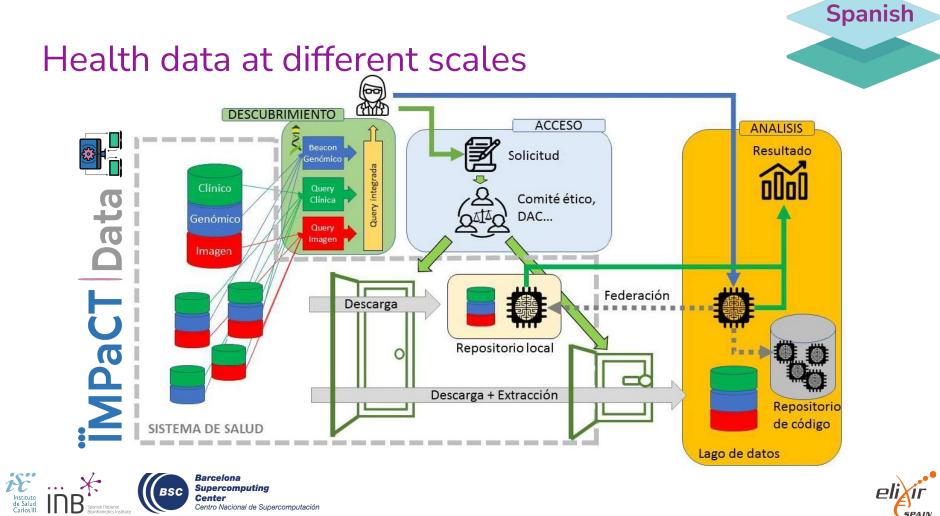
IMPaCT (Infrastructure for Personalized Medicine associated to Science and Technology) aims to set the foundations of the future national genome medicine in Spain.

- Divided into three complementary programs: Preventive Medicine, Genomics Medicine and **Data Science**.
- BSC coordinates the Data Science programme (<u>46 partners + 20 other</u> <u>organizations</u>), which aims to focus in the interception of clinical information, genomics data and biomedical imaging.
- The Data Science program will strongly rely in existing standards and mechanisms to favour **interoperability**, e.g. **OMOP**, **FHIR**, **openEHR**.
- Connects with other efforts like the **National Plan for Natural Processing Language** (among others domains from electronic health records).





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Perspective

European

International

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- Genomics data would be generated by the healthcare systems.
- Strong focus on facilitating the pheno-clinical annotations to genomics data
- Existing solutions for federated access to genomics, e.g. EGA, beacon, can be potentially extended to other domains.
- Strong connection with 1+MG/B1MG & associated projects.





https://inb-elixir.es http://elixir-europe.org





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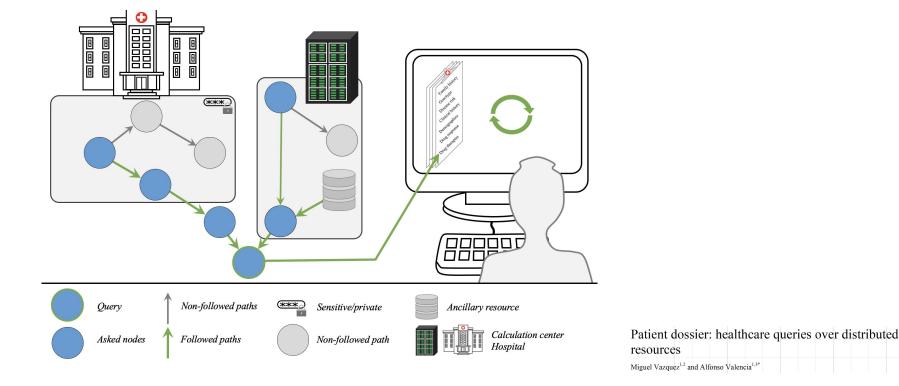




SP21-00001 – CR-BDI

The overall goal :Transparent access to normalised and interoperable data and the appropriate compute

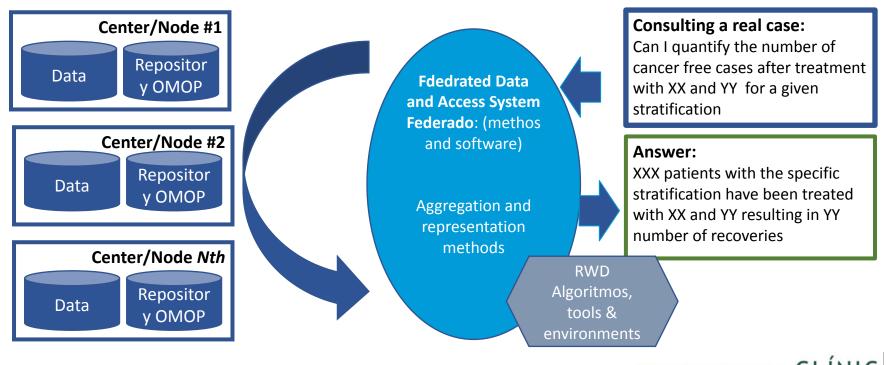






SP21-00001 – CF

Example of potential use: Building a Virtual Cohort in a Federated Environment



A federated operation is executed in each of the centers / nodes on their private OMOP repositories – after consultation with the ethic committee(s). **Requires interoperable data**

Hospital Universitario SaudMadrid 12 de Octubre

CRG Centre for Genomic

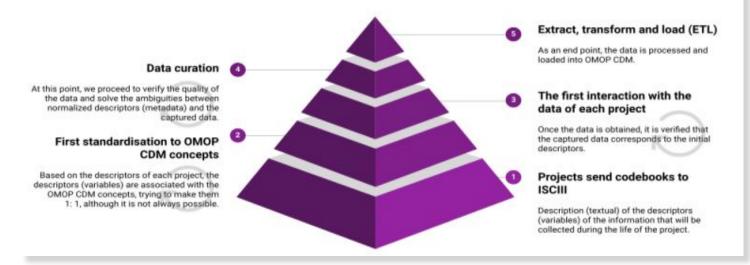
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Ejemplo de la dificultad de la interoperabilidad semántica.



Harmonizing, standardizing and sharing COVID-19 data.



60 funded projects by ISCIII: 51 clinic-epidemiological + 9 host+viral sequencing A team of 6 experts curator for 2 years + informatics support to normalise 1/3 of them

