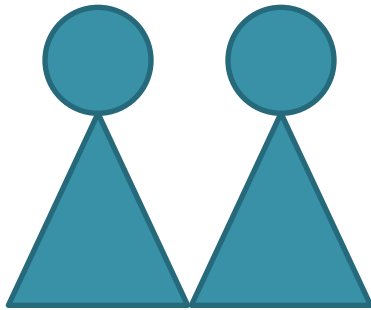
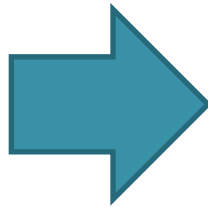


# Initiatives to Speed up Data Sharing

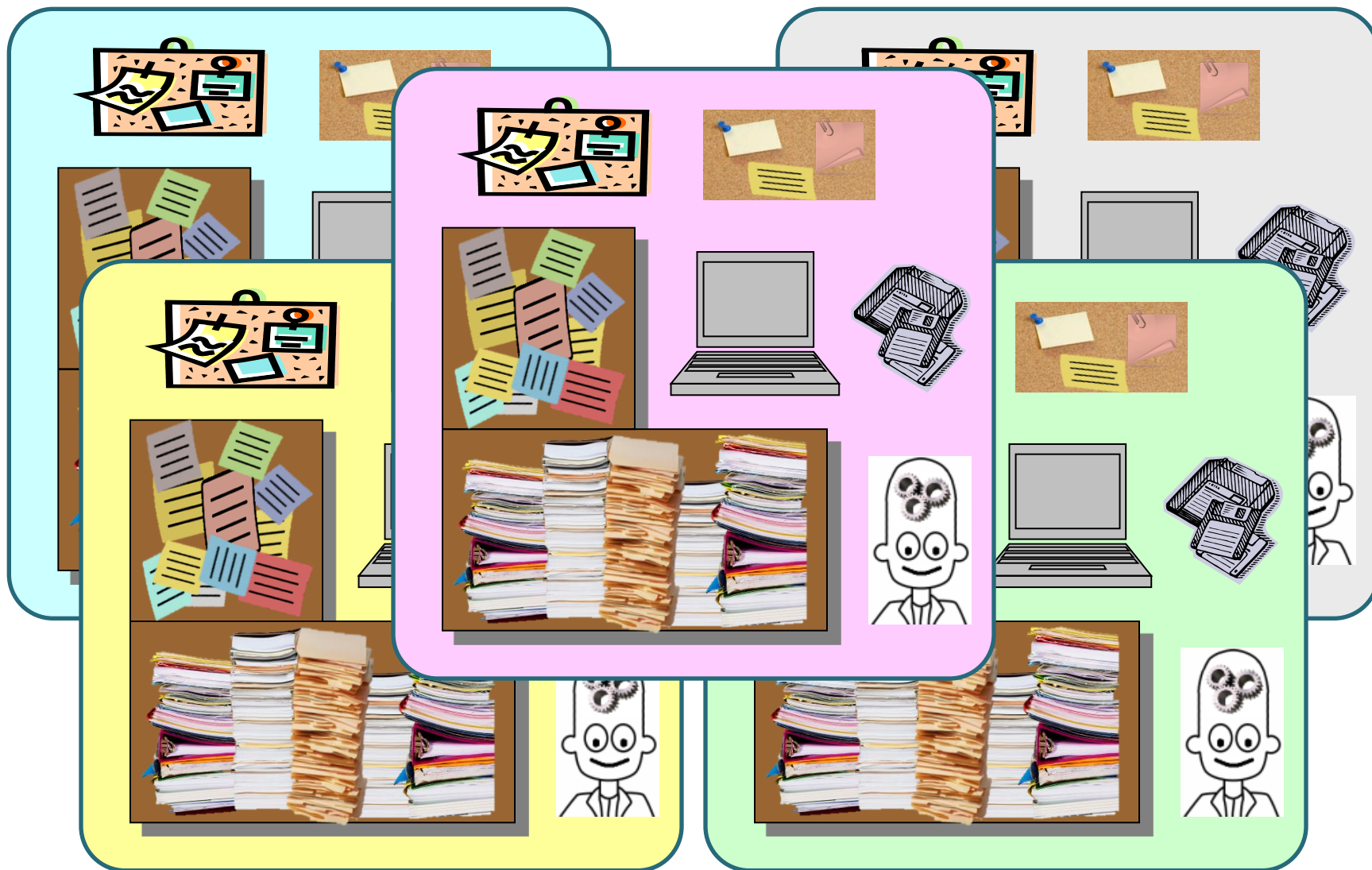
- Anthony Brookes
- ICORD 2014, Ede, Netherlands
- 9 October 2014



**Single Team**



**Data**

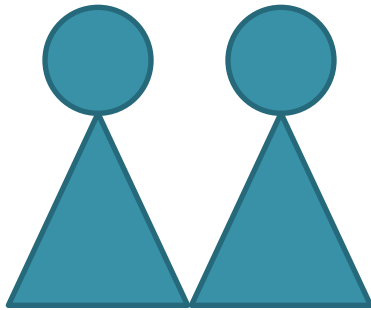


## Consortia / Networks

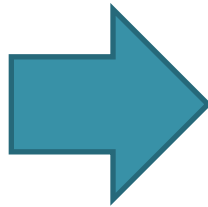


**IRDiRC**

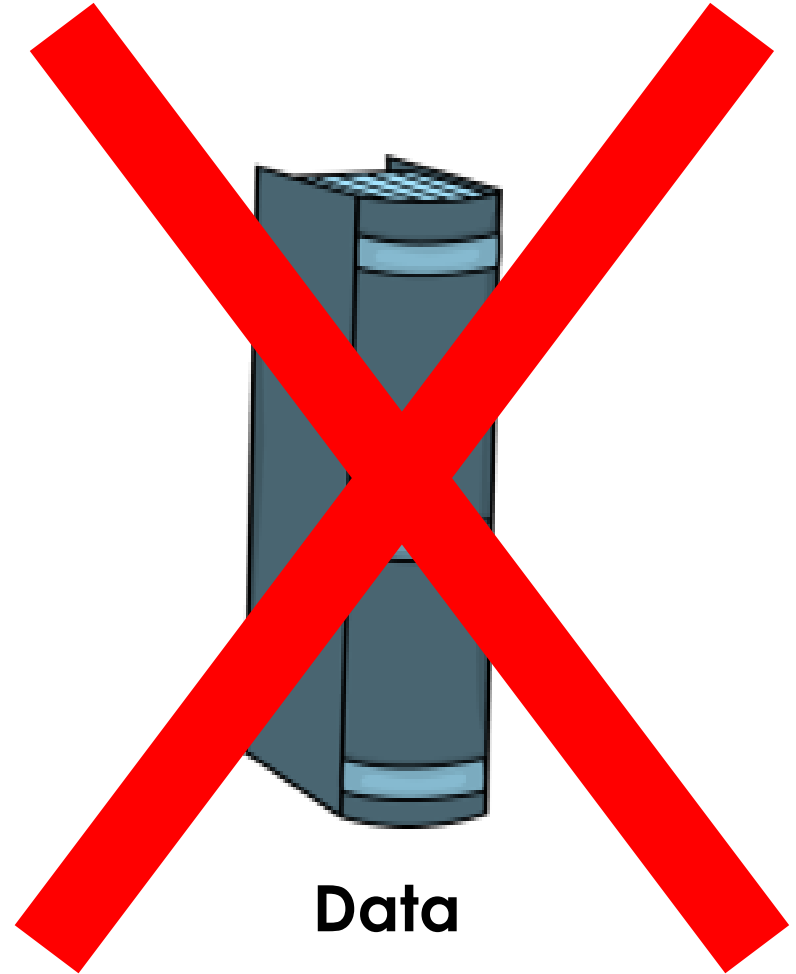
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**Single Team**



**Data**



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**Federated**



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# Rationale

- ▶ Research & healthcare produces an enormous amount of data
- ▶ These data have significant 'value' – unless shared we cannot develop optimum knowledge, diagnostics and treatments, while ensuring efficient utilization of scarce resources
- ▶ Datasets include data and metadata relating to phenotypes, genomic variants, other 'omic' data, natural histories, clinical trial data, etc
- ▶ Resources include patient and family material (extracted DNA, cell lines, pathological samples), technical protocols, informatics infrastructure, and analysis tools

# Barriers to Data Sharing

- ▶ Technical and Financial issues
  - ↪ Storing, transferring, securing terabytes
  - ↪ Providing logistics for sharing data
- ▶ Ethical and Legal issues
  - ↪ Absent/Unclear policies for sharing
  - ↪ Bridging public and private networks
  - ↪ Different national rules/policies
- ▶ Cultural issues
  - ↪ Reluctance to share valuable asset (researchers, clinicians/institutions)

**CAN NOT**

**MUST NOT**

**WILL NOT**



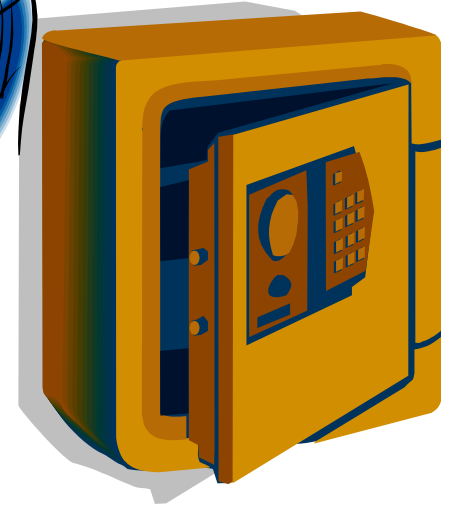


# Openly Shared



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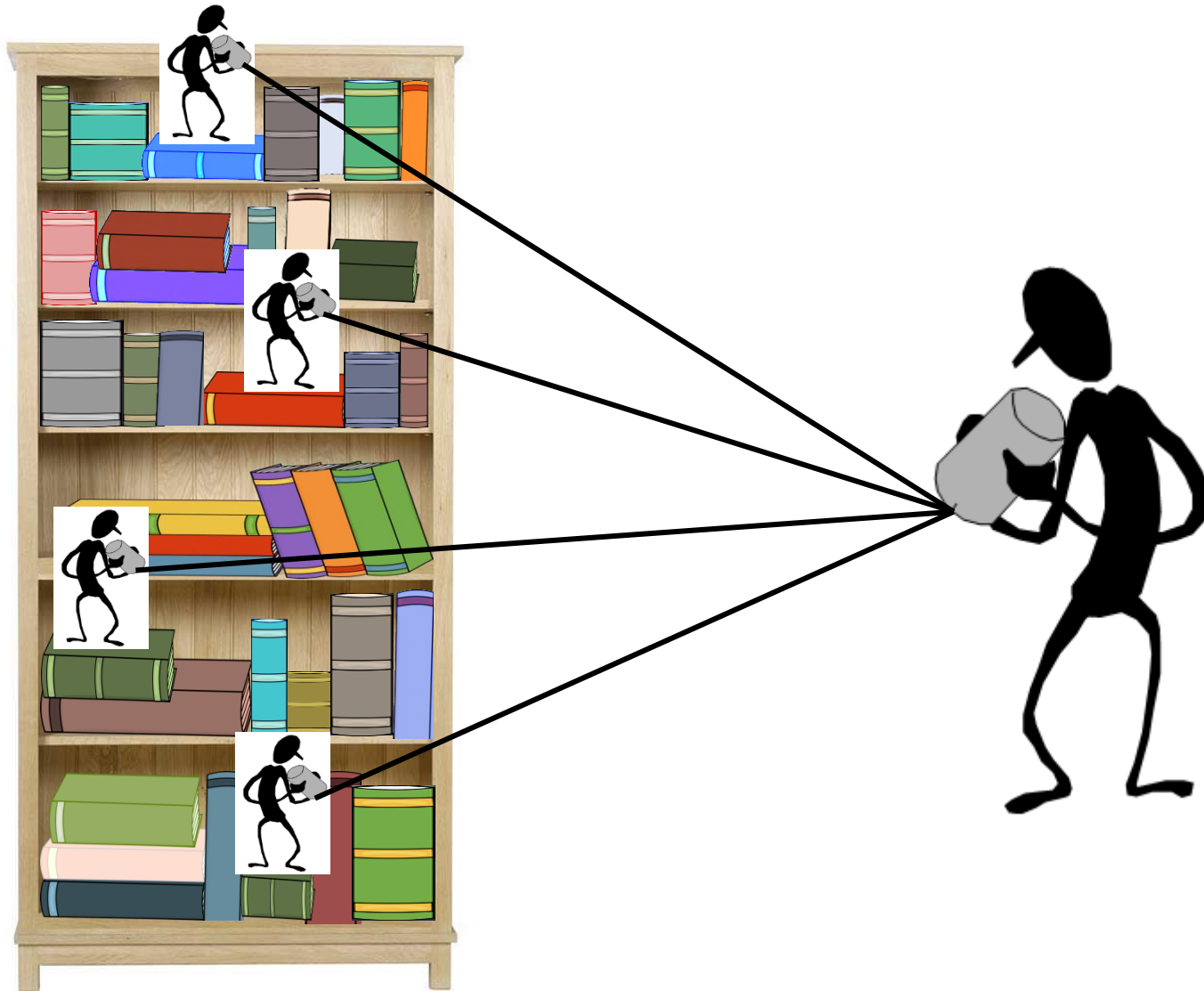
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# Controlled Access

**Open Access** and **Controlled Access** approaches  
are important....

....but **other options** exist, which are  
not only useful but arguably **essential**



## Remote Data Analysis



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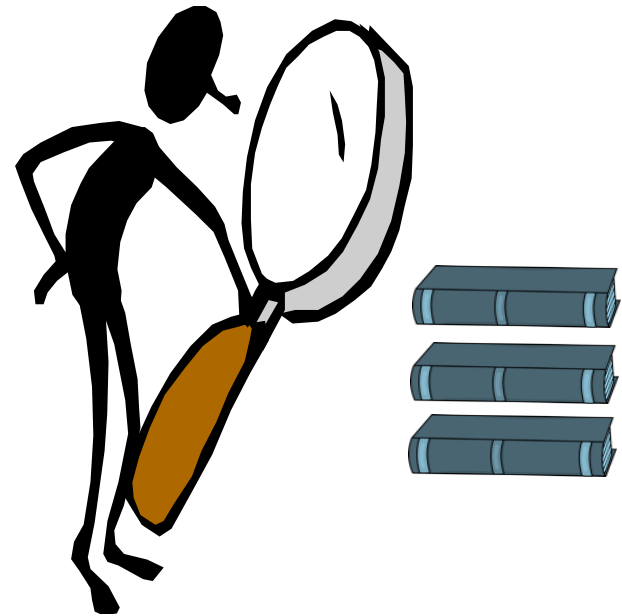
**Focus on Knowledge & Visualisation**



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**Find the Data (catalog approaches)**



## Data Discovery



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# IRDiRC principles (1)

## Sharing and collaborative work

- ▶ Informed consent based procedures
- ▶ Rapid release of data
- ▶ Interoperability of data
- ▶ Using maximally open access databases

## Scientific standards, requirements and regulations

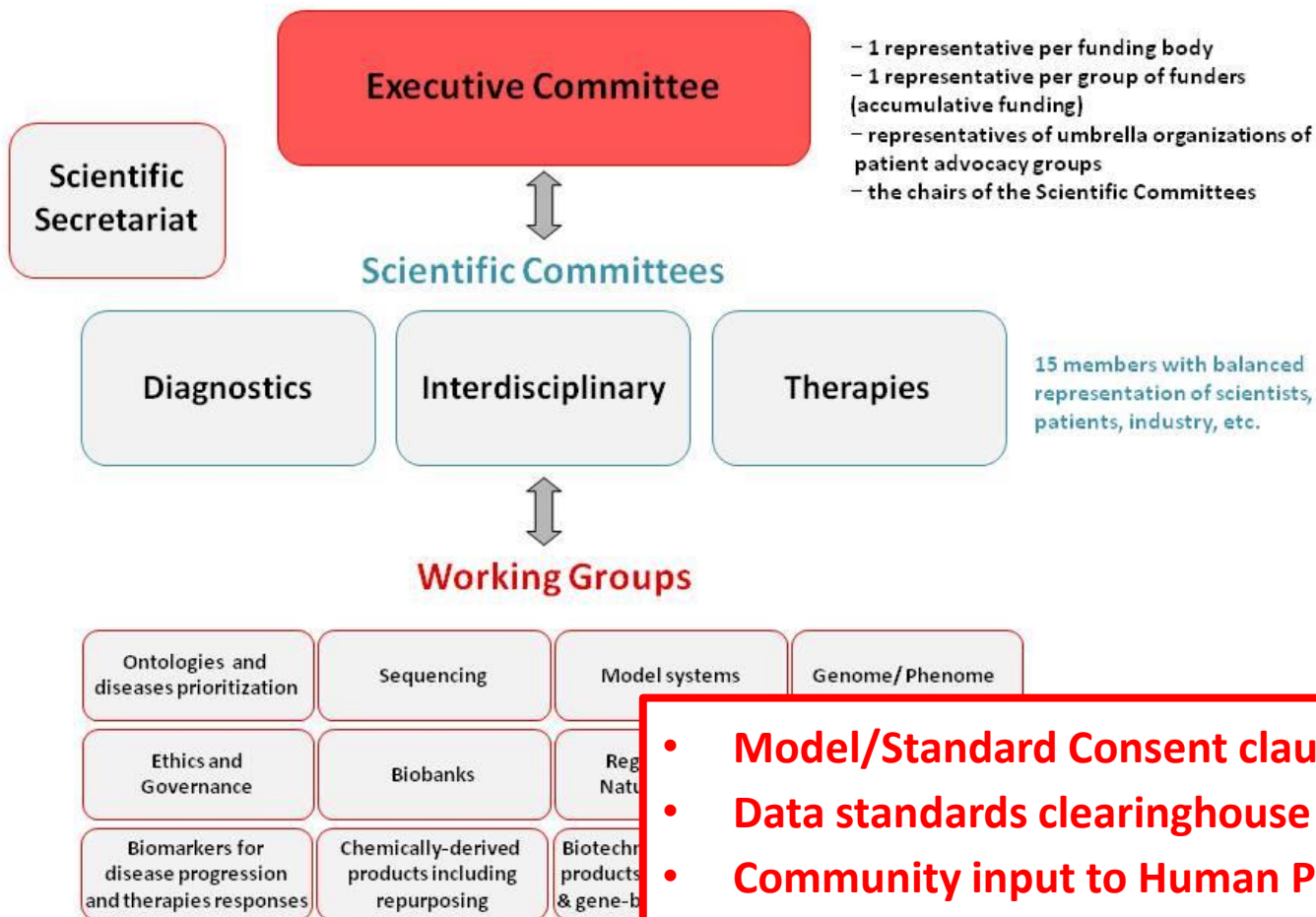
- ▶ Projects should adhere to existing standards
- ▶ Standard development - especially consents, metadata, minimal content, patient IDs, ontologies & validated biomarkers
- ▶ Upon sharing/publication, always cite utilised databases & biobanks



# IRDiRC principles (2)

## ► Guidelines & Policies:

- ↪ Data generated from research projects, including source data, should be deposited in appropriate open or controlled access public databases.
- ↪ Projects should adhere to standards endorsed by IRDiRC
- ↪ Data producers acknowledge their responsibilities to release data rapidly and to publish initial analyses in a timely manner.



- **Model/Standard Consent clauses**
- **Data standards clearinghouse**
- **Community input to Human Phenotype Ontology**
- **Matchmaker Exchange (v1.0 => v2.0)**
- **Minimum open data conventions**
- **Globally unique patient IDs**
- **Bio-resource metrics and impact system**
- **Population Controls Variant Resource**

# ClearingHouse project (1)

- ▶ Catalog: list of available data standards
  - ↪ In development – release in January 2015 on the IRDiRC website
- ▶ Dynamic: catalog with an added dimension
  - ↪ Contains a list of data standards currently available
  - ↪ Allows users to select the most appropriate data standards to apply
  - ↪ Allows standards submissions from users
  - ↪ Allows users to connect/collaborate on standards creation
  - ↪ Includes use cases and exemplar applications
  - ↪ Informs researchers about standards outside their specific RD fields

# ClearingHouse project (2)

- ▶ Five main fields of application
  - ↳ Standards in Genomics and other OMICS
  - ↳ Standards in Phenotyping
  - ↳ Standards in Outcome Measures for clinical trials
  - ↳ Standards in Human Data Registration
  - ↳ Open and controlled access databases to store data
- ▶ Align with other ongoing efforts
  - ↳ RD-Connect, Orphanet
  - ↳ PCORI, Comete
  - ↳ ELIXIR, BBMRI, GA4GH, Data FAIRport



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# Matchmaker Exchange (1)



In research and clinical settings, many RD patients are difficult to diagnose in isolation. Finding a similar (geno and/or pheno) patient elsewhere may provide sufficient evidence to identify the causative gene. 'Matchmaker Exchange' aims to enable those similar patient pairings to be identified via a standardized APIs and procedural conventions.

# Matchmaker Exchange (2)

## ▶ Tiered Informed Consent

- ↪ Explicit patient consent may not be needed, dependent on the potentially identifiable information made discoverable
- ↪ Subsequent sharing would need explicit informed consent

## ▶ Requirements & conventions

- ↪ Data provider and match requestor MUST provide contact details
- ↪ Recommended that searches and matches are logged

## ▶ ‘Data Submission’ API

- ↪ Requestor sends in their patient’s data, these data are retained for future matches, basis of match is not controllable or revealed

## ▶ ‘Data Query’ API

- ↪ Requestor sends in a question and thereby controls the basis of the match, with an option to deposit data to enable future matches



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# Café Variome (1)



*Share the 'existence' rather than the 'substance' of data*

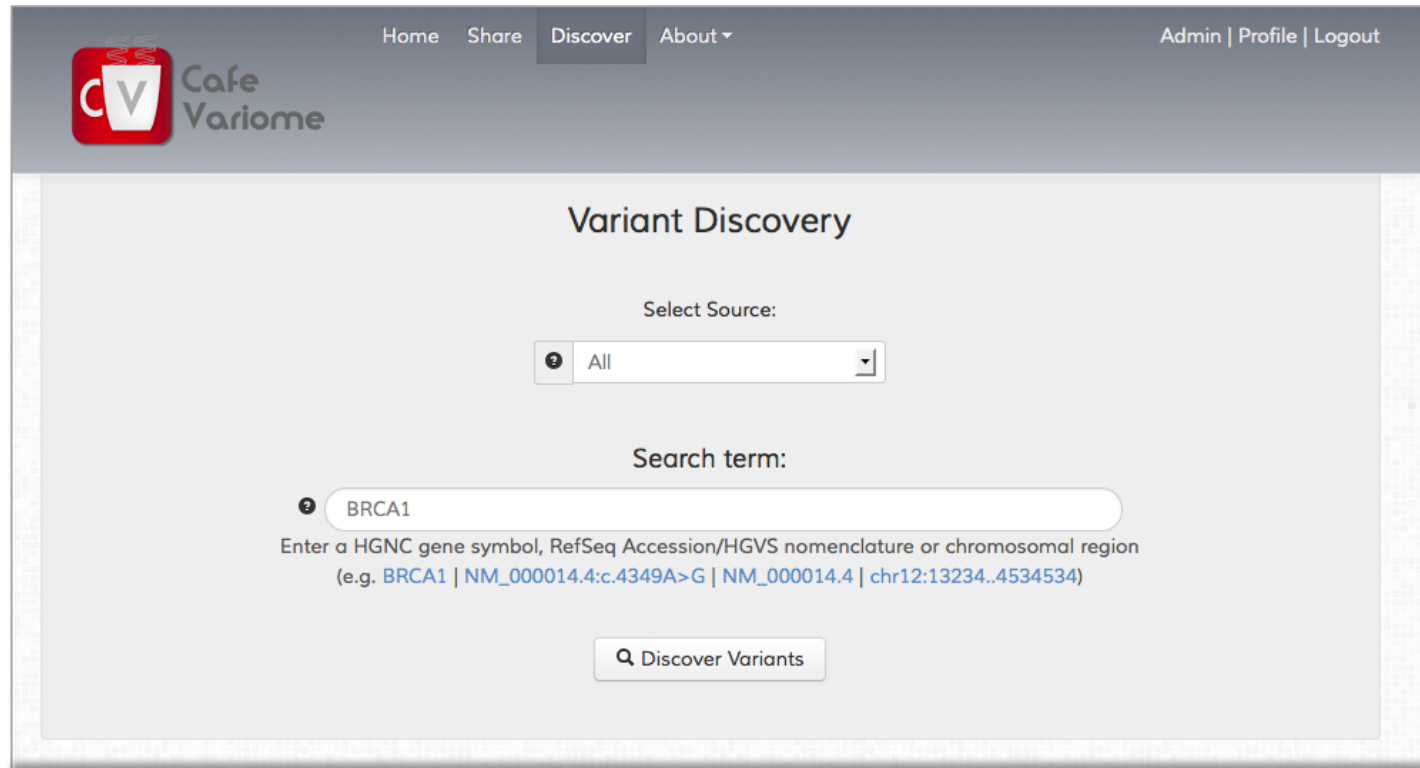
*This technology sits atop/alongside existing local DBs to bring the discoverability and connectivity, without replacing or altering the local solutions*



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# Café Variome (2)



The screenshot shows the Café Variome website interface. At the top, there is a navigation bar with links for Home, Share, Discover (highlighted), and About. On the right of the navigation bar are links for Admin, Profile, and Logout. The Café Variome logo is on the left. The main content area is titled "Variant Discovery". It features a "Select Source:" dropdown menu currently set to "All". Below this is a "Search term:" input field containing "BRCA1". A help icon (?) is to the left of the input field. Below the input field, there is a prompt: "Enter a HGNC gene symbol, RefSeq Accession/HGVS nomenclature or chromosomal region (e.g. BRCA1 | NM\_000014.4:c.4349A>G | NM\_000014.4 | chr12:13234..4534534)". At the bottom of the search area is a button labeled "Discover Variants" with a magnifying glass icon.

Home Share **Discover** About ▾ Admin | Profile | Logout

 Café Variome

## Variant Discovery

Select Source:

ⓘ All ▾

Search term:

ⓘ BRCA1

Enter a HGNC gene symbol, RefSeq Accession/HGVS nomenclature or chromosomal region  
(e.g. BRCA1 | NM\_000014.4:c.4349A>G | NM\_000014.4 | chr12:13234..4534534)

🔍 Discover Variants




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# Café Variome (3)

 **Café Variome**

Home | Share | **Discover** | About ▾

Admin | Profile | Logout

## Variant Discovery

Select Source:

2 All ▾

Search term:

2 BRCA1

Enter a HGNC gene symbol, RefSeq Accession/HGVS nomenclature or chromosomal region  
(e.g. [BRCA1](#) | [NM\\_000014.4:c.4349A>G](#) | [NM\\_000014.4](#) | [chr12:13234..4534534](#))

🔍 Discover Variants

Source	Open Access		Restricted Access		Linked Access	
<a href="#">1000 Genomes Project</a>	0	✖	0	✖	0	✖
<a href="#">dbSNP</a>	1401	📄	0	✖	0	✖
<a href="#">Diagnostic Variants</a>	0	✖	11	📄	0	✖

# Café Variome (4)

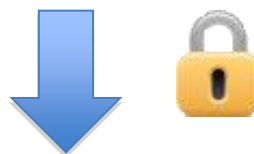
Open Discovery – Reporting Existence of Variants in Sources

Open Access



Core info for each variant record is shown & made available for download

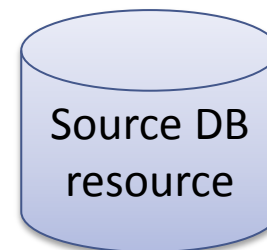
Restricted Access



Core or full record details are provided per record, if:

- User is pre-approved by group access permissions set by data owner
- Access is approved after facilitated email request to the data owner

Linked Access



No data, only link to the data source is reported.

Access then control managed by source db

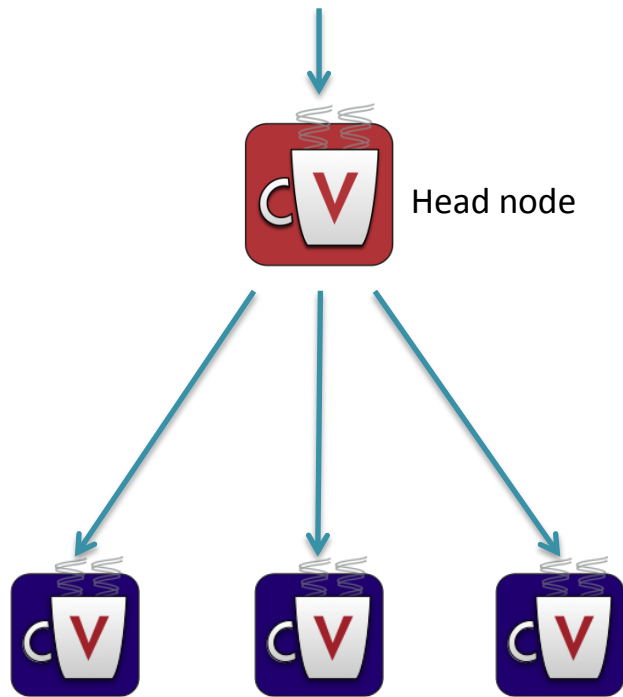
# Café Variome (5)

## Variant Report for vx62

Cafe Variome ID	vx62
Source link	-
Gene symbol / LRG	<a href="#">BRCA1 (LRG_292)</a>
Reference sequence	<a href="#">NM_007294.3</a>
HGVS description	c.4956G>A
Phenotype	Breast-ovarian cancer, familial, 1
Individual ID	-
Gender	-
Source/submitter ID	diagnostic
Genomic location	chr17:41222975-41222975 <a href="#">View in UCSC Genome Browser</a>
Comment	Submitted from Gensearch tool during Cafe Variome pilot study

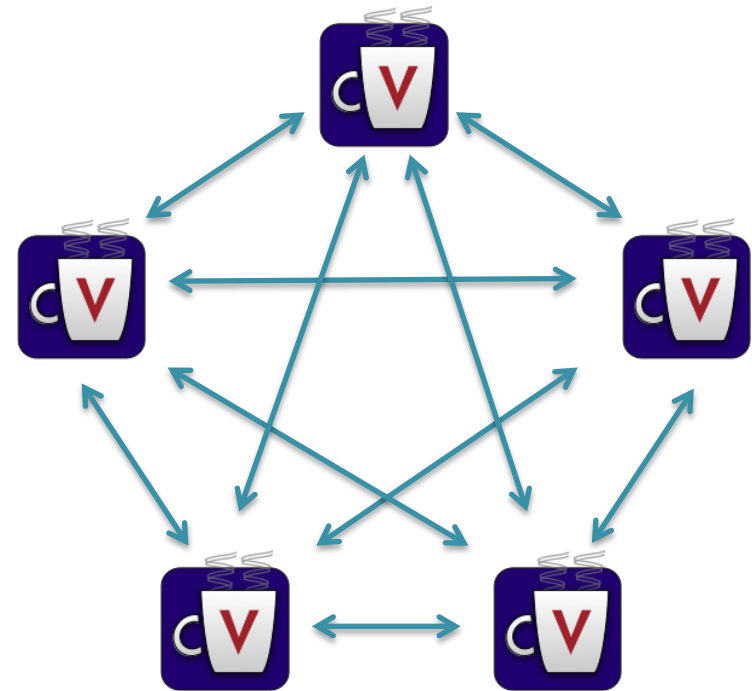
# Café Variome (6)

## External searches



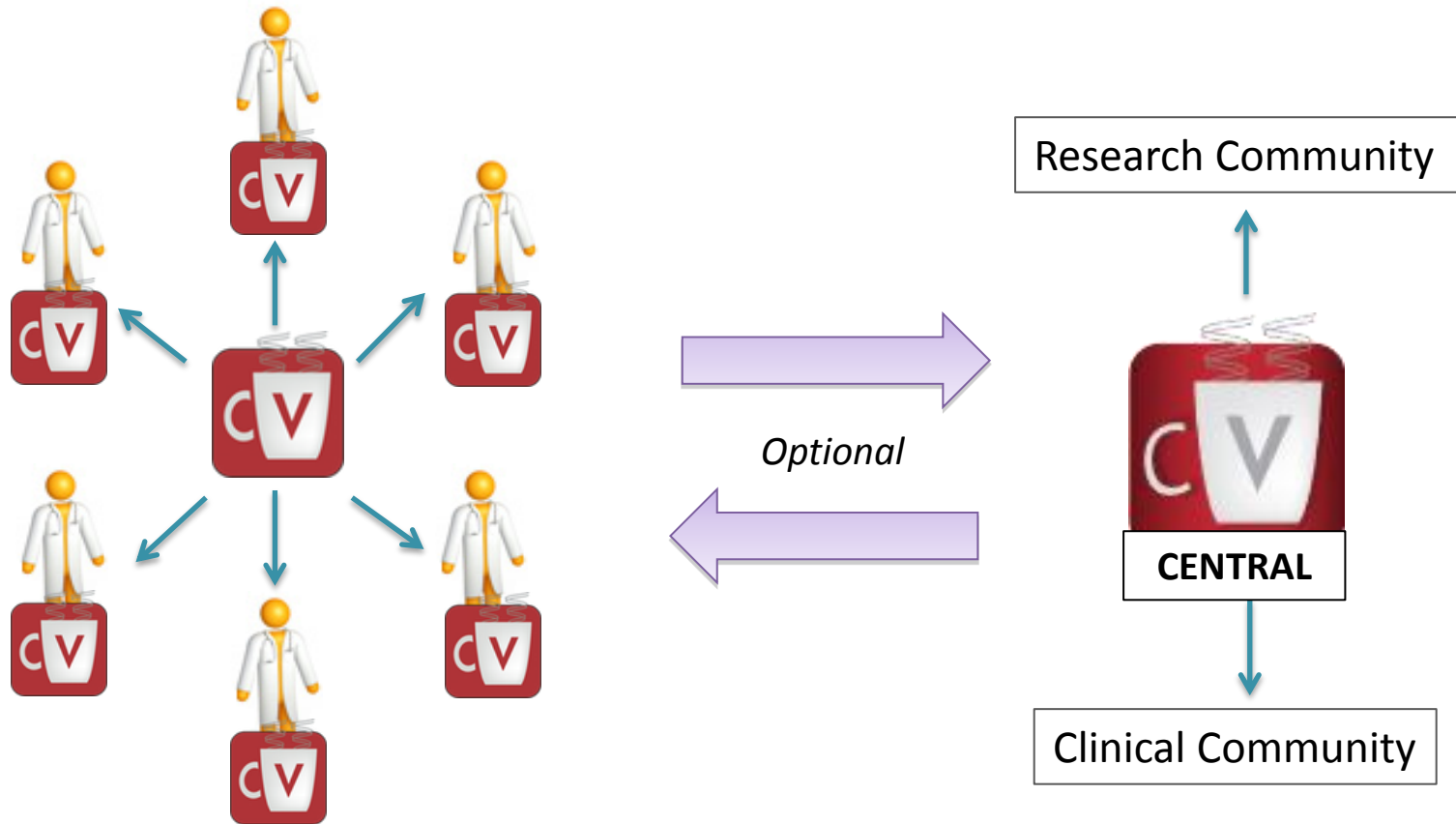
- ▶ Searches are performed through one nominated head node

## Internal searches



- Searches can be performed from any node in the network

# Café Variome (7)



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# Café Variome (8)

## **Disease consortia / diagnostic networks:**

- ▶ Ehlers Danlos Syndrome Consortium (Ghent Uni, Belgium & others)
- ▶ Brugada Syndrome Network (lead by University of Girona, Spain)
- ▶ Sheffield Children's NHS Trust (Osteogenesis imperfecta)
- ▶ Congenital Adrenal Hyperplasia (lead by Medizinische Universität Innsbruck, Austria)
- ▶ Danish diagnostic network (lead by Aarhus University)
- ▶ Netherlands diagnostic network (lead by University of Groningen)

## **“Cafe Variome enabled” diagnostic software:**



- ▶ Gensearch (Phenosystems)
- ▶ Alamut Visual (Interactive Biosoftware)







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# Café Variome (9)



umcg

HomeDiscoverContact




[Logout](#)

## Variant Discovery


Select Source:




All

Search term:

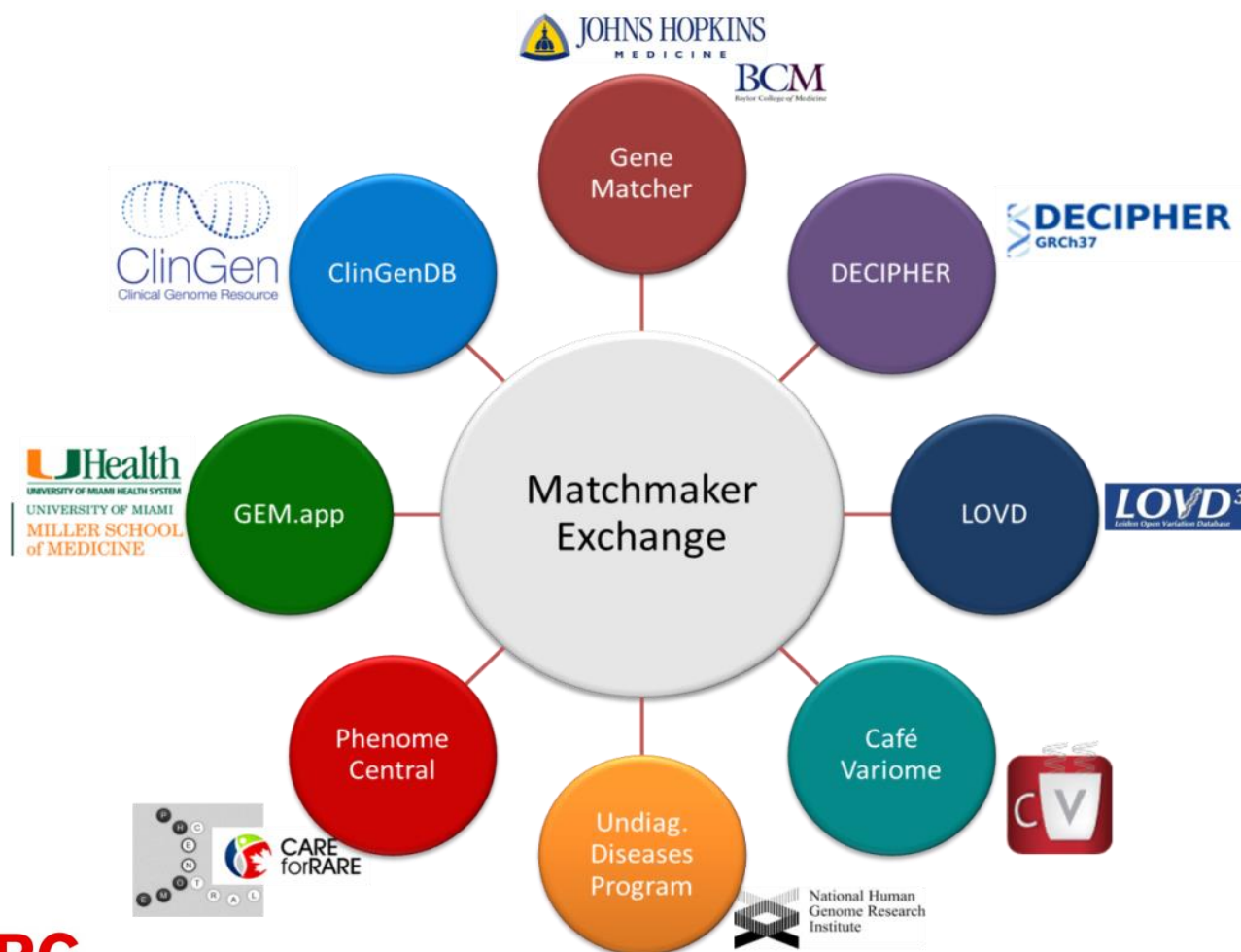
TTN

View top [gene](#) or [reference](#) content and use in your search.  
Alternatively search by chromosomal region e.g. [chr17:41196312..41277500](#),  
or HGVS nomenclature e.g. [NM\\_007294.3:c.5561T>C](#)

 Discover Variants

Source	openAccess		restrictedAccess		linkedAccess	
<a href="#">Cardio Kit</a>	662		0		0	

# Café Variome (10)



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