



IRDiRC

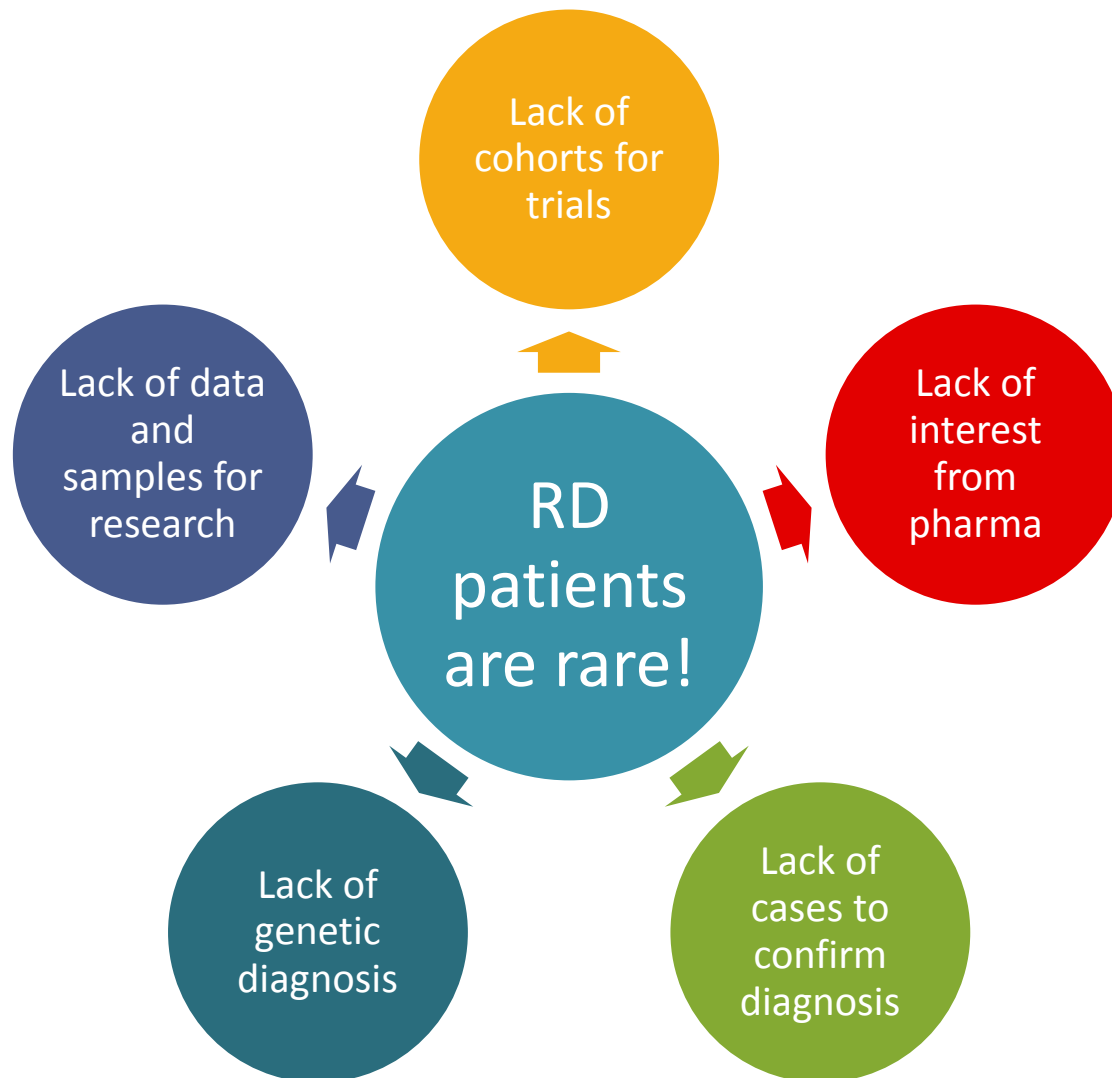
INTERNATIONAL
**RARE
DISEASES
RESEARCH**
CONSORTIUM

Cross-cutting bottlenecks and solutions in rare disease research

Hanns Lochmüller, Newcastle University
Chair (outgoing), Interdisciplinary Scientific Committee
8 February 2017



Bottlenecks in rare disease research



Many bottlenecks are cross-cutting

...across diseases and across research domains

- ▶ A lot of them come down to data
- ▶ Not just scarcity of data, but lack of options to reuse the data that does exist
 - ↪ Privacy protection issues, particularly across borders
 - ↪ Lack of infrastructure for data sharing
 - ↪ Lack of standards and interoperability
 - ↪ Reluctance to share unpublished data
 - ↪ Lack of capacity to analyse large amounts of data
 - ↪ Challenges of linking different datasets in different places



IRDiRC

INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

Many European and global initiatives are working on solutions

...IRDIRC works with all relevant initiatives through its scientific committees and task forces

RD  Connect

elixir 

orphanet 
Inserm 


 **BBMRI-ERIC**
Biobanking and
BioMolecular resources
Research Infrastructure

 EuroBioBank

 European
Reference
Networks

 **ECRIN**
EUROPEAN CLINICAL RESEARCH
INFRASTRUCTURE NETWORK

NeurOmicS 

 CERBEL
SHARED SERVICES
FOR LIFE-SCIENCE

EUReN  Omics

 **TREAT-NMD**
Neuromuscular Network

 **IRDIRC**
INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

 **EPIRARE**
European Platform for Rare Disease Registries



Global Alliance
for Genomics & Health

IRDiRC scientific committees

...bring together international scientific expertise to address the bottlenecks

▶ **Diagnostics committee**

(Kym Boycott, Gareth Baynam)

↪ Bottlenecks in diagnosis of RD



▶ **Therapeutics committee** (Diego Ardigò)

↪ Bottlenecks in RD therapy development



▶ **Interdisciplinary committee**

(Hanns Lochmüller, Petra Kaufmann)

↪ “Everything else?”



IRDiRC

INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

Interdisciplinary Scientific Committee (ISC)



Hanns Lochmüller (Chair, outgoing)

•University Newcastle upon Tyne (UK)



Edmund Jessop

• NHS England, UK



Petra Kaufmann (Chair, incoming)

•NCATS/ORDR, NIH (USA)



Bartha Maria Knoppers

•McGill University (Canada)



Angel Carracedo

•University of Santiago de Compostela (Spain)



Jeffrey Krischer

•University of South Florida (USA)



Gema Chicano

•EURORDIS, AADE (Spain)



Samantha Parker

•Lysogene (France)



Jack Goldblatt

•Genetic Services and the Familial Cancer Program of Western Australia (Australia)



Rumen Stefanov

•Medical University of Plovdiv (Bulgaria)



Steven Groft

•ORDR/ NCATS, NIH (USA)



Domenica Taruscio

•Italian National Centre for Rare Diseases (Italy)



Ken Ishii

•Japan Agency for Medical Research and Development (Japan)

IRDiRC task forces

...bring together nominated experts from different backgrounds, affiliations and geographical areas on an ad hoc basis

- ▶ To work on selected, actionable topics/research areas and push forward policy change
- ▶ Collaborate through teleconferences and workshops
 - ↳ Production and dissemination of reports
 - ↳ Implementation of outcomes
 - ↳ Publication in peer-reviewed journals
 - ↳ Presentation at conferences

Task force:

Privacy-preserving record linkage

- ▶ Development of mechanisms to enable linkage of records belonging to the same individual to enable research data sharing across multiple projects and institutions
- ▶ Product: Guidelines on the technical and ethical-legal requirements of patient identifiers in Rare Disease Research; recommendations for the most practical, streamlined and minimalistic approach that maximises uptake whilst complying with relevant legal regulations.
- ▶ Joint IRDiRC-GA4GH collaboration



Task force:

Automatable Discovery and Access

- ▶ Associate clinical data with the scope of consent given for use of that data
- ▶ Develop standardized and computer-readable data use types for use in consent forms
- ▶ Product: The Automatable Discovery and Access Matrix (ADAM) provides a standardized way to unambiguously represent consent and other conditions of use, making such information computer-readable and hence directly available for digital communication, searching and automation activities.
- ▶ Joint IRDiRC-GA4GH collaboration



IRDiRC
INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM



Global Alliance
for Genomics & Health

IRDiRC policies and guidelines

...mandate that researchers funded under IRDiRC address data sharing and reuse

- ▶ “RD research should be collaborative. Resources, data and results should be shared among IRDiRC research projects and made publicly available to the broader community, and duplication should be avoided.”
- ▶ “RD research should involve patients and/or their representatives in all relevant aspects of the research.”
- ▶ “International, national, regional and local legislation/regulations need to be adhered to with respect to data protection and ethical approvals.”
- ▶ Data producers acknowledge their responsibilities to release data rapidly and to publish initial analyses in a timely manner. IRDiRC members will encourage and facilitate rapid data release”



IRDiRC

INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

<http://www.irdirc.org/reports-guidelines/policies-guidelines/>

Sharing: Benefits

- ▶ Overcoming the “rare disease problem”
 - ↳ Cohort size
 - ↳ Powering trials
 - ↳ Finding confirmatory cases
- ▶ Reducing costs
- ▶ Reducing duplication of effort
- ▶ Facilitating validation of results
- ▶ Enabling engagement with experts and the patient community

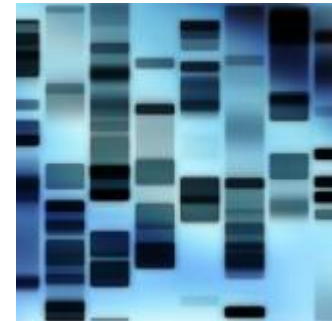


IRDiRC

INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

Sharing: What?

- ▶ Raw data from all types of studies
 - ↪ Genomic data
 - ↪ Phenotypic data
 - ↪ Natural history data
 - ↪ Clinical trial data
- ▶ Biosamples (blood, DNA, tissue samples, cell lines...)
- ▶ Linked data and samples
- ▶ Brokering access to patients
- ▶ ...



IRDiRC

INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

Sharing: Barriers

▶ General

- ↪ Privacy protection issues: “do I have the patient’s permission?”
- ↪ Lack of infrastructure: “I want to share data but where do I put it?”
- ↪ Lack of standards and interoperability

▶ Academia

- ↪ Culture of protecting research results: “someone else might scoop my publication!”
- ↪ Lack of incentives for sharing

▶ Industry

- ↪ IP issues/competition (when sharing own data)
- ↪ Concerns over data quality, regulatory compliance (when reusing data from academia or patients)

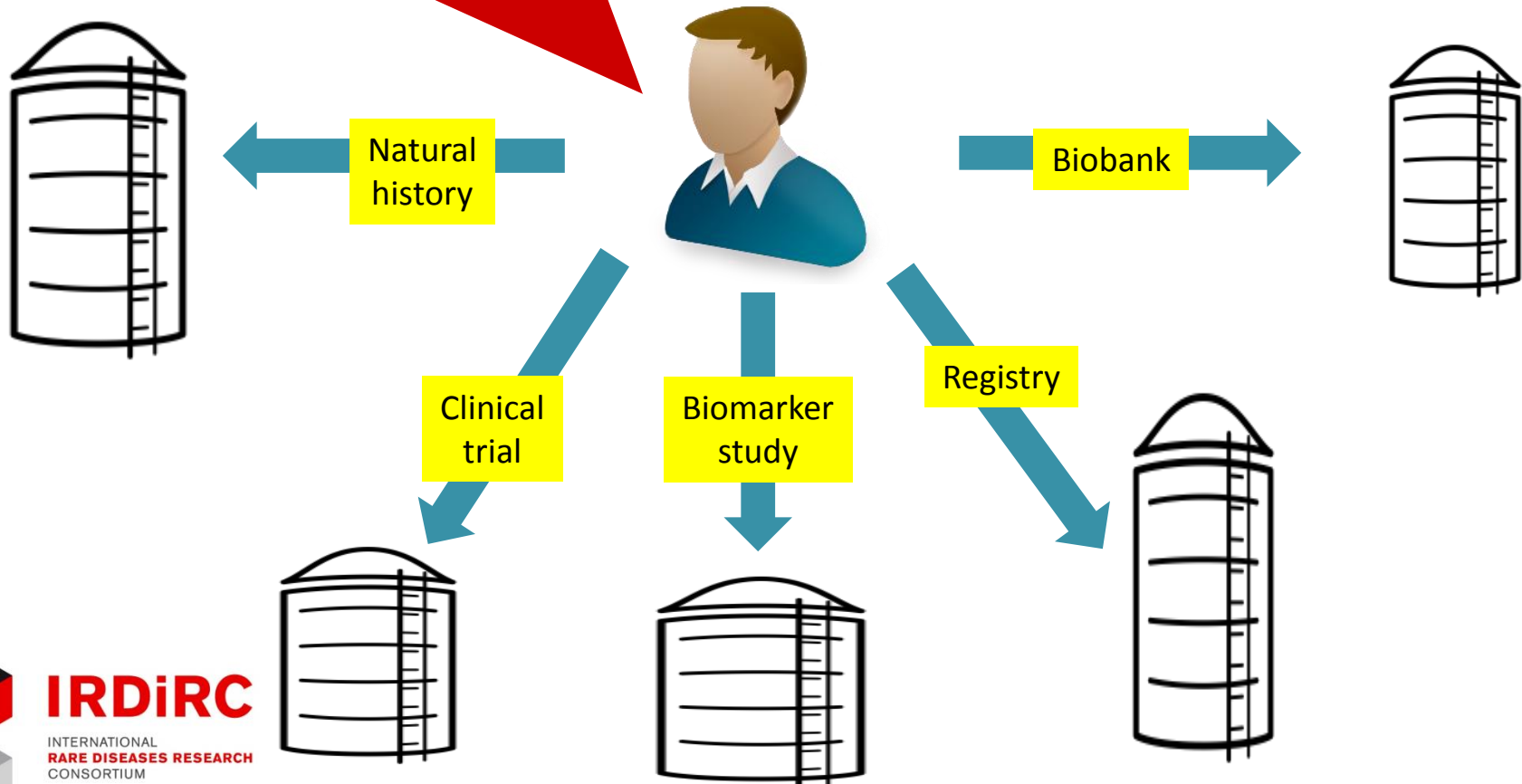


IRDiRC

INTERNATIONAL
RARE DISEASES RESEARCH
CONSORTIUM

What happens to the data of a rare disease patient?

Where does my data go? Who can access my data? Is my data safe? Will my data be useful?





RD-Connect: Infrastructure for RD research data sharing

15

An integrated platform connecting databases, registries, biobanks and clinical bioinformatics for rare disease research

Overarching objectives:

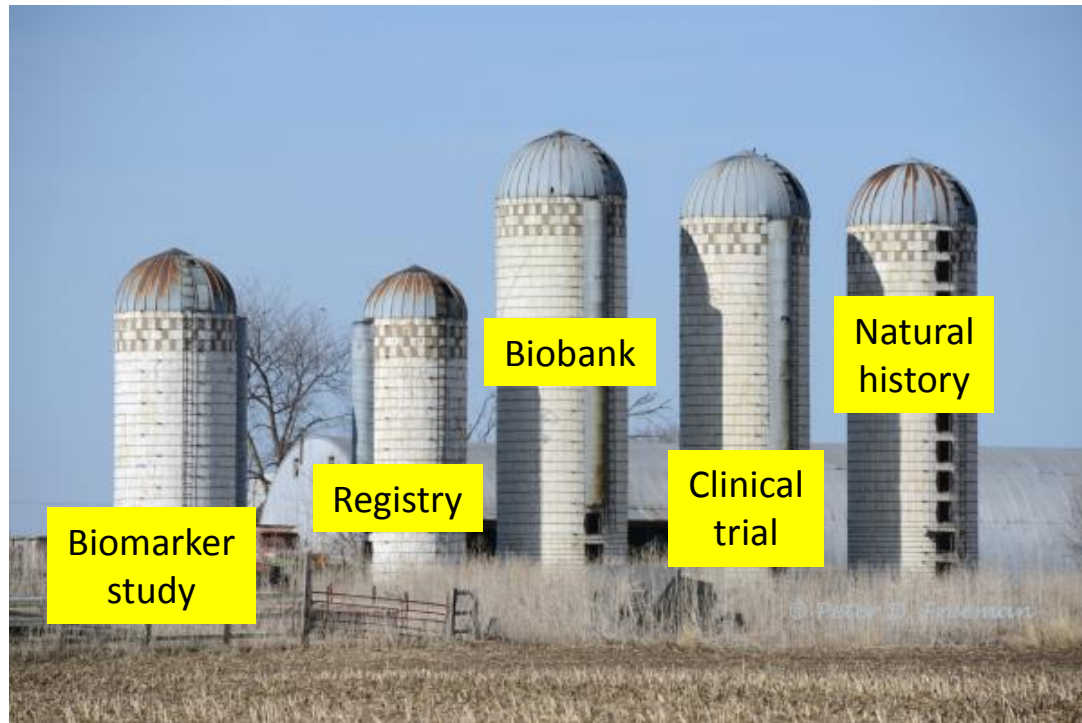
- Contribution to the IRDiRC objectives of delivering 200 new therapies for rare diseases and means to diagnose most rare diseases by the year 2020
- Development of an integrated, quality-assured and comprehensive platform in which complete clinical profiles are combined with -omics data and sample availability for rare disease research, in particular IRDiRC-funded research.



RD-Connect's guiding principle

16

Overcoming silos

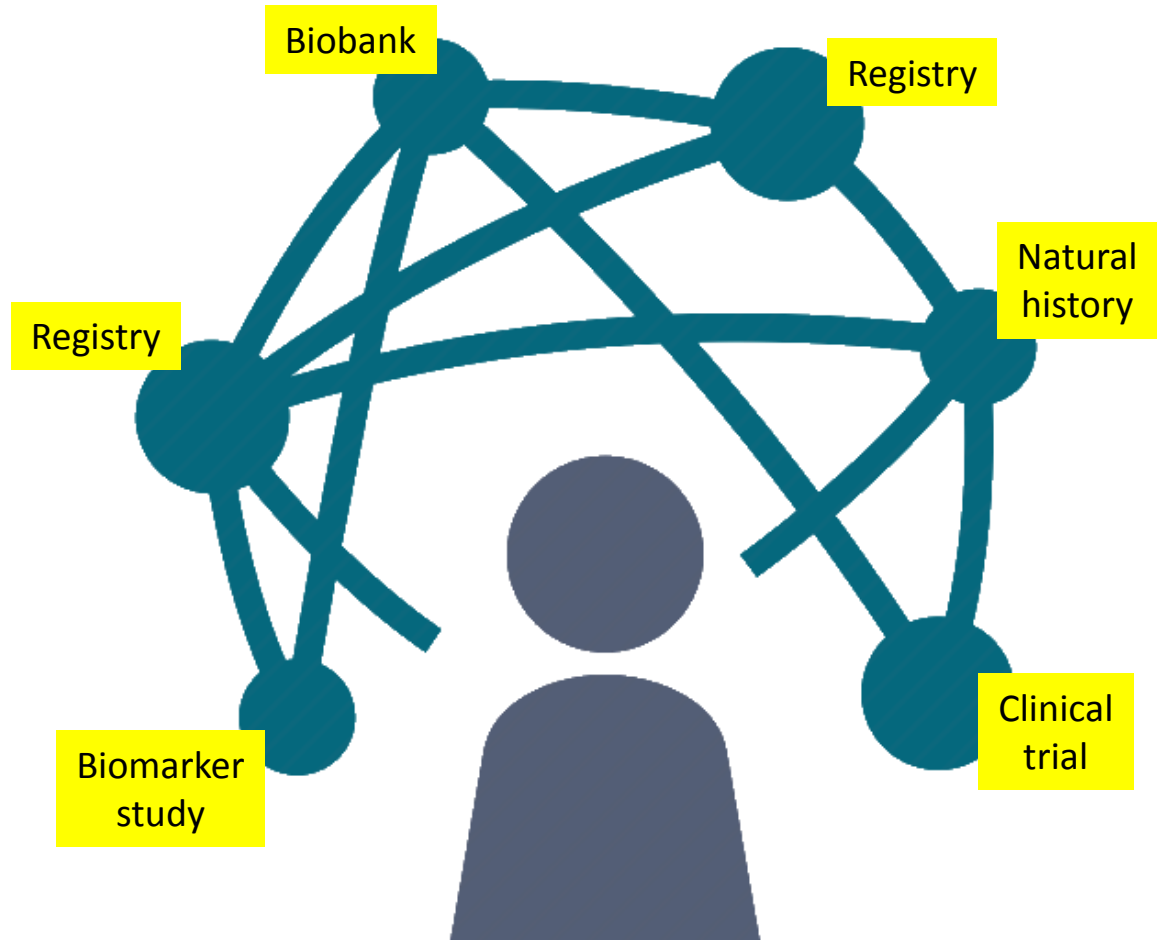


Data sharing for research and better data analysis



Enabling data linkage and reuse

17





RD-Connect's main aims

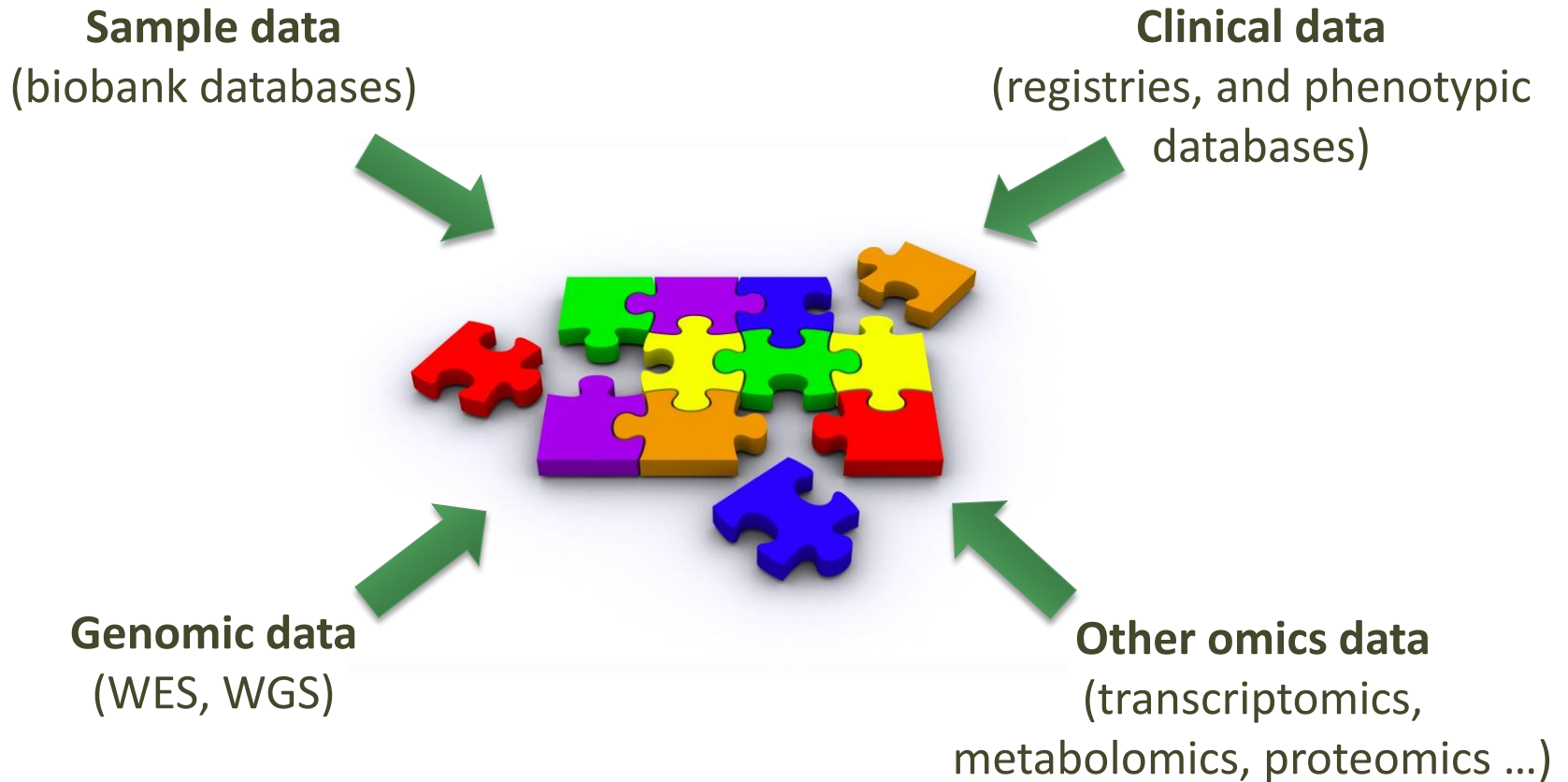
18

- Creation of central system and repository for **reprocessing, storing** and **analysing** omics data
 - Raw data hosted at European Genome-phenome Archive (EGA)
 - Raw data reprocessed through standard analysis pipeline for consistency
 - Reprocessed data accessible via National Centre for Genomic Analysis (CNAG) Barcelona platform with user-friendly online analysis interface
- Integration of phenotypic data
- Integration of biosample data
- Development of new bioinformatic tools
- Ethical and legal considerations for data sharing
- Patient input
- Outreach and impact: interaction with rare disease community



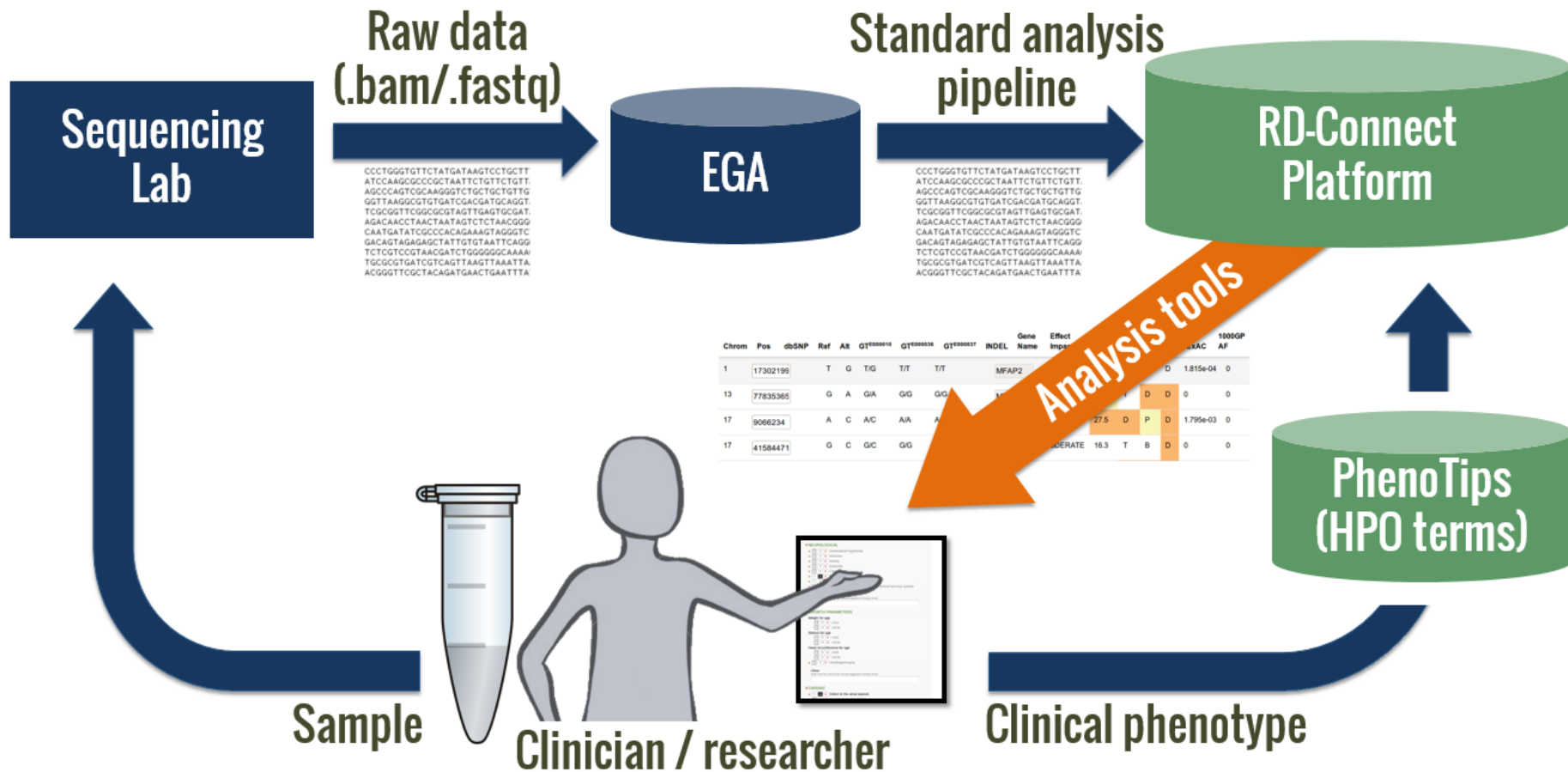
Data in the RD-Connect platform

19





Genomic data in RD-Connect





RD-Connect genomic analysis platform

Search Samples

LOG OUT



Genomics

RESET RUN QUERY

Variant Type: coding high moderate Population: gp1_af exac SNV->MT: A D SNV->SIFT: D SNV->PP2: D P

- Sample selection ? >
- Variant Type ? >
- Population ? >
- SNV Effect Prediction ? >
- Gene and Chromosome Coordinates >

Chrom	Pos	Ref	Alt
1	17302199	T	G

Functional Predictive Population Samples ALFA Diseasecard

Gene Name	Gene BioType	Transcript ID	Transcript BioType	Effect	Effect Impact	Function Class
MFAP2	CODING	ENST00000375535	protein_coding	NON_SYNONYMOUS_CODING	MODERATE	MISSENS
MFAP2	CODING	ENST00000375534	protein_coding	NON_SYNONYMOUS_CODING	MODERATE	MISSENS
MFAP2	CODING	ENST00000438542	protein_coding	NON_SYNONYMOUS_CODING	MODERATE	MISSENS

Results 5 EXPORT ALL

First Previous 1 Next Last

Samples

Chrom	Pos	dbSNP	Ref	Alt	GTE000010	GTE000038	GTE000037	INDEL	Gene Name	Effect Impact	CADD	SIFT	PP2	MT	ExAC	1000GP AF
1	17302199		T	G	T/G	T/T	T/T		MFAP2	MODERATE	21.1	D	P	D	1.0E-4	0
13	77835389		G	A	G/A	G/G	G/G		MYCBP2	MODERATE	24.7	T	D	D	0	0
17	9066234		A	C	A/C	A/A	A/A		NTN1	MODERATE	27.5	D	P	D	0.0017	0
17	41584471		G	C	G/C	G/G	G/G		DHX8	MODERATE	16.3	T	B	D	0	0
19	39062819		G	C	G/C	G/G	G/G		RYR1	MODERATE	16.8	D	D	D	0	0

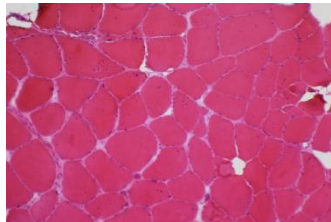


Exome sequencing and data sharing: new congenital myopathy gene

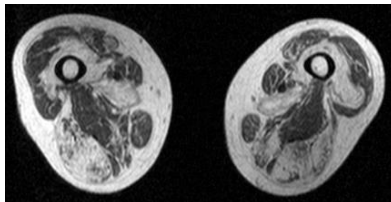
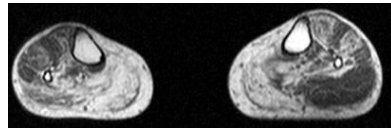
22

Newcastle case

- Childhood onset
- Proximal muscle weakness, mainly lower limbs
- Slow progression
- CK: normal or mildly elevated
- Muscle biopsy: internal nuclei, fibre splitting and fibre type 1 predominance
- Pattern resembling DNM2 patients



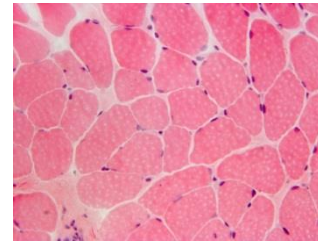
51 years



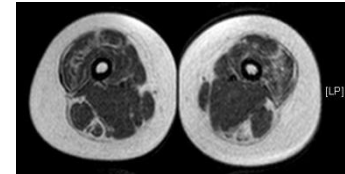
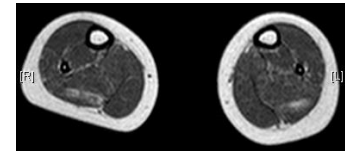
65 years

London case

- Antenatal onset with reduced foetal movement
- Proximal muscle weakness, mainly lower limbs
- Axial weakness
- Joint laxity of hands and ankles
- Slow improvement
- Muscle biopsy: minicores, central cores and some internal nuclei



4 years



4 years

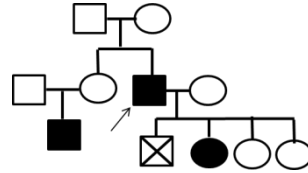


Exome sequencing and data sharing: new congenital myopathy gene

23

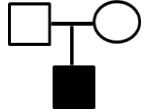
Newcastle case

- Stop gain
- novel (absent from 62k)
- chrX:153049846 G>A; p.Trp415Ter



London case

- Essential Splice Site
- novel (absent from 62k)
- chrX:153050629 G>A



SRPK3

- Serine/arginine protein kinase
- Muscle specific, regulated by myocyte enhancer factor 2 (MEF2)
- Known to regulate mRNA splicing and nuclear lamina proteins
- KO mice develop centronuclear myopathy (Nakagawa et al 2005)
- Preliminary data in zebrafish morpholino knockdown shows slow movement and muscle disorganization (unpublished)
- Four new mutations found (manuscript in preparation)



Ana Töpf

**Room 106 from 16:00: European Perspective on Sharing –Omics
Data for Personalized Medicine in Rare Diseases**

Ivo Gut, Centro Nacional de Análisis Genómico (CNAG), Spain



Biosample sharing

24

- **(1) Cataloguing** and registration of rare disease biobanks
 - Biobanks can sign up and give details of their biobank in an “ID card”
 - Allows biobanks to participate in RD-Connect infrastructure and research
 - Standardised assessment procedure, MTAs etc.
- **(2) Sharing **sample-level data**** in a common database
 - Not just sample numbers but drill-down right to individual samples
 - Researchers can find the samples they need for their research
 - Allows data from omics experiments to be traced back to the sample it came from for further research



Biosample database

25

- RD-Connect biosample database contains sample-level data from all participating biobanks

The screenshot shows the molgenis Data Explorer interface. The main content area displays a table with the following data:

Sample ID	Material Type	Studies	Diseases
CDBDCDFB-8B54-4564-AE1C-4608A07CCC07	Whole blood	Test study 1	Ackerman syndrome
ACC33FB8-CF63-40B5-A10C-784EE2AFDCB4	Whole blood	Test study 2	Ackerman syndrome
21CE39DA-E154-4B4B-9577-E7A1C0E8A6E8	Whole blood	Test study 1, Test study 2	Ackerman syndrome
9B043903-8072-4CD4-9295-C6EE6474E0A8	Whole blood	Test study 1, Test study 2	Ackerman syndrome
1C76306E-14E5-41A9-B210-732E6F783F56	Whole blood	Test study 1	Ackerman syndrome
014062E4-4069-4DCF-B2ED-4FD10FB5F2C5	Whole blood	Test study 2	Ackerman syndrome
FB40F8A1-A744-4667-A81D-71E2B88AC004	Whole blood	Test study 1, Test study 2	Ackerman syndrome
8DA832B1-300A-4873-A44C-83FB405D172B	Whole blood	Test study 1, Test study 2	Ackerman syndrome
FC69F51C-7339-4C97-B53A-9580FE81C8B2	Whole blood	Test study 1	Ackerman syndrome
3A5B8C0-8554-4EBF-BC12-7184571CE47C	Whole blood	Test study 2	Ackerman syndrome

10 items found
Download as CSV



Clinical and phenotypic data

26

- Phenotype is **more important than ever** in the context of clinical outcome measures and next-generation sequencing analysis
- Requires transformation into a “computable” form
- Requires linkage from different sources (multiple registries, phenotypic databases...)

➡ **FAIR DATA**



NEUROLOGICAL

- Generalized hypotonia
- Seizures
- Ataxia
- Dystonia
- Chorea
- Specificity**
- Spinal dysraphism**
- Morphological abnormality of the central nervous system

Other (enter free text and choose among suggested ontology terms)

GROWTH PARAMETERS

Weight for age

- <-3rd
- >97th

Stature for age

- <-3rd
- >97th

Head circumference for age

- <-3rd
- >97th

- Hemispheropathy

Other (enter free text and choose among suggested ontology terms)

CARDIAC

- Defect in the atrial septum

Face of progression:

- Congenital onset
- Juvenile onset
- Embryonal onset
- Adult onset
- Neonatal onset
- Young adult onset
- Middle age onset
- Late onset

Comments:

No complications

Image / photo (optional):

Medical report (optional):



What is FAIR data?

27

Findable - (meta)data is uniquely and persistently identifiable. Should have basic machine readable descriptive metadata.

Accessible - data is reachable and accessible by humans and machines using standard formats and protocols.

Interoperable - (meta)data is machine readable and annotated with resolvable vocabularies/ontologies.

Reusable - (meta)data is sufficiently well-described to allow (semi)automated integration with other compatible data sources.

SCIENTIFIC DATA **IN PRESS**

The FAIR Guiding Principles for scientific data management and stewardship

Mark D. Wilkinson, Michel Dumontier, IJsbrand Jan Aalbersberg, Gabrielle Appleton, Myles Axton, Arie Baak, Niklas Blomberg, Jan-Willem Boiten, Luiz Bonino da Silva Santos, Philip E Boume, Jildau Bouwman, Anthony J Brookes, Tim Clark, Mercè Crosas, Ingrid Dillo, Olivier Dumon, Scott Edmunds, Chris T Evelo, Richard Finkers, Alejandra Gonzalez-Beltran, Alasdair J G Gray, Paul Groth, Carole Goble, Jeffrey S. Grethe, Jaap Heringa, Peter A.C. 't Hoen, Rob Hooft, Tobias Kuhn, Ruben Kok, Joost Kok, Scott J. Lusher, Maryann E. Martone, Albert Mons, Abel L. Packer, Bengt Persson, Philippe Rocca-Serra, Marco Roos, Rene van Schaik, Susanna-Assunta Sansone, Enk Schultes, Thierry Sengstag, Ted Slater, George Strawn, Morris A. Swertz, Mark Thompson, Johan van der Lei, Enk van Mulligen, Jan Velterop, Andra Waagmeester, Peter Wittenburg, Katherine Wolstencroft, Jun Zhao, and Barend Mons

Open data is about MORE THAN DISCLOSURE it must be Fair

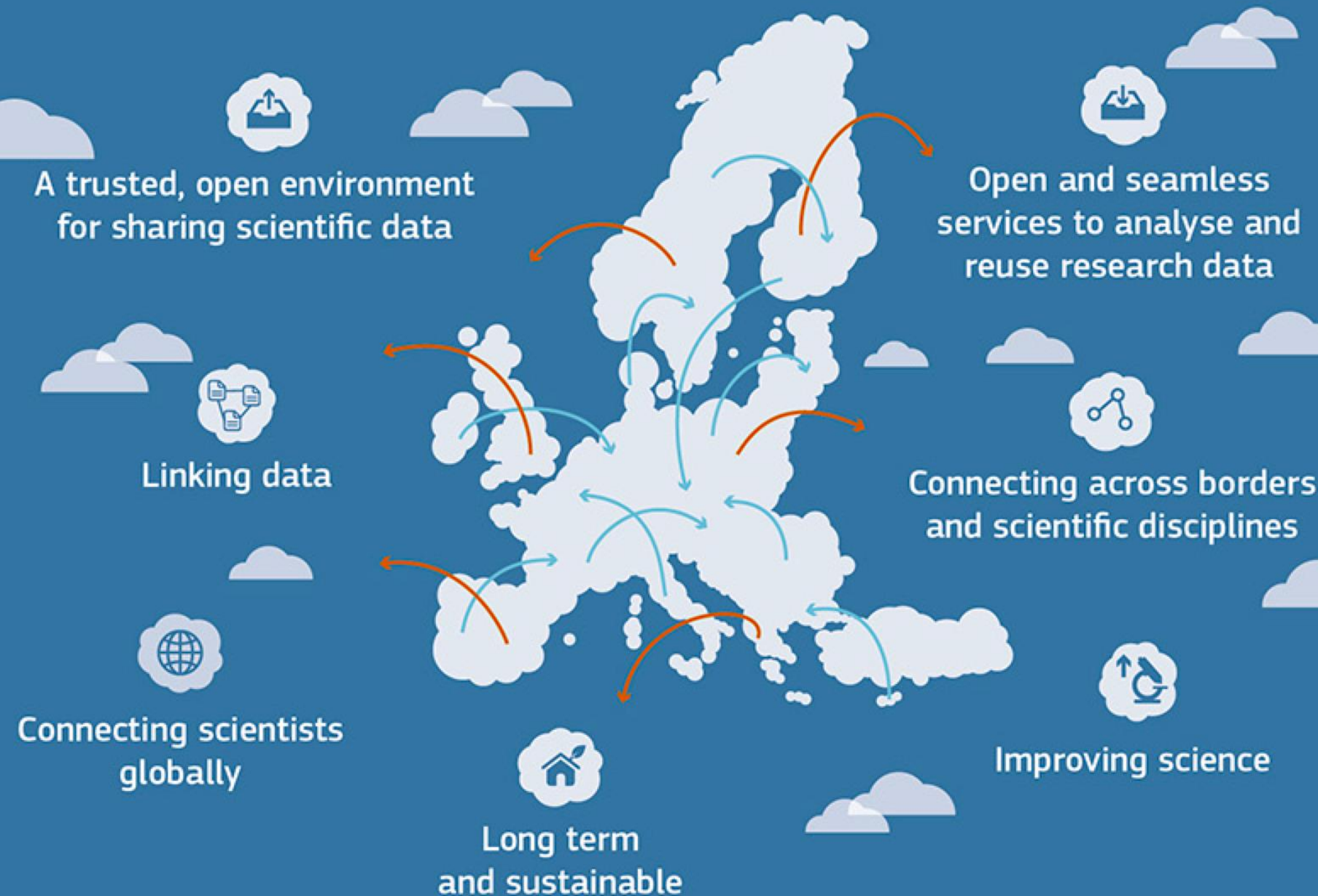
- Findable
- Accessible
- Interoperable
- Reusable

<http://www.nature.com/sdata/> nature publishing group

03 October 2017

EUROPEAN OPEN SCIENCE CLOUD

BRINGING TOGETHER CURRENT AND FUTURE DATA INFRASTRUCTURES





Prerequisites for sharing and reuse

- Standards and infrastructure for biosample sharing and reuse



- Standards and infrastructure for data sharing and reuse



- Patient involvement and consent and privacy issues





When consent is inadequate...

30

SARAH ZHANG SCIENCE 04.11.16 11:00 AM

nature
biotechnology

GENETIC SUPERHEROES WALK AMONG US, BUT STILL NO ONE

S

Attempted recontact of candidate resilient individuals

We were unable to recontact any of the 13 candidate resilient individuals identified in this study, often due to the absence of a recontact clause in the original informed consent forms used for the studies from which these individuals were identified.

Hanlin Zhou¹, Lifeng
Hardik Shah^{1,2}
Luo

The genetic superheroes mutations but not the disease

...or disease-causing mutations in afflicted
...to identify healthy individuals resilient to highly
...prehensive screen of 874 genes in 589,306 genomes led to the
...for 8 severe Mendelian conditions, with no reported clinical manifestation of
...demonstrate the promise of broadening genetic studies to systematically search for well
...ing the effects of rare, highly penetrant, deleterious mutations. They also indicate that incomplete
...Mendelian diseases is likely more common than previously believed. The identification of resilient individuals
...provide a first step toward uncovering protective genetic variants that could help elucidate the mechanisms of Mendelian
diseases and new therapeutic strategies.



Data sharing charter

31

EJHG Open

European Journal of Human Genetics (2015) 23, 721–728
© 2015 Macmillan Publishers Limited All rights reserved 1018-4813/15
www.nature.com/ejhg



POLICY

International Charter of principles for sharing bio-specimens and data



Deborah Mascalzoni^{*,1,2}, Edward S Dove³, Yaffa Rubinstein⁴, Hugh JS Dawkins^{5,6,7,8}, Anna Kole⁹, Pauline McCormack¹⁰, Simon Woods¹⁰, Olaf Riess¹¹, Franz Schaefer^{12,13}, Hanns Lochmüller¹⁰, Bartha M Knoppers³ and Mats Hansson¹

- Ethical foundations for data and bio-specimen sharing
- Material and Data Transfer Agreement to ensure uniformity of access across projects and countries

Room 106 from 16:00: How to Promote Data Sharing in Rare Disease while Protecting Privacy

Mats Hansson, Uppsala University, Sweden



The General Data Protection Regulation

32

- GDPR is a regulation under EU law, with direct applicability. It will enter into force on 25 May 2018.
- The GDPR provides that the free movement of personal data within the European Union shall be neither restricted nor prohibited for reasons connected with the protection of natural persons with regard to the processing of personal data.
- The GDPR allows Member States to maintain or introduce further conditions, including limitations, with regard to the processing of genetic data, biometric data or data concerning health. However, this should not hamper the free flow of personal data within the Union.



How do we address this?

33

- Large-scale initiative to create a code of conduct for research data sharing in compliance with the GDPR



NATURE | COLUMN: WORLD VIEW

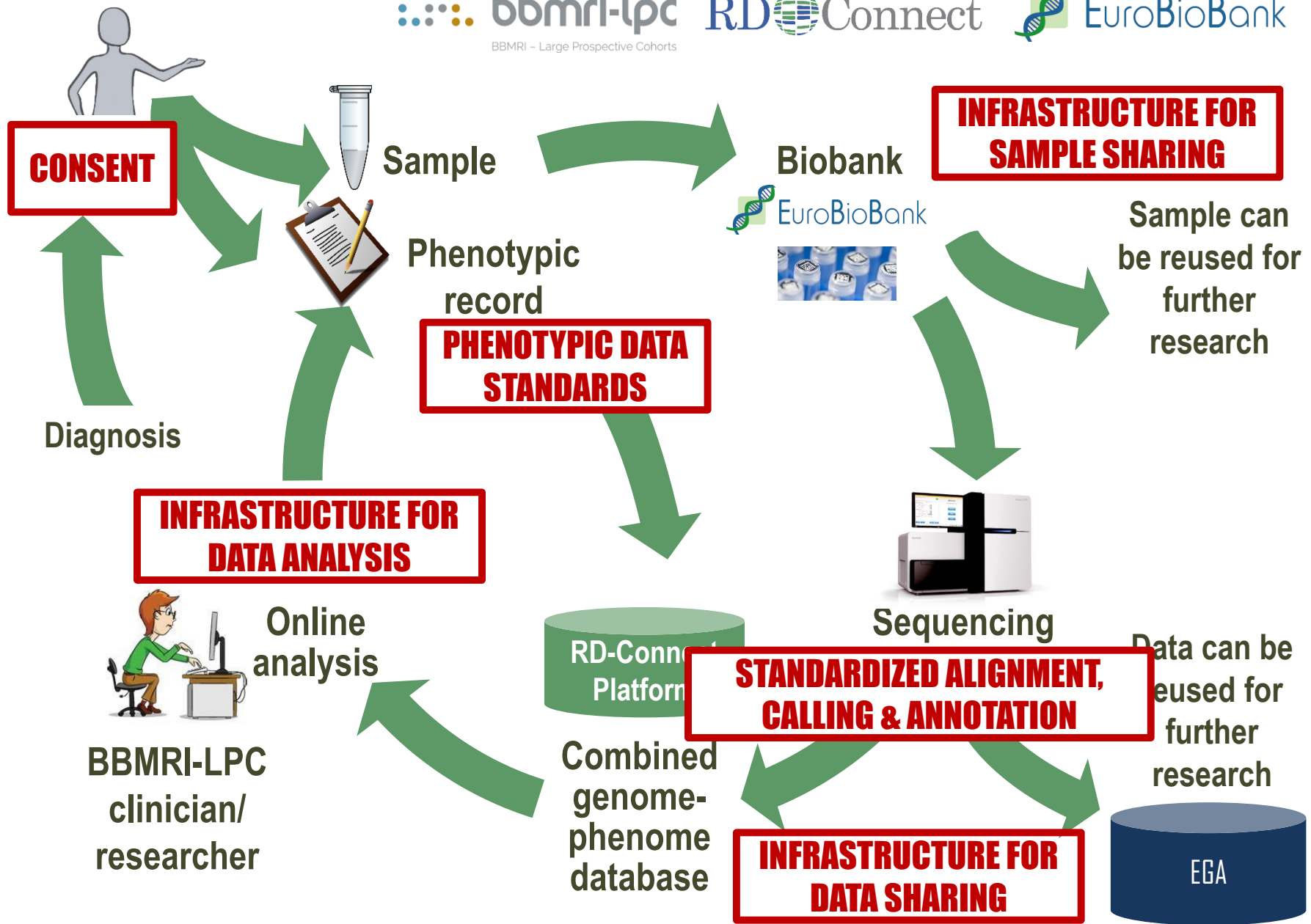


BBMRI-ERIC

We must urgently clarify data-sharing rules

Scientists have worked hard to ensure that Europe's new data laws do not harm science, but one last push is needed, says **Jan-Eric Litton**.

A paradigm for best practice in data sharing in genomic studies?





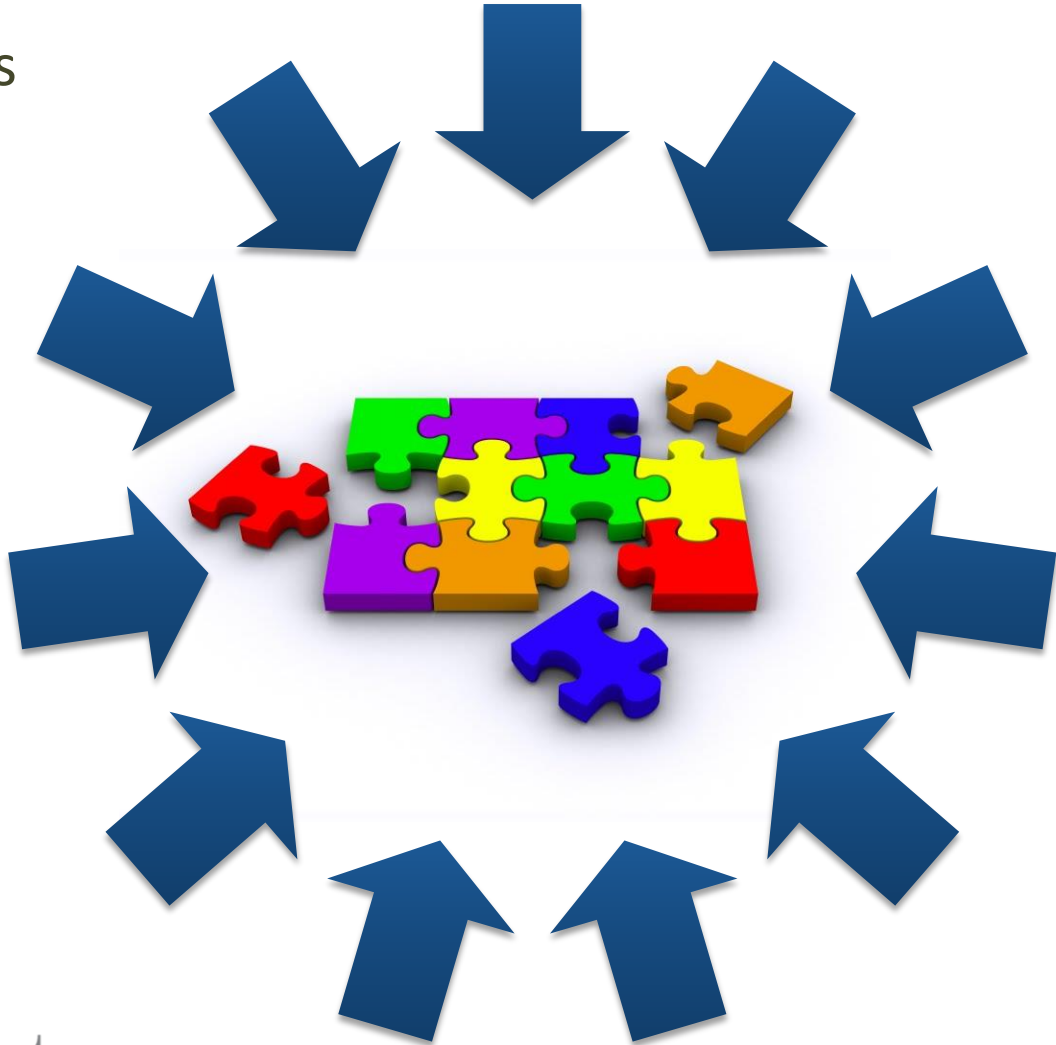
- A mechanism for implementing cross-border healthcare established by the European Commission under Directive 2011/24/EU of 9 March 2011
- Networks of healthcare providers that have been recognised by their own member state as centres of expertise for a particular disease area
- *“European reference networks for rare diseases should serve as research and knowledge centres, updating and contributing to the latest scientific findings, treating patients from other Member States and ensuring the availability of subsequent treatment facilities where necessary.”*
- December 2016: networks approved under 23 different disease domains (24 expected soon)
- Formal kickoff March 2017





ERN data in RD-Connect

RD-Connect has agreed with ERN coordinators to include data from all ERNs (genomic, biosample, phenotypic/registry data)



Supports ERNs in their research and diagnostic goals

Enables data sharing for research



Scientists are invited to

37

- ❑ Deposit WES/WGS/panel raw data from sequencing projects for integration into the RD-Connect platform
- ❑ Request an account to look at genomic data in the platform
- ❑ Use the RD-Connect platform for gene discovery
- ❑ Let our developers know if you want the functionality of the platform improved/adapted for your research
- ❑ Add a registry/biobank to the RD-Connect catalogue (ID card)
- ❑ Participate in multi-omics user groups, co-develop the functionality that you are interested in (use cases)
- ❑ Make sure future projects are fit for sharing (consent)
- ❑ Use the RD-Connect impact and dissemination channels



Clinicians are invited to...

38

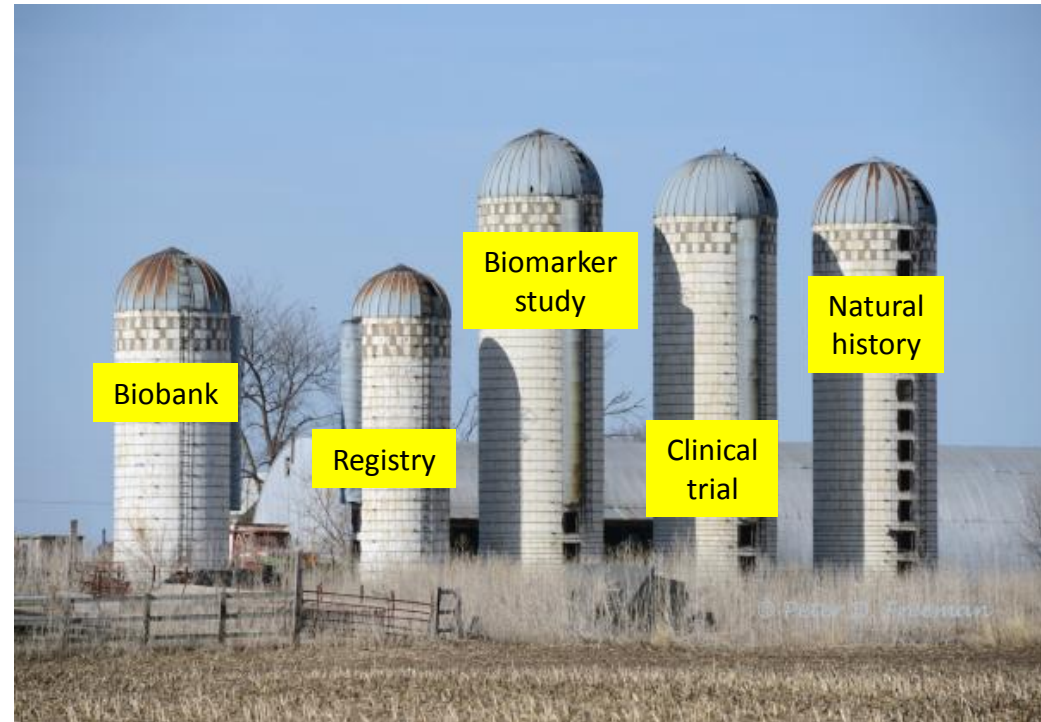
- Use appropriate consent for NGS and data sharing
- Use standardized ontologies to describe a patient's phenotype
- Collect samples from patients in a standardized way and deposit them in appropriate biobanks
- Get involved with the interpretation of genome/exome/panel results (genome rounds)
- Feed back results to your patients and point them towards lay-friendly information, encourage their participation
- Include patients in other research (registries, cohorts, natural history, clinical trials, etc)
- Use the RD-Connect impact and dissemination channels



The bottom line: data sharing benefits research

39

- Data sharing enhances research and data analysis
- Gene and modifier discovery
- Samples for further research
- Genotype-phenotype correlation
- Biomarkers, therapeutic targets...





Learn more in Berlin

<http://meeting.rd-neuromics.eu>

40

Joint meeting and outreach day for RD-Connect
NeurOmics, EURenOmics and E-RARE

- RD-Connect: 1-2 May
- Outreach day: 3 May
- NeurOmics and EURenOmics: 4-5 May

RD  Connect

Neur  Omics

EURen  Omics





Questions/feedback

41



Coordinator:

Hanns Lochmüller – hanns.lochmuller@ncl.ac.uk



Project manager:

Libby Wood – elizabeth.wood2@ncl.ac.uk



Data helpdesk – personalised support!

John Dawson – john.dawson@ncl.ac.uk



Technical questions:

Sergi Beltran – sergi.beltran@cnag.crg.eu



Research questions:

Rachel Thompson – rachel.thompson@ncl.ac.uk



Thanks to:

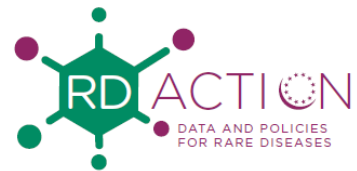
The Newcastle JWMDRC team

All our international collaborators

The IRDiRC scientific committee chairs

The interdisciplinary committee

The IRDiRC secretariat



@ConnectRD

@RareDiseasesEU

