



#### WHY FAIR FOR RARE DISEASES?

SPEAKER: MARCO ROOS



**RD-Connect Community Webinars** 



#### **Lieze Thielemans**





### Medical student Lieze Thielemans (Imperial College, London)





#### Radboudumc

### Preliminary evidence of unexpected haemolysis in patients with hereditary haemorrhagic telangiectasia:

### Development of FAIR Data Stewardship for Rare Vascular Diseases in Europe

Lieze Thielemans

Supervised by: Prof. Claire Shovlin, Prof. Leo Shultze Kool and Dr Marco Roos

## Hereditary haemorrhagic telangiectasia & Iron deficiency anaemia



### Possible mechanisms

1) Excessive bleeding

2) Decreased absorption

3) Destruction of iron stores

### Null hypothesis

"Haemolysis does **not** occur in the HHT cohort, and that there is **no** association with iron infusions or blood transfusions to treat iron deficiency"

### What Lieze did and could not do

Manually extracted data from medical records

- $\rightarrow$  big effort for small data set
- → choice of statistics driven by this big effort, assumptiondriven, not data driven
- → impossible to compare results with data from other patients

### Conclusion

### Local data and other people's data not readily available for analysis

### Multiply this with all researchers investigating biomedical data













### Share data, put data together







### Share data, put data together Analyse data, answer questions





### Aim: Answer questions efficiently and correctly

photos: MDs, patient representatives, local data stewards involved in FAIRification pilots (DMD, VASCERN, BOND)





- "What are the differences in age of loss of ambulation as a result of steroid use in DMD patients across EU countries?"
- "How do patients with the HHT phenotype respond to radiotherapy in other hospitals; what associations with iron infusions do other patients with iron deficiencies have"
- "What is the current information about the course and treatment of vascular malformations and hemangiome in all registries?"
- "What number of fractures is the most common in patients carrying mutations on the COL1A1 gene across Europe?"
- "What are the associations between genetic variant, disease severity and phenotypes in Rett syndrome?"
- "Where can I obtain tissue samples for transcriptome analysis from donors with similar symptoms as my patients?"





### Why is this not easy?





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# The biggest bottleneck for data sharing







### is the need to share data







### the *perceived* need to *physically* share data







Data sharing guidelines, embargo's,
 Data access forms, etc.

Common data element debates

Aligning policies between institutes and across borders

Data warehousing attempts

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### Absolute need to enable analysis over resources





- Sparse
- Highly distributed
- Heterogeneous
- Different format
- Poorly interoperable
- Sensitive
- .....



### A different approach

#### The Personal Health Train paradigm







### If sharing is hard...







### Don't share











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#### (under well-defined conditions)





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### Interoperable







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### Reusable







### for humans and computers



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### Don't share, be FAIR at the source







### Dekker's example

Better prediction of treatment prognosis



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### Australia **Rethink palliative treatments in good prognosis patients**

Netherlands **Rethink curative treatments in poor prognosis patients** 













Machine learning algorithm on data from multiple hospitals.... that were never shared and never put together!! RD@Connect elixir \*\*\*\*\*\*





#### **Demonstrator**



Where can I obtain **biosamples** of donors with **an abnormality in head or neck**?

In which **biobanks** can I find these samples?







- det number of biosamples from donors with a specific phenotype
- 🧈 Get number of persons with a specific phenotype
- Get number of biosamples from donors with a specific disease
- Get number of biosamples from donors with a specific phenotype and from a specific region
- 🛫 Get biosamples from donors with a specific phenotype and specific sampletypes
- 🚁 Get biosamples from donors with a specific disease and a specific karyotype
- → Get biosamples from donors with a specific disease, a specific karyotype and specific sampletypes
- 🧈 Get biosamples from donors with a specific disease, a specific karyotype, a specific breakpoint localization and a s
- Get diseases sharing phenotypes
- 🛫 Get biosamples from donors sharing phenotypes

Powered by : SCALEUS -- ID-Cards -- FAIRDataPoint



#### Step 1 > Retrieve:

- 🛫 Get number of biosamples from donors with a specific phenotype
- 🥏 Get number of persons with a specific phenotype
- tion for the second sec
- Get number of biosamples from donors with a specific phenotype and from a specific region
- 🖢 Get biosamples from donors with a specific phenotype and specific sampletypes
- t Get biosamples from donors with a specific disease and a specific karyotype
- Get biosamples from donors with a specific disease, a specific karyotype and specific sampletypes
- 🧈 Get biosamples from donors with a specific disease, a specific karyotype, a specific breakpoint localization and a s
- 🥏 Get diseases sharing phenotypes
- at biosamples from donors sharing phenotypes

# Step 2 > By which value? Region type e.g. Paternopoli Phenotype type e.g. Wide mouth



Step 1 > Retrieve:

- 🛫 Get number of biosamples from donors with a specific phenotype
- Get number of persons with a specific phenotype
- 捷 Get number of biosamples from donors with a specific disease
- 🥩 Get number of biosamples from donors with a specific phenotype and from a specific region
- 🧈 Get biosamples from donors with a specific phenotype and specific sampletypes
- 🛃 Get biosamples from donors with a specific disease and a specific karyotype
- 捷 Get biosamples from donors with a specific disease, a specific karyotype and specific sampletypes
- 🧈 Get biosamples from donors with a specific disease, a specific karyotype, a specific breakpoint localization and a s
- 🬛 Get diseases sharing phenotypes
- 🬛 Get biosamples from donors sharing phenotypes

Step 2 > By which value?		
Region	type	Pi v
		Pistoia
Phenotype	type	Pietrasanta



Step 1 > Retrieve: Get number of biosamples from donors with a specific phenotype Get number of persons with a specific phenotype Get number of biosamples from donors with a specific disease Get number of biosamples from donors with a specific phenotype and from a specific region Get biosamples from donors with a specific phenotype and specific sampletypes Get biosamples from donors with a specific disease and a specific karyotype Get biosamples from donors with a specific disease, a specific karyotype and Wide mouth Get biosamples from donors with a specific disease, a specific karyotype, a sp 1 Get diseases sharing phenotypes Short neck Get biosamples from donors sharing phenotypes Seizures Hypertelorism Anteverted nares Step 2 > By which value? Abnormality of head or neck Abnormality of the face Region type Phenotypic abnormality e.g. Wide mouth ¥. Phenotype type


#### Linked Data Demonstrator

#### Step 1 > Retrieve: Get number of biosamples from donors with a specific phenotype Get number of persons with a specific phenotype Get number of biosamples from donors with a specific disease Get number of biosamples from donors with a specific phenotype and from a specific region Get biosamples from donors with a specific phenotype and specific sampletypes Get biosamples from donors with a specific disease, a specific karyotype Get biosamples from donors with a specific disease, a specific karyotype and specific sampletypes Get biosamples from donors with a specific disease, a specific karyotype, a specific breakpoint localization and a s Get diseases sharing phenotypes

Get biosamples from donors sharing phenotypes





Process

numberOfSamples	phenotype	disease	biobank	registry	region
5	Downslanted palpebral fissures	Ring chromosome 14	Galliera Genetic Bank	Ring14 Clinical database	Pistoia
5	Anteverted nares	Ring chromosome 14	Galliera Genetic Bank	Ring14 Clinical database	Pistoia
1	Mandibular prognathia	Angelman syndrome	Galliera Genetic Bank	Tuscany registry of congenital defects	Pistoia
3	Depressed nasal bridge	Ataxia-telangiectasia	Biobank of the Institute of Rare Diseases Research/Institute of Health Carlos III (IIER-ISCIII)	CoF-AT study: a French cohort on ataxia-telangiectasia	Pistoia
5	Depressed nasal bridge	Ring chromosome 14	Galliera Genetic Bank	Ring14 Clinical database	Pistoia
2	Anteverted nares	Ataxia-telangiectasia	Biobank of the Institute of Rare Diseases Research/Institute of Health Carlos III (IIER-ISCIII)	CoF-AT study: a French cohort on ataxia-telangiectasia	Pistoia



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Rare developmental defect during emb	-Rare developmental defect during emb Show siblings						
Chromosomal anomaly		E (exact mapping (the terms and the concepts are equivalent)) OMIM:616606 NTBT (narrower term maps to a broader					
-Autosomal monosomy		term) ICD-10:Q93.2					
Ring chromosome		Attributed ICD-10:Q93.2 E (exact mapping (the terms and the concepts are equivalent))					
-Rare genetic disease		UMLS:C2930916					
-Chromosomal anomaly		hasDbXref					
-Autosomal anomaly		MeSH:C535487, UMLS:C2930916,					



Process

#### Step 3 > Result:

numberOfSamples	phenotype	disease	biobank	registry	region
5	Downslanted palpebral fissures	Ring chromosome 14	Galliera Genetic Bank	Ring14 Clinical database	Pistoia
5	Anteverted nares	Ring chromosome 14	Galliera Genetic Bank	Ring14 Clinical database	Pistoia
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Class Hierarchy				
Thing + <u>Phenotype</u> + <u>abnormal phenotype</u> + <u>Phenotypic abnormality</u>				





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# Personal Health Train video:

## https://youtu.be/mktAtHmy-FM





# **Ecosystem of communicating FAIR data stations**





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## **FAIR data station**

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Contains data at the source

not limited to a common or minimal set

- F: Exposes **description** to be findable
- A: Controls access
- I: Content is **prepared for** *analysis across FAIR data stations*
- R: Content is **richly described** for efficient and correct *reuse*











Rett syndrome



DMD pilot LUMC (Leiden)



DMD pilot UMCL (Ljubljana)



Hevas











VASCA CDEs





Rett syndrome



LUMC DMD







LUMC DMD



Hevas



Open PHACTS



Rizzoli pilot



C RDF Platform

































## **FAIR data station**









Your FAIR data station



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# Machine readable?

#### or how do we help computers to help us?







#### What is 'machine readable'



Mr Spock Famous Star Trek character 台





#### What is 'machine readable'



**Computers are like Baby Spocks** 

- know nothing
- can learn a lot
- everything has to be 100% explicit, logical and unambiguous









## Rare disease data linkage plan





#### **FAIRification process**







# Making data machine readable









# Making data machine readable

sources Research





Keywords:	Search terms		
Class: Epileptic spasms			
Term IRI: <u>http://purl.obolibrary.org/obo/HP_00110</u> Definition: A sudden flexion, extension or mixed extension myoclonic movement but not as sustained as a tonic seiz Annotations	297 on-flexion of predominantly proximal and truncal muscles which is usually more sustained than a rure [database_cross_reference: HPO;jalbers][database_cross_reference: HPO;jalbers]		
database_cross_reference: UMLS:C0037769; UMLS:C16     has_exact_synonym: Salaam convulsions; Salaam seizur     has_obo_namespace: human_phenotype     has_related_synonym: West syndrome     http://www.geneontology.org/formats/obolnOwl#create     formats/obolnOwl#create     formation of infacy and childhood known as West Syndrome. West S     demonstrated by electroencephalography).  Class Hierarchy      thig     * <u>Phenotype     * abnormal phenotype     * Abnormality.oft     * Abnormality.oft </u>	527366; SNOMEDCT_US:28055006; MSH:D013036 res res res res res res res res	Machine readable	Human readable

human phenotype ontology











**Rare disease data stewards** 

FAIR software engineers

# LUMC FAIR data stewardship





LUMC FAIR data stewards

FAIR software engineers

LUMC librarians and Data Managers





"Now! *That* should clear up a few things around here!"

#### FAIR is

- efficient and correct computer
   analysis across rare disease data
   sources
- being clear & explicit about what data elements mean
- encoding data with a globally understood computer language







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# TH ٢N ~

"Now! *That* should clear up a few things around here!"

#### FAIR is

making Baby Spock happy





# Support for FAIR





# Adopting FAIR principles



\* Contact: fair-rd-info@elixir-europe.org or the RD-Connect community contact

![](_page_70_Picture_0.jpeg)

# FAIR project blueprint

Tasks

	Task	Period (months)	Associated Milestone Deliverable	Comments
Start of preparation phase	Define driving research questions and target data for FAIRification (use case)	1	M1	
	Technical assessment of requirements for the BYOD	1-2	M2	
	Select BYOD experts	3	M2	<disease d=""> experts, <disease D&gt; database experts, FAIR data experts</disease </disease>
	Prepare minimal reference ontology for BYOD	2-4	M2	
End of preparation phase	BYOD <disease d=""> data owners and FAIR data experts</disease>	4	М3	
Start of implementa tion phase	Technical assessment of requirements for implementing a FAIR Data Point for the <disease d=""> resource</disease>	4-5	M4, D1	
	Develop and test <disease D≻ FAIR Data Point</disease 	4-11	M4, D1	Agile development including pre-releases of FDPs for testing
	Design and execute data analysis for testing FAIR Data Points as substrate for knowledge discovery on <disease d=""> (proof-of-principle)</disease>	9-11	М5	Executed by collaborating research scientists
End of	Release documented	11-12	D1	By <disease d=""></disease>

## https://goo.gl/bJqH1d

RD@Connect

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![](_page_71_Picture_0.jpeg)

# Supporting infrastructure 1: you!

![](_page_71_Picture_2.jpeg)

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![](_page_71_Figure_3.jpeg)

![](_page_71_Picture_4.jpeg)

![](_page_71_Picture_5.jpeg)

![](_page_71_Picture_6.jpeg)

![](_page_71_Picture_7.jpeg)

#### CROSS-BORDER HEALTHCARE DIRECTIVE

ERNs are being set up under the 2011 Directive on patients' rights in cross-border healthcare. This Directive also makes it easier for patients to access information on healthcare and thus increase their treatment options.

![](_page_71_Picture_10.jpeg)

![](_page_71_Picture_11.jpeg)

![](_page_71_Picture_12.jpeg)

![](_page_71_Picture_13.jpeg)


## Infrastructure 2: collaborating infrastructures







## Infrastructure 3: ELIXIR platforms, ELIXIR nodes

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Consultancy: align with cross-national standards

National nodes are service providers Example: FAIR services by NL





RD

#### Infrastructure 4: FAIR data services by tools and people (DTL, UPM, ISS, LUMC, ELIXIR-NL/UK/SL, BBMRI, RD-Connect, FAIR-dICT, ...)



### Infrastructure 4: organise our own FAIR service ecosystem







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**Foster** and strategically oversee the expansion of the adoption of FAIR data principles by the RD community towards a critical mass of FAIR data, providing a home for stakeholders seeking advice on FAIR data stewardship and guiding the transition of the rare disease community towards understanding, embracing and refining the FAIR Principles and Goals.





#### Organisation











## Future (EJP/ELIXIR/...)

### □ Address FAIR more fully

- Metadata
- FAIR metrics
- Automating ELSI
- Filling gaps for analytics
- Scaling up
  - Data steward network
  - 'more FAIR' guidelines (Annika Jacobsen *et al.*)
  - **\square** Routine tools  $\rightarrow$  FAIR data generating tools (e.g. registry software)

□ Approach: real-life cases in interdisciplinary collaboration







# SAVE THE DATE

# International Summer School on Rare Disease Registries and FAIRification of Data

Mid/End of September 2019

Istituto Superiore di Sanità – Rome (Italy)

#### Thank you







https://rd-connect.eu/about-rd-connect/become-member/



L U M C FAIR data engineering team

Rajaram Kaliyaperumal, Kees Burger, Nuno Nunes, Shamanou van Leeuwen, Mark Thompson, Luiz Bonino, Mark Wilkinson, Michel Dumontier



#### **RDs GO FAIR seed group:**

Claudio Carta, Ronald Cornet, David van Enckevort, Marc Hanauer, Ian Harrow, Victoria Hedley, Gulcin Gumus, Dipak Kalra, Veronica Popa, Ana Rath, Marco Roos, Yaffa Rubinstein, Gary Saunders, Rachel Thompson, Mark Wilkinson

#### Training material:

ELIXIR, FAIR-dICT, DTL, Claudio Carta, Mascha Jansen, Celia van Gelder, Erik Schultes, Albert Mons

Use case collaborators Rachel Thompson, Libby Wood, Claudio Carta, Marco Crimi, Estrella Gomes, Marina Mordenti, Luca Sangiorgi, David van Enckevort, Fleur Kelpin, Claire Shovlin, Lieze Thielemans, Hevas, Leo Schultze Kool, Carine van Vleuten, Erik Niks, VSOP, Annika Jacobsen, Freddie Ehrhart, Andra Waagmeester; Heimo Muller, Robert Reihs; Pedro Sernadella, Jose Oliveira; Marc Hanauer, Ana Rath; Roxana Merino; Matthias Brochausen; Developers of Castor, RDRF, OSSE, MolGenis; participants Bring Your Own data workshops and patient representatives, rare disease linked data and ontology task force **ELIXIR**: Chris Evelo and team (Maastricht), Carole Goble and team (Manchester), Ivo Gut and team (CNAG), Helen Parkinson and team (EBI), Olivier Poch and team (Strassbourg), Orphanet, Brane Leskosek and team (Ljubljana)

The BioSemantics group and the Human Genetics Department LUMC