

# **Data Sharing: Progress by improving data 'control' ?**

**Anthony J Brookes**

TMF Data Integration/Sharing Workshop  
12-13<sup>th</sup> July 2016

**DATA ARE 'IMPORTANT' and 'VALUABLE'**

*and so*

**MANY OTHERS WANT YOUR DATA**

*therefore*

**GIVE ALL YOUR DATA AWAY**

**Quo Vadis ?**

## Issues that restrict sharing data

- **OUGHT NOT:** Data owners may not be allowed to share data (e.g., ethical, legal, institutional)
- **CAN NOT:** Data owners may not have time nor funding to manually submit data, and/or submission process and requirements too complicated
- **WANT NOT:** Data owners receive little or no recognition or reward for releasing data, risk undermining their competitive edge, and hence have little incentive to try



Studies



## About HGVS

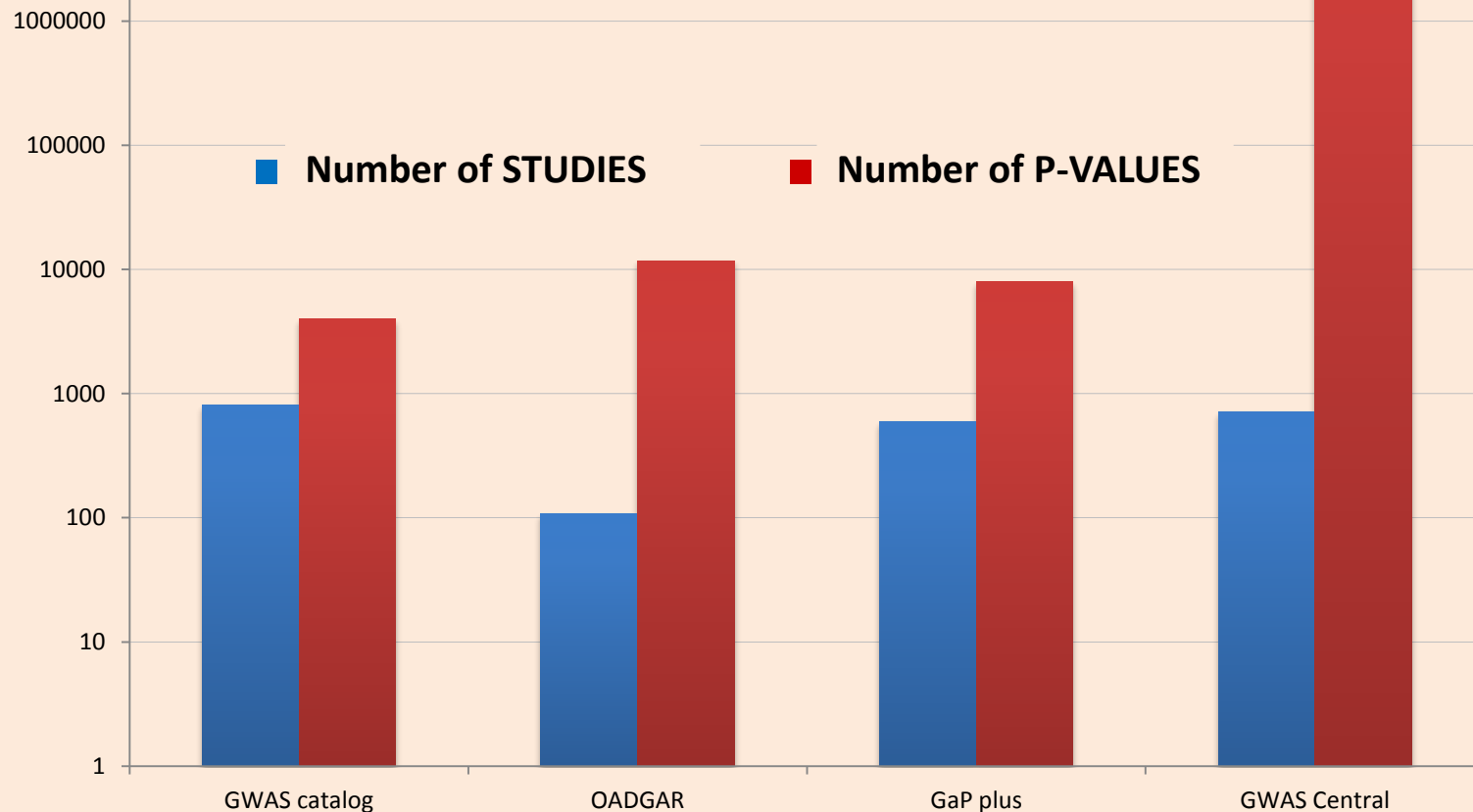
The Human Genome Variation Society (HGVS) provides summary level findings from large and small. We actively generate projects, and encourage community. [See more..](#)



## Frequently Asked Questions

- How is the database structured?
- How do I find Studies?
- How do I find Markers?
- How do I use the Browser?
- How do I submit my data?

- *comprehensive genetic association database*
- *aggregate data & extensive metadata*
- *links to data sources for primary data*



# GWAS CENTRAL 'Publicity Project'

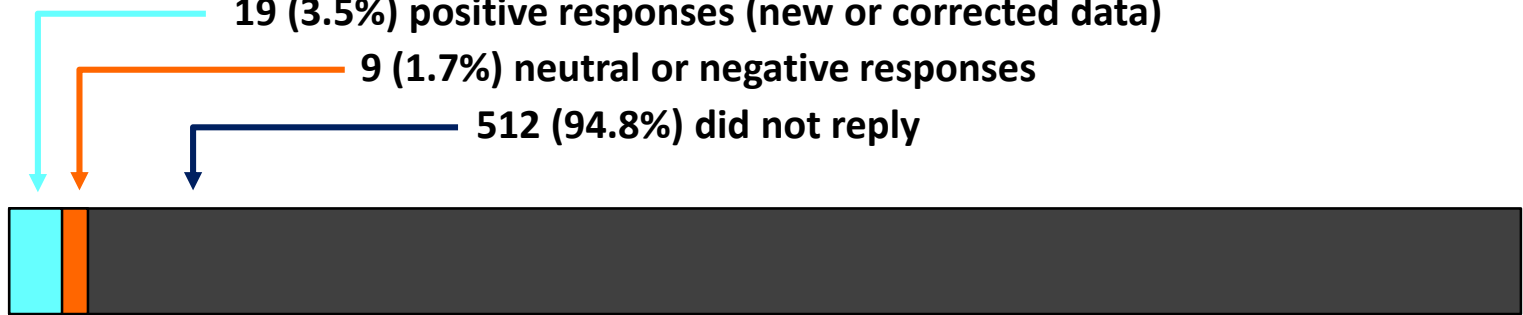
March 2011

570 e-mails sent to authors of 700 studies [30 undeliverable]

19 (3.5%) positive responses (new or corrected data)

9 (1.7%) neutral or negative responses

512 (94.8%) did not reply



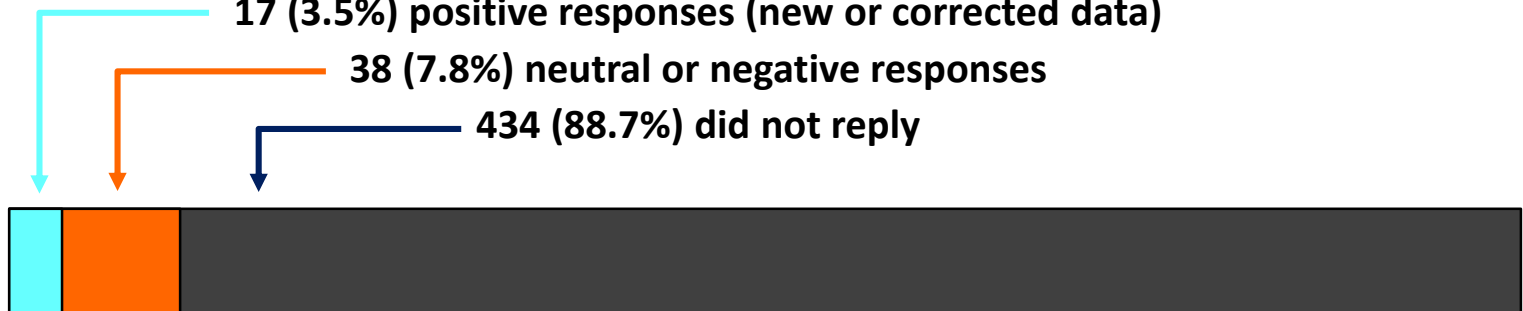
January 2012

505 e-mails sent to authors of 512 studies [16 undeliverable]

17 (3.5%) positive responses (new or corrected data)

38 (7.8%) neutral or negative responses

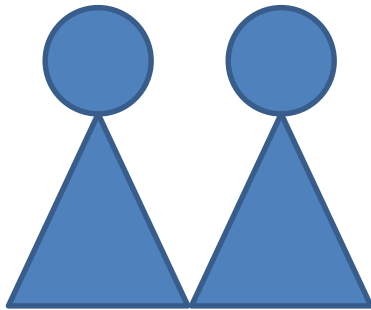
434 (88.7%) did not reply



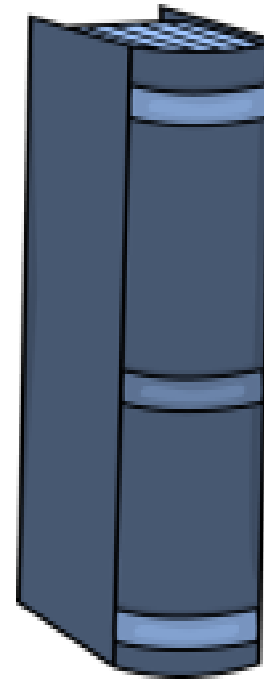
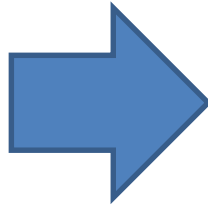
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- WANT NOT: Data owners receive little or no recognition or reward for releasing data, risk undermining their competitive edge, and hence have little incentive to try

**Are all data digitised, organised, structured...  
to make them 'sharable' ?**

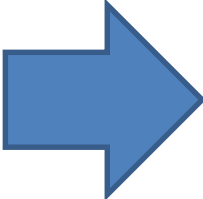
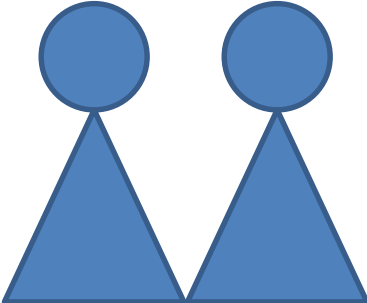


**Research Team**



**Data**

# Or are data generally chaotic & unstructured ?



**Research Team**

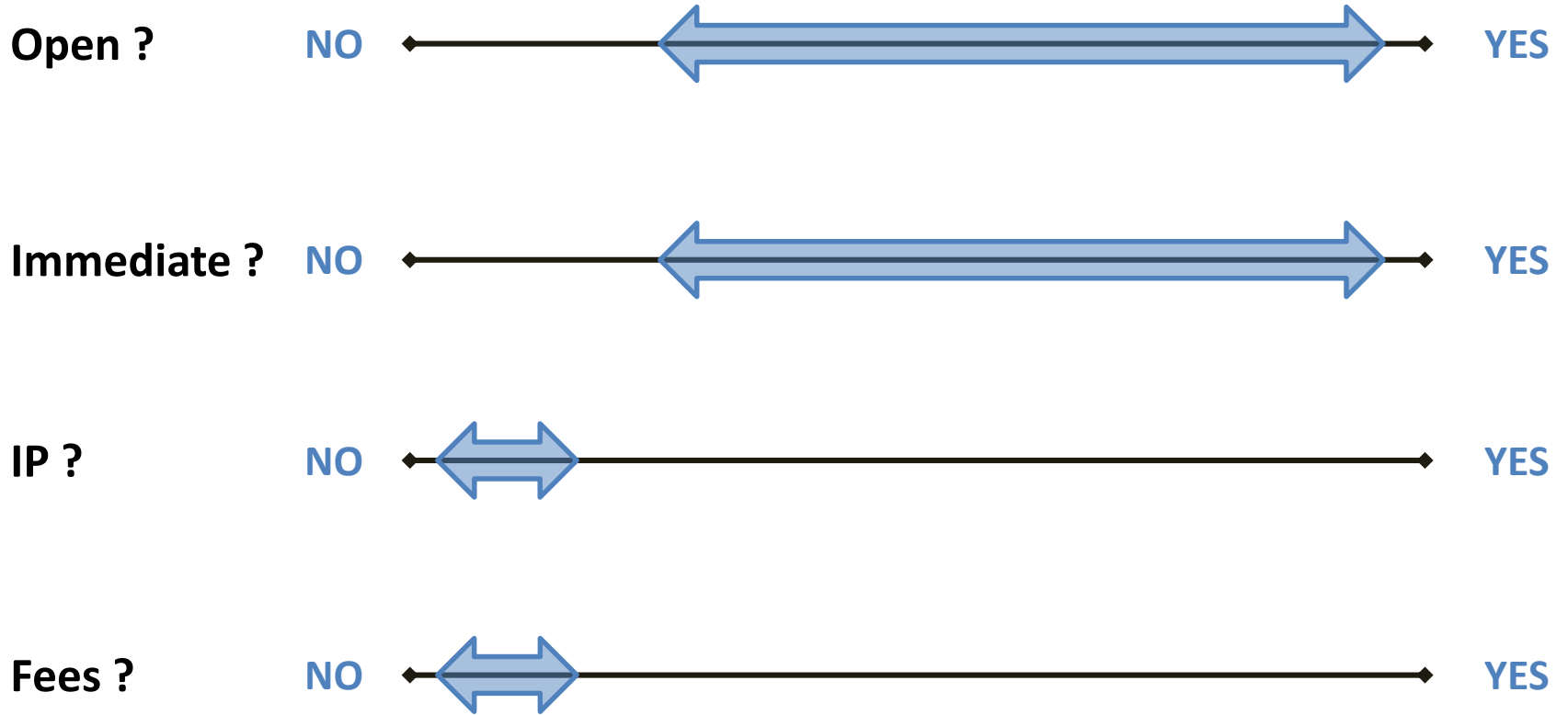
**Data**



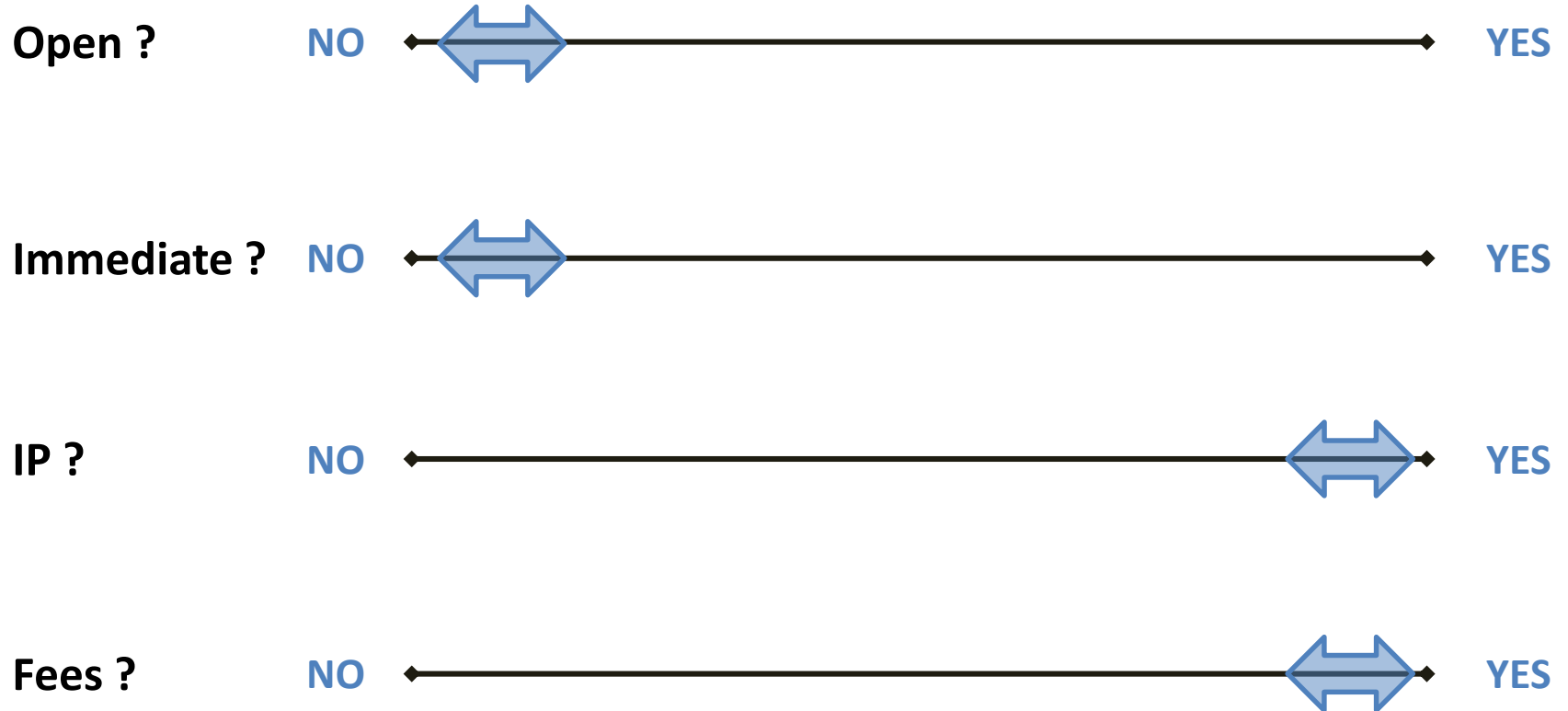
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# SHARING DATA



# SHARING NEW METHOD, BIOREAGENT, TECHNOLOGY, DRUG . . .



# Drazen/NEJM Editorial...

Raised general concerns about open data sharing, namely





- working separately, someone not involved in the original data collection may **misinterpret** the original data parameters or biases
- researcher "parasites" could use data of others to **unfairly compete** and/or disprove the original hypothesis

So they concluded that **data analysis should happen “symbiotically”**

-----  
*Later added...*

*[As per ICMJE proposal] NEJM will require authors to **make ‘available’ the data that underlie the reported results of their work within 6 months of publication***

5 December 2011 Last updated at  
21:22

1.3K Share    

## Everyone 'to be research patient', says David Cameron

..personal data



"Let me be clear, this does not threaten privacy, it doesn't mean anyone can look at your health records, but it does mean using anonymous data to make new medical breakthroughs.



the guardian

home UK world politics sport football opinion culture busi ≡ all

Media & Tech Network Open data economy

# Google's NHS deal does not bode well for the future of data-sharing

***“This is people's most personal information and many will be horrified by the idea it is being shared with Google - encrypted or not”***

Joy



the guardian

home > tech UK world politics sport football opinion culture b ≡ all

## Data protection

# NHS to scrap single database of patients' medical details

Care.data scheme to close after Fiona Caldicott review calls for tougher measures to keep information confidential



# Data FAIRport

Find, Access, Interoperate & Re-use Data

<http://www.datafairport.org/>

Home

Latest News

Work Packages

Workshop participants

Join

## FAIR Principles Work Packages

The Data FAIRport program will consist of the following workpackages:

- **WP1 - Detailed plan of approach & funding strategy.** WP1 will focus on producing a detailed Plan of Approach for the process towards the September deliverables and beyond (assuming a positive decision to move forward). This WP will include [read more](#)

- **WP2 - Key Stakeholders & Advocacy.** WP2 will focus on developing a strategy for engagement and alignment of the visions of Enablers and onboarding of stakeholders. It needs to produce a [read more](#)

- **WP3 - Tech exemplars.** WP3 will focus on developing one or more exemplars to be presented during the RDA meeting in September 2014. Aspects needing attention include [read more](#)

Overview and review (sounding board, non executive)

Niklas Blomberg, George Strawn, Abel Packer, Jan velterop, Olivier Dumon, Myles Axton, Frank van Harmelen

(criteria: no pet technologies, role in endorsement, publisher view)

WP1

Bengt Persson  
Barend Mons

Editor:  
Arie Baak

Anthony Brookes  
Johan van der lei  
Thierry Sengstag  
Ted Slater  
Tim Clark  
Paul Groth  
Scott Lusher

WP2

Barend Mons  
Tim Clark

Editor:  
Arie Baak

Maurice Bouwhuis  
Ted Slater  
Carole Goble  
Jan Willem Boiten  
Rene van Schaik  
Joost Kok  
Jaap Heringa

WP3

Carole Goble  
Paul Groth

Tech Leads:  
Mark Wilkinson,  
Michel Dumontier

Morris Schwartz  
Erik van Mulligen  
Joel Kuiper  
Paolo Ciccarese  
Luiz Olavo Bonino  
Others (MW)

Reflection on Governance implications, secretariat, redaction, hosting etc.

Arie Baak, Albert Mons, Ruben Kok, Mascha Jansen, Femke Francissen, Jacintha van Beemen

(criteria: hosting/investing, supporting work packages)

## A Critical Insight / Solution... ???

**Possession**

(not sharing)



**Control**

(power & opportunity)

**So, we need to disconnect possession and control,  
so that data can be released (in whole or in part)  
whilst not undermining the data owner's  
reasonable control of the data**



## (1) Alternative Forms of data

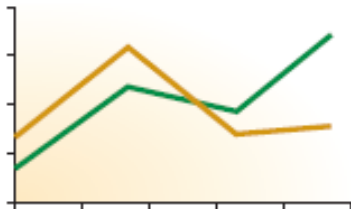
...AAACGTTGGACCGCGT...  
...TTTGCAACCTGGCGCA...



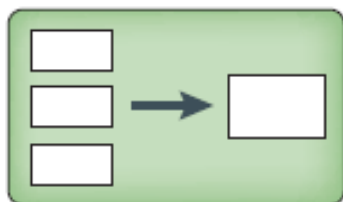
### Metadata

Disease  
Age  
Gender  
Consent

### Graphics

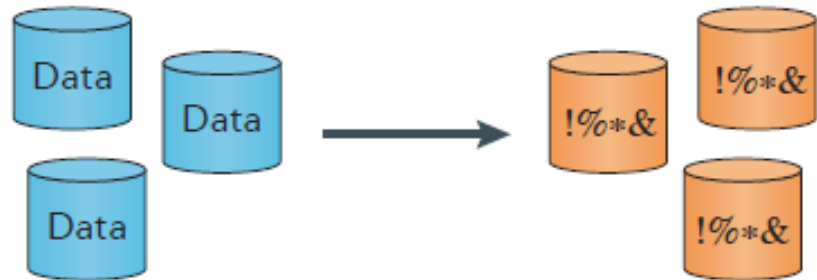


### Aggregates

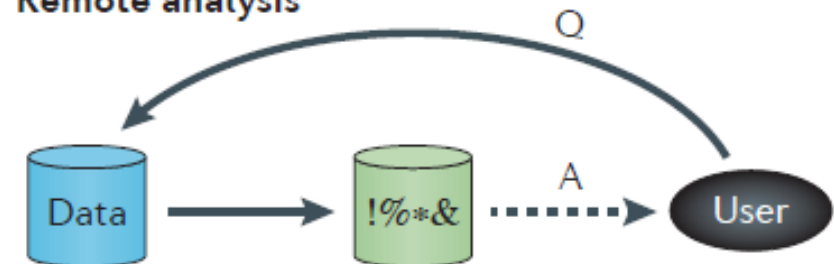


## (2) Encryption based solutions

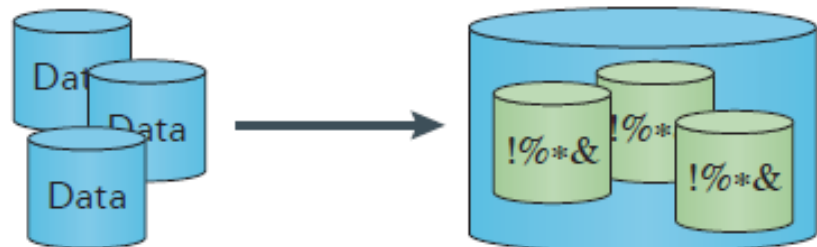
### Encryption



### Remote analysis



### Pooling



### (3) Automatable Discovery and Access Matrix (ADA-M) v1.0



Global Alliance  
for Genomics & Health



- 'Atomic' – smallest sensible, standardised concepts which can be combined into a data use conditions profile, encompassing
  - Mode of Sharing
  - Permissions
  - Terms
  - Meta-conditions
- Various cross-mapping exercises completed, e.g., to datasets managed by EGA (Jordi Rambla De Argila), Consent Codes (S. Dyke), DUOS (Anthony Philippakis, Gregory Rushton), and a database of consent clauses (E. Forbes)
- Alpha testing by many teams after broad email notification Jan 2016, enabling stepwise feedback and refinement (now v1.0)
- Various collaboration opportunities identified and being developed

## (3) Potential applications



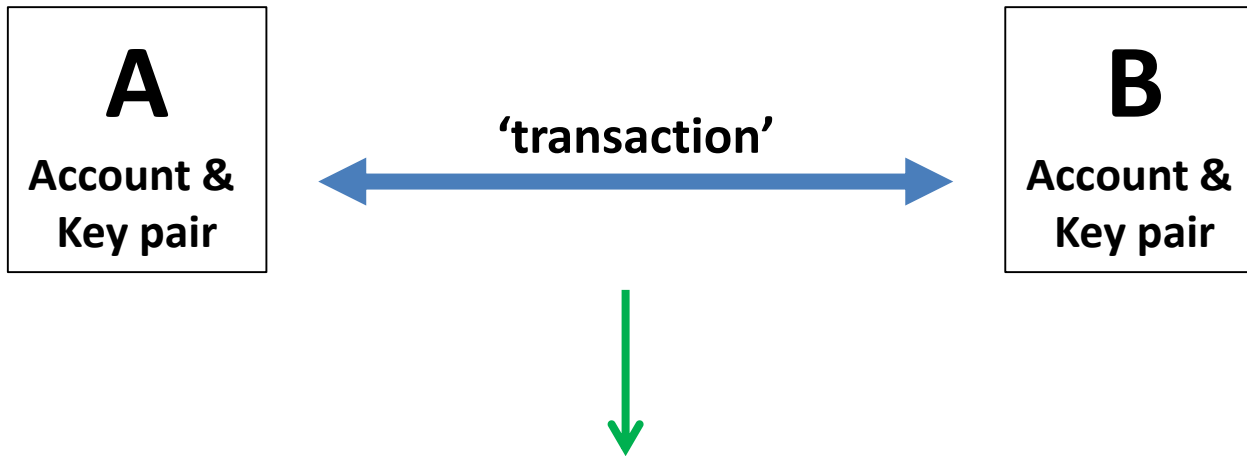
1. As a descriptor  
ADA-M used to communicate the use conditions profile of a dataset
2. Enhance discovery  
provide extra level of information to underpin 'discovery' queries
3. Automated data sharing:  
align access requests to ADA-M profiles, and share if conditions are met

### (3) ADA-M

Permissions:	
use within countries/locations	"Unrestricted" or "Limited"
<i>within specified countries/locations</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by organisations	"Unrestricted" or "Limited"
<i>for specified categories of organisation</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by non-profit organisations	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>by specified non-profit organisations</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by profit organisations	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>by specified profit organisations</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by categories of person	"Unrestricted" or "Limited"
<i>for specified categories of person</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by academic professional	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>by specified categories of academic professional</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by clinical professional	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>by specified categories of clinical professional</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by profit-making professional	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>by specified categories of profit-making professional</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use by non-professional	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>by specified categories of non-professional</i>	Free text list, with optional suffix "[Obligatory]" after each list entry
use for non-profit purpose	"Unrestricted" or "Unrestricted[Obligatory]" or "Limited" or "Limited[Obligatory]" or "Forbidden"
<i>for specified non-profit purposes</i>	Free text list, with optional suffix "[Obligatory]" after each list entry

Terms:	
There are no requirements for any formal approval, contract or review conditions to be satisfied	"True" or "Untrue"
<i>Formal approval, contract or review conditions are to be met, as specified</i>	Free text list
There are no requirements regarding publication of results, or included references or acknowledgements	"True" or "Untrue"
<i>Publication or disclosure of derived results is subject to restrictions, as specified</i>	Free text list

Meta-Conditions:	
Interpretation rule if multiple Obligatory permissions are specified	"Meet all Obligatory permissions" or "Meet at least one Obligatory permission"
There are no other use restrictions/limitations in force which are not herein specified	"True" or "Untrue"
<i>Other permissions/limitations may apply as specified</i>	Free text list
No special evaluation required for access requests involving sensitive/restricted populations	"True" or "Untrue"



**'A' agrees a debt returnable to 'B' (IOU)**

**'A' pays money to 'B' (cheque)**

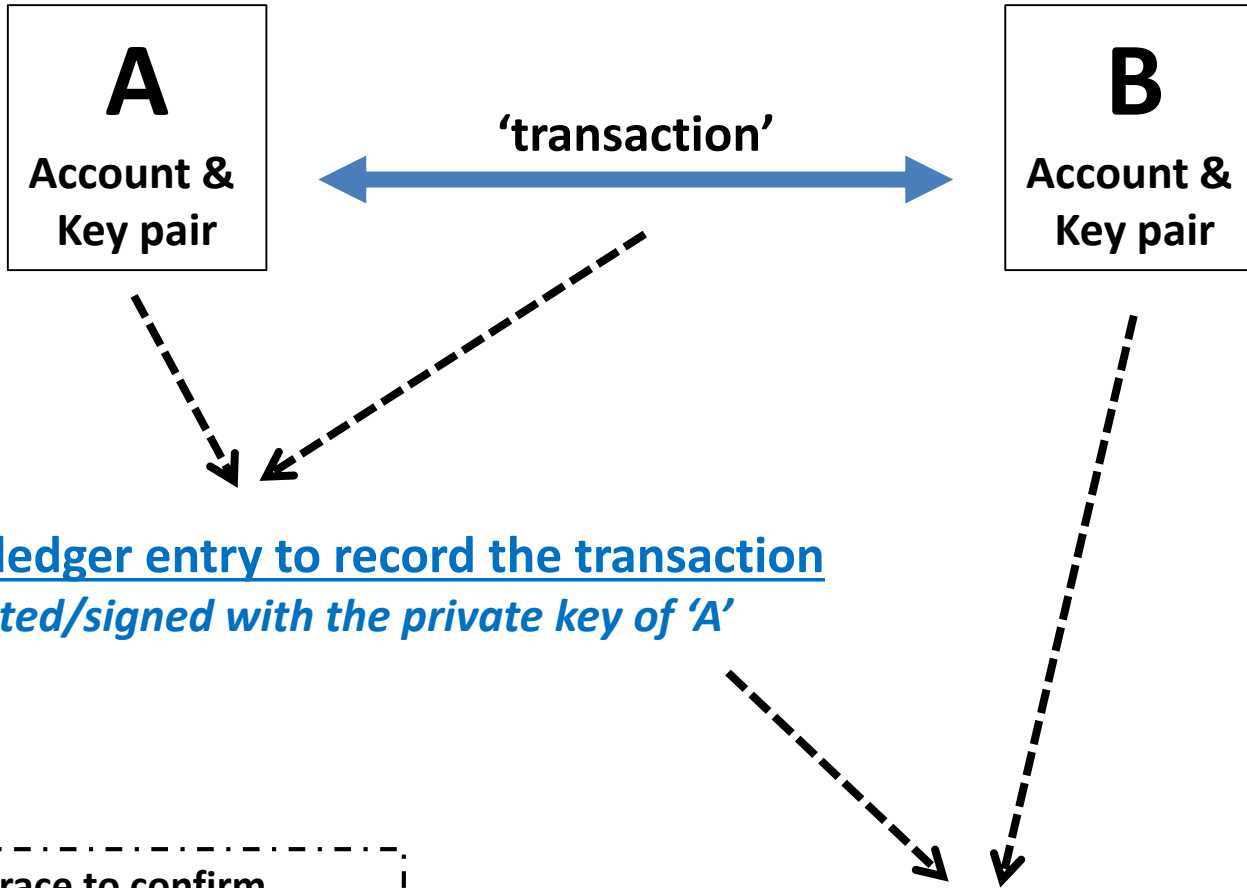
**'A' receives/accesses an item from 'B' (receipt)**

*'A' receives/accesses data (token) from 'B',  
intended for use XYZ*

## **(4) BLOCK-CHAIN**

- **A fully transparent, public ledger, of transactions**
- **Eliminates the 'middle man', and makes terms of all interactions visible**

(4)



'A' makes a ledger entry to record the transaction

*- encrypted/signed with the private key of 'A'*

Peers (miners) race to confirm many entries as a group

- *by checking source*
- *by checking payment history of currency integral to the block chain*

Upon validation the miner

- *adds a new block to the chain*
- *claims the set of validation fees*

'B' can check the statement, to establish that:

- *'A' produced the statement (via A's public key)*
- *payment by A is valid (via 'Block Chain')*
- *'A' is in good standing (via a 'user registry')*
- *terms are agreeable (via 'computer readable metadata')*

# **(5) DISCOVERY**

**= a distinct discipline**

*Share the 'existence'  
rather than the 'substance'  
of the data  
or knowledge  
or sample  
or subject  
or resource  
or standard...*

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*NATURE REVIEWS GENETICS* | REVIEW

((( ARTICLE SERIES: **Computational tools**

# Human genotype–phenotype databases: aims, challenges and opportunities

**Anthony J. Brookes & Peter N. Robinson**

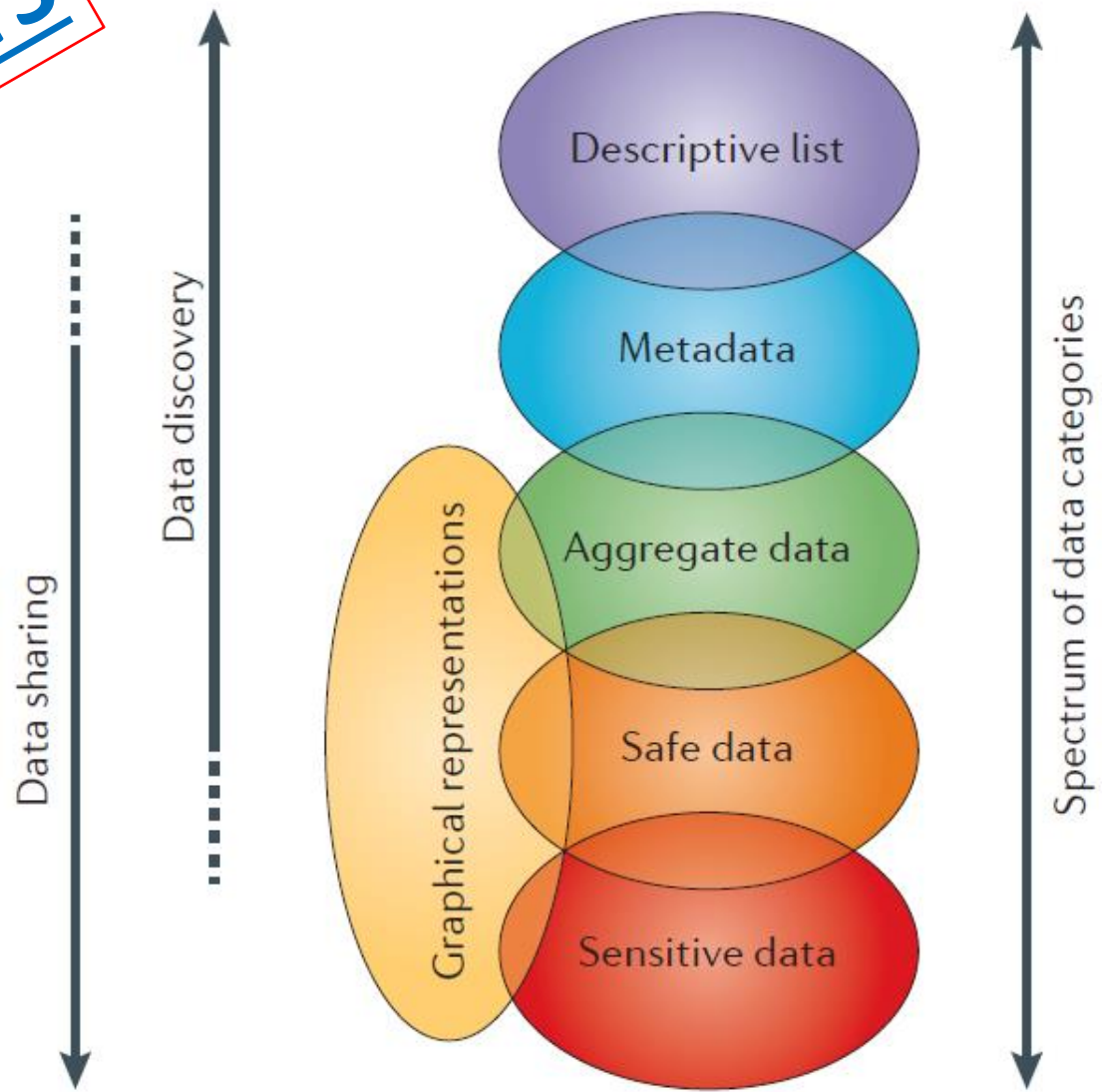
**Affiliations** | **Corresponding author**

*Nature Reviews Genetics* (2015) | doi:10.1038/nrg3932

Published online 10 November 2015



**TARGETS**

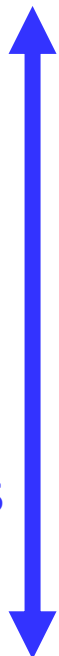


# **OUTPUTS**

**SUBJECTS  
SAMPLES**



**DATASETS**



- Links (e.g., to PI, to data)**
- Ways to request data**
- Yes/No answers**
- Record counts (optionally adjusted, thresholded)**
- Record IDs**
- Summary level statistics**
- Graphical displays (e.g., dotplots, barcharts)**
- Limited data**
- Extensive data**

# European Genome-phenome Archive

All 

Examples: EGAS00000000001, Cancer

[EGA home](#) [About](#) [Studies](#) [Datasets](#) [Data access committees](#) [Data providers](#) [Submit to EGA](#) [Contact Us](#)

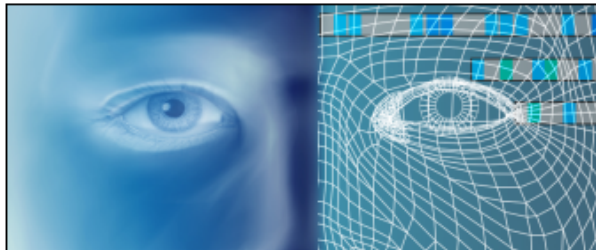
The European Genome-phenome Archive (EGA) allows you to explore **datasets** from genomic **studies**, provided by a range of **data providers**. Access to datasets must be approved by the specified **Data Access Committee (DAC)**.

## Help

- [Users FAQ](#)
- [Submitters FAQ](#)
- [Using your EGA account](#)

[NCBI](#) [Resources](#)  [How To](#) [Sign in to NCBI](#)

dbGaP

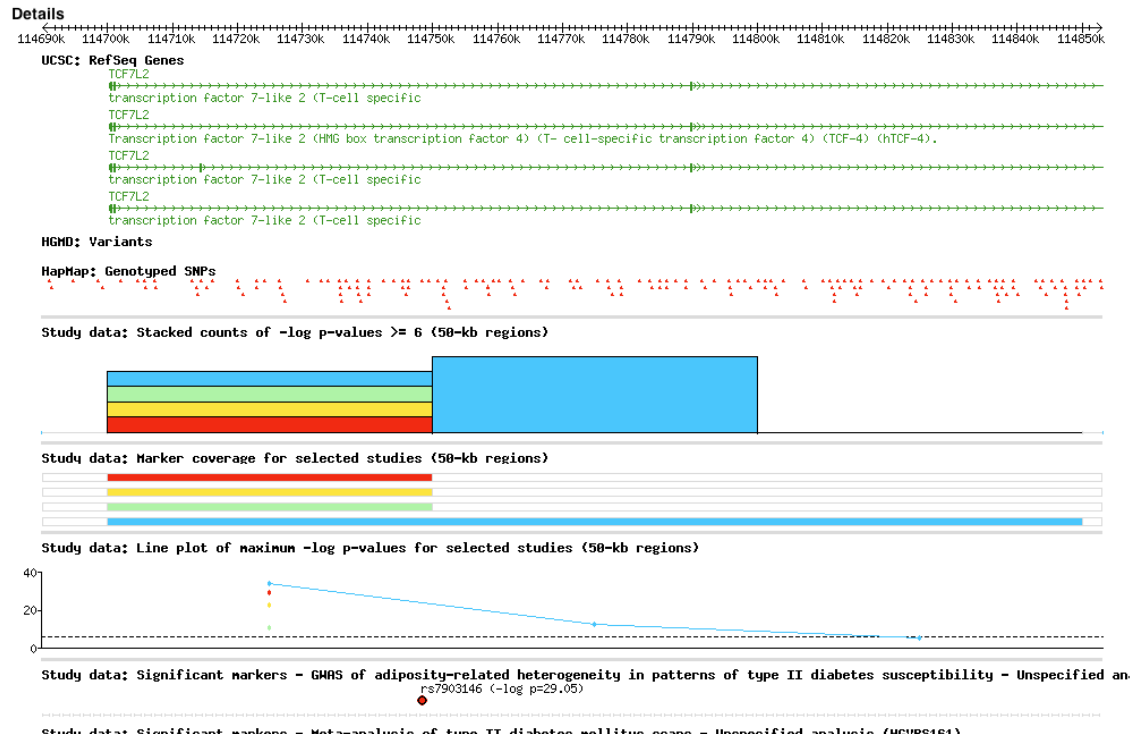
dbGaP [Limits](#) [Advanced](#)[Help](#)

## dbGaP

The database of Genotypes and Phenotypes (dbGaP) was developed to archive and distribute the results of studies that have investigated the interaction of genotype and phenotype.

[Getting Started](#)[Access dbGaP Data](#)[Important Links](#)

# GWAS Central (www.gwascentral.org)



Study	Phenotype	Go to Markers	No. markers with $-\log p$ -value $\geq 3$
log10 IgE (kU/L) (HGVST306)	log10 IgE (kU/L)	➔	421
Systolic Blood Pressure (mm Hg) (HGVST307)	Systolic BP (mm Hg)	➔	457
Adult Body Mass Index (kg/m <sup>2</sup> ) (HGVST308)	Adult BMI (kg/m <sup>2</sup> )	➔	402
Adult height (cm) (HGVST309)	Adult height (cm)	➔	505
FEV1 (litres) (HGVST310)	FEV1 (litres)	➔	417
4 kHz hearing threshold (dB) (HGVST311)	4 kHz hearing threshold (dB)	➔	457
Cholesterol (mmol/L) (HGVST312)	Cholesterol (mmol/L)	➔	497
Glycosylated haemoglobin (HbA1c) (%) (HGVST313)	log10 HbA1c (%)	➔	624

# Beacon Project (GA4GH)

## *Lead - Marc Fiume*

- a beacon answers the question, have you observed this allele?
- the 0.2 Beacon query is shown on the right

```
protocol BEACON {  
  
  /**  
   * A request for information about a specific site  
   */  
  record QueryResource {  
    /** Allele string  
     * string allele;  
  
    /** The chromosome of the request */  
    string chromosome;  
  
    /** 0-based allele locus */  
    long position;  
  
    /** The version of the reference */  
    string reference;  
  
    /** The name of the targeted population */  
    union{ null, string } dataset = null;  
  }  
}
```

# Beacon-of-Beacons (GA4GH, DNASTACK)

Advanced Options


















GRCh37 - 13 : 32954208 T>A

Search

Response All None  
 Found 2  
 Not Found 30  
 Error 6

Organization All None  
 AMPLab, University of California  
 BGI  
 BioReference Laboratories  
 Broad Institute  
 Centre for Genomic Regulation

Show All

	1000 Genomes - Thousand Genomes YRI Trio DNASTack	Not Found
	AMPLab - 1000 Genomes Project AMPLab, University of California	Not Found
	Biobase - HGMD University of California, Santa Cruz	Not Found
	BioReference BioReference Laboratories	Not Found
	DNASTack	Not Found
	EBI - 1000 Genomes Project, UK10K, GoNL, EVS, GEUVADIS, UMCG Cardio GenePanel EMBL European Bioinformatics Institute	Not Found
	European Genome-phenome Archive Centre for Genomic Regulation	Not Found
	ExAC Broad Institute	Not Found
	GIGAScience	Error
	GIGAScience #1 BGI	Error
	GIGAScience #2 BGI	Error
	Google - 1000 Genomes Project Google	Not Found
	Google - 1000 Genomes Project Phase 3 Google	Not Found
	Google - Illumina Platinum Genomes Google	Not Found
	Google Genomics Public Data	Not Found
	ICGC - Cancer Projects Ontario Institute for Cancer Research	Not Found
	Kaviar	Found

## Plus...

- ❖ **Biobank catalogs (e.g., BBMRI, UKCRC-TDC)**
- ❖ **Health data discovery (e.g., EMIF, Jerboa, PopMedNet, i2b2, OHDSI)**
- ❖ **Research data (e.g., MME, NGS-Logistics, Orphanet, VarWatch)**
- ❖ **Patient data (e.g., PEER, RD-Connect, PatientsLikeMe)**



# Cafe Variome

Informatics

## Cafe Variome: General-Purpose Software for Making Genotype–Phenotype Data Discoverable in Restricted or Open Access Contexts



Owen Lancaster<sup>1</sup>, Tim Beck<sup>1</sup>, David Atlan<sup>2</sup>,  
Morris Swertz<sup>3</sup>, Dhiwagaran Thangavelu<sup>1</sup>,  
Colin Veal<sup>1</sup>, Raymond Dalglish<sup>1</sup>  
and Anthony J Brookes<sup>1,\*</sup>

Article first published online: 25 AUG 2015

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Issue



**Human Mutation**

Special Issue: The Matchmaker  
Exchange

**Volume 36, Issue 10, pages  
957–964, October 2015**



# Query Builder Interface

The interface consists of eight stacked search fields, each with a left-pointing arrow on the right side. Below each field are two buttons: 'AND' (light gray) and 'OR' (blue). At the bottom of the interface are two buttons: 'Reset' (light gray) and 'Build Query' (blue).

GENOME COORDINATE

AND OR

ACCESSION COORDINATE

AND OR

DNA SEQUENCE OF VARIANT

AND OR

PROTEIN SEQUENCE OF VARIANT

AND OR

GENE SYMBOL

AND OR

HGVS NAME

AND OR

PHENOTYPE

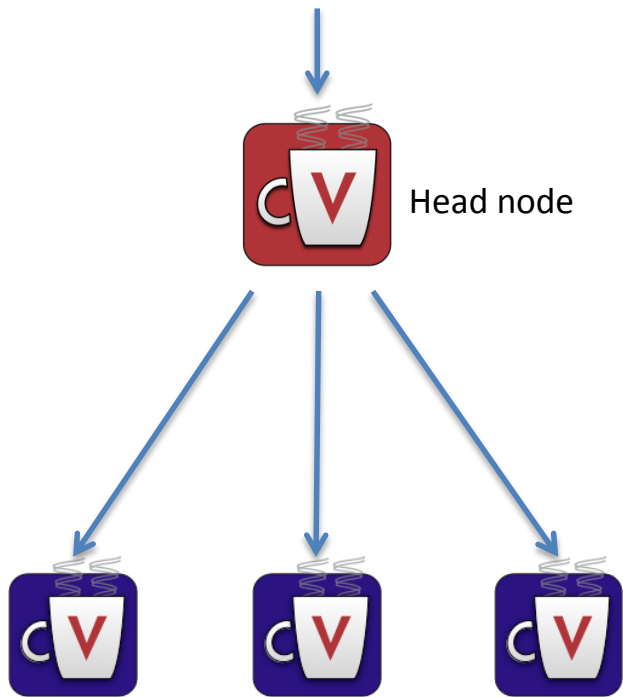
AND OR

OTHER SEARCH FIELDS

Reset Build Query

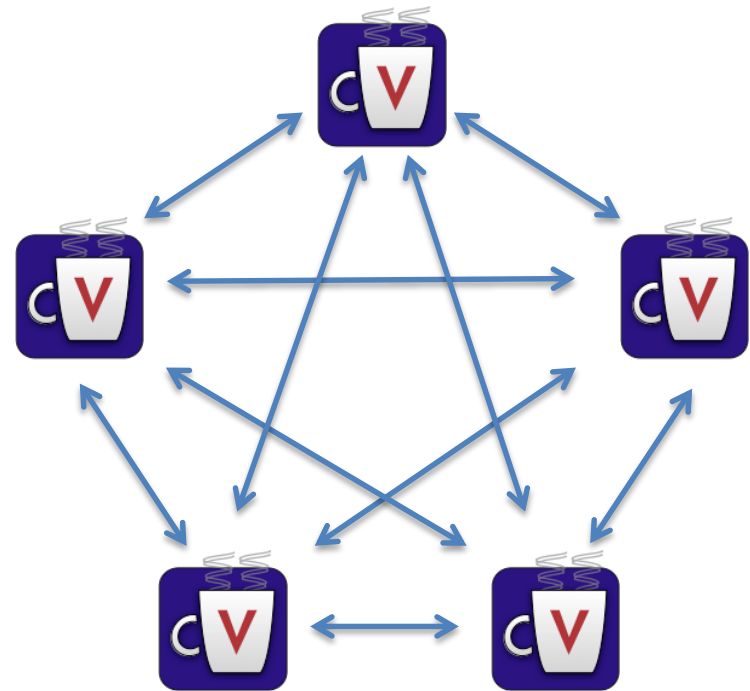
# Node Search Options

## External searches

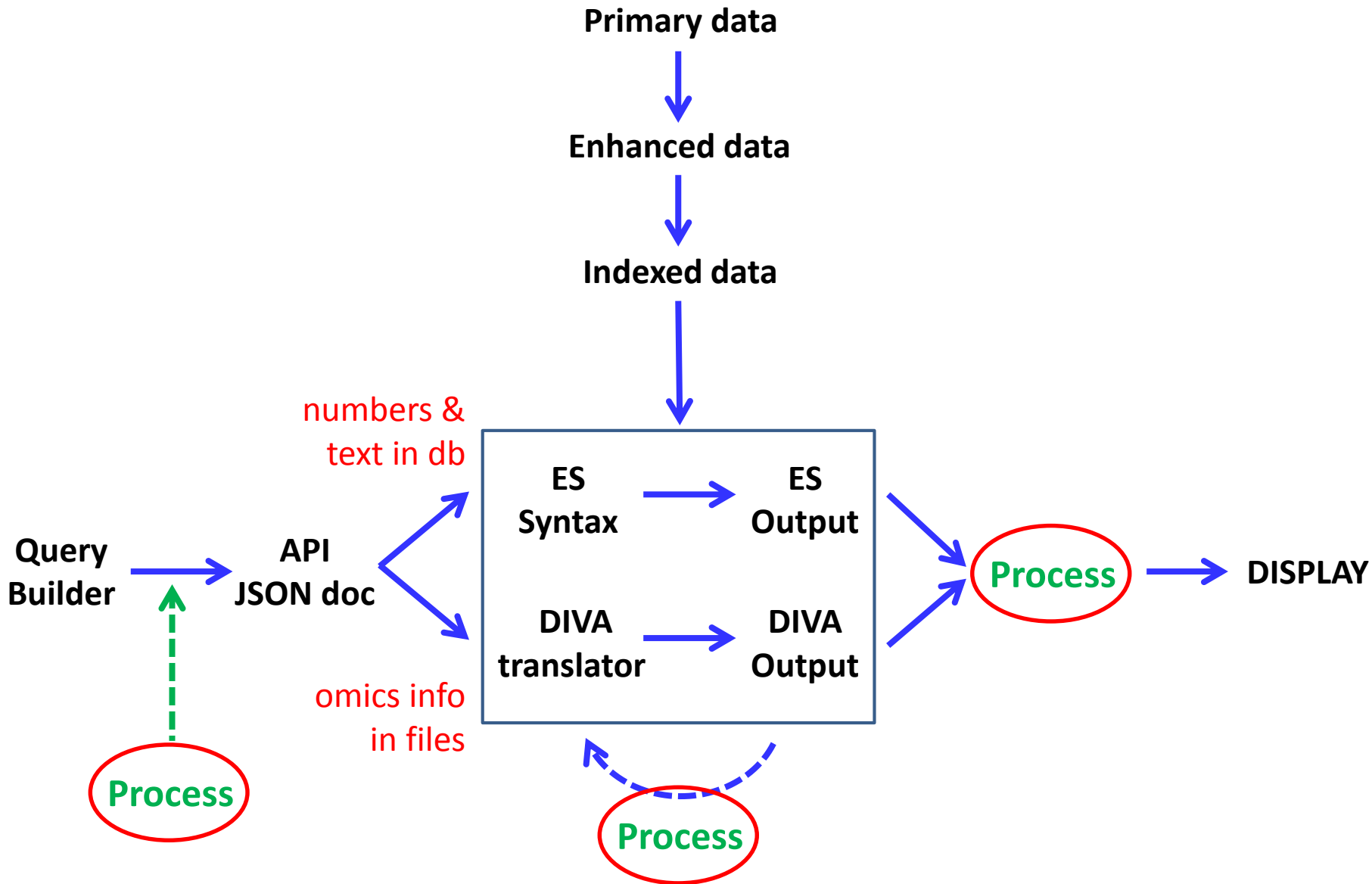


- Searches are performed through one nominated head node

## Internal searches



- Searches can be performed from any node in the network



# Geno-Pheno Query-by-Method API

Anthony Brookes

Morris Swertz

(Isaac Kohane)

(Marc Fiume)

(Johan van der Lei)

```
"query" : {
  "gender" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "gender" : {
        "ontologyGender" : {"id" : "<ontology term code>",
                           "term" : "<ontology term string>",
                           "source" : "<ontology source name>"},
        "cursiveGender" : {"term" : "FEMALE|MALE", "source" : ""}
      }
    },
    ...
  ]
  "sex" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "sex" : {
        "ontologySex" : {"id" : "<ontology term code>",
                        "term" : "<ontology term string>",
                        "source" : "<ontology source name>"},
        "cursiveSex" : {"term" : "FEMALE|MALE", "source" : ""}
      }
    },
    ...
  ]
  "age" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "age" : {"value" : "", "units" : ""}
    },
    ...
  ]
  "inheritanceMode" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "inheritanceMode" : {
        "ontologyInheritanceMode" : {"id" : "<ontology term code>",
                                     "term" : "<ontology term string>",
                                     "source" : "<ontology source name>"},
        "cursiveInheritanceMode" : {"term" : "", "source" : ""}
      }
    },
    ...
  ]
  "diseaseFeature" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "diseaseFeature" : {
        "ontologyDiseaseFeature" : {"id" : "<ontology term code>",
                                     "term" : "<ontology term string>",
                                     "source" : "<ontology source name>"},
        "cursiveDiseaseFeature" : {"term" : "", "source" : ""}
      }
    },
    ...
  ]
  "geneRegion" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "geneRegion" : {
        "ontologyGeneRegion" : {"id" : "<ontology term code>",
                                 "term" : "<ontology term string>",
                                 "source" : "<ontology source name>"},
        "cursiveGeneRegion" : {"term" : "", "source" : ""}
      }
    },
    ...
  ]
  "geneConsequence" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "geneConsequence" : {
        "ontologyGeneConsequence" : {"id" : "<ontology term code>",
                                      "term" : "<ontology term string>",
                                      "source" : "<ontology source name>"},
        "cursiveGeneConsequence" : {"term" : "", "source" : ""}
      }
    },
    ...
  ]
  "pathogenicityClass" : [
    {
      "querySegmentID" : "",
      "operator" : "",
      "pathogenicityClass" : {"class" : "", "source" : ""}
    },
    ...
  ]
  "queryStatement" : "(1 AND 2) OR 3"
}
```



# Phenotype Semantics

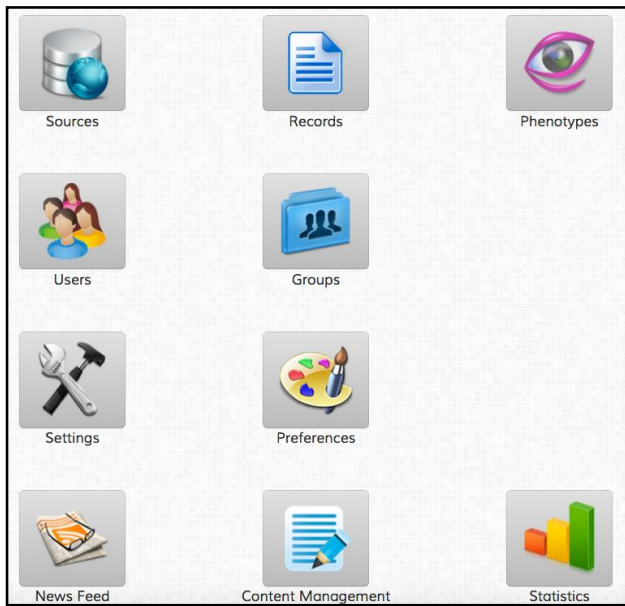
- Allow phenotypes to be described using **public ontologies**
  - Many terms from many ontologies can be associated with one entity
- Allow phenotypes to be described using a **local vocabulary or list**
- Enable hierarchical viewing and querying of the phenotype ontology data



Installation wizard

# Multiple Admin Options

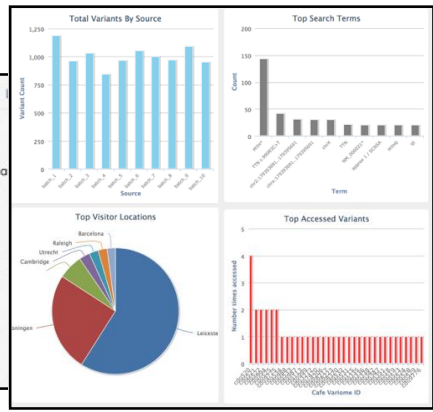
Record and source management



User, group and record access control management



Core system settings, defining displayed and searchable fields, bulk import template configuration



Appearance preferences, content management system and statistics reporting

# Query Builder in action

DNA

EXACT Reference +

Age [years]	>	64	-
APOE4 [most recent result]	=	2	-
Gender	IS	M	-
--Select an attribute--	=	--Select a value--	+

--Select an attribute--

- ADAS-COG [count of results]
- ADAS-COG [most recent result]
- ADAS-COG [results exist]
- Age [months]

Reset Build Query



IS Enter a HGVS description +

AND OR

PHENOTYPE

--Select an attribute--	IS	--Select a value--	-
AND OR			
--Select an attribute--	IS	--Select a value--	+ -

# Controlled Display of Matched Record Counts & Data (if permitted)

(Gender:male)

Source	openAccess		linkedAccess		restrictedAccess	
Amsterdam 01			0		0	
Barcelona 01			0		0	
Mock Cohort 01	13		0		0	
Stockholm 01			0		0	

Open Access

Data provided

Cofe Variant ID	Gene	Reference	HDV5	Phenotype(s)	Source ID
v001	FB	NM_001012.2	c.283A>G	Hemophilia A	diagnostic
v004	FB	NM_001012.2	c.148C>G	Hemophilia A	diagnostic
v007	FB	NM_001012.2	c.884C>T	Hemophilia A	diagnostic
v008	FB	NM_001012.2	c.884C>T	Hemophilia A	diagnostic
v009	FB	NM_001012.2	c.884C>T	Hemophilia A	diagnostic
v010	FB	NM_001012.2	c.1768G>C	Hemophilia A	diagnostic
v011	FB	NM_001012.2	c.1768G>C	Hemophilia A	diagnostic
v012	FB	NM_001012.2	c.4788A>G	Hemophilia A	diagnostic
v013	FB	NM_001012.2	c.3781C>G	Hemophilia A	diagnostic
v014	FB	NM_001012.2	c.853A>C	Hemophilia A	diagnostic

Linked Access

No data provided,  
only link to data source

Source DB

Restricted Access

You may request  
pre-approval  
for these data



# CafeVariome Discovery

Coordinator has access to all counts, but no access to data itself


The screenshot displays the CafeVariome Discovery search interface. At the top, a green header labeled 'PHENOTYPE' contains two filter rows. The first row has a dropdown for 'Gender' set to 'female' and a red minus button. The second row has a dropdown for 'MMSE score [lowest]' set to '< 29' and green plus and red minus buttons. Below these are 'AND' and 'OR' buttons. A grey header labeled 'OTHER SEARCH FIELDS' is below. At the bottom, there are 'Reset' and 'Build Query' buttons. The query text is '((Gender:female) AND (MMSE\_score\_[lowest]:<29))'. Below the query is a table with columns: Source, openAccess, linkedAccess, and restrictedAccess. The table has three rows for mockdata\_1, mockdata\_2, and mockdata\_3, each with counts and download icons.

Source	openAccess	linkedAccess	restrictedAccess
mockdata_1 (Cafe Variome Demo 4)	0	0	10
mockdata_2 (Cafe Variome Demo 4)	0	0	6
mockdata_3 (Cafe Variome Demo 4)	0	0	35



# CafeVariome Discovery

User 2 has full access to own data,  
but no access to counts or data from other datasets

**PHENOTYPE** ▾



Gender ▾ IS ▾ female ▾ 

AND OR
















MMSE score [lowest] ▾ < ▾ 29 ▾  

AND OR

**OTHER SEARCH FIELDS** ◀

 Reset  Build Query


((Gender:female) AND (MMSE\_score\_[lowest]:<29))

Source	openAccess		linkedAccess		restrictedAccess	
mockdata_1 (Cafe Variome Demo 4)						
mockdata_2 (Cafe Variome Demo 4)	6		0		0	
mockdata_3 (Cafe Variome Demo 4)						








# EDS Consortium Cafe Variome

The screenshot shows the homepage of the EDS Consortium Cafe Variome. The header features the EDS logo (Ehlers-Danlos syndrome Consortium) and a 'CV' icon. Navigation links include 'Home', 'Discover', and 'Contact'. Utility icons for search, settings, email, user profile, and 'Logout' are present. A sidebar on the left contains a 'News' section with three entries: 'EDS Consortium Meeting - Glasgow June 6th 2015...' (01 April 2015), 'Ghent University COL3A1 Variants...' (10 July 2014), and 'EDS Cafe Variome goes live...' (19 June 2014). The main content area has a large heading 'Welcome to the EDS Cafe Variome' followed by a paragraph explaining the installation's purpose for controlled discovery of EDS patients and variants. It also states that individual research groups can deposit data with controlled access levels. A note mentions that no data is currently accessible to anyone outside the consortium, with a link to 'View current source statistics here.' A prominent green button at the bottom of the main area says 'Start Discovering Variants'.

**EDS**   
Ehlers-Danlos syndrome  
Consortium

Home Discover Contact

    Logout

 News

[EDS Consortium Meeting - Glasgow June 6th 2015...](#)  
01 April 2015

[Ghent University COL3A1 Variants...](#)  
10 July 2014

[EDS Cafe Variome goes live...](#)  
19 June 2014

[Read more...](#)


## Welcome to the EDS Cafe Variome

This Cafe Variome installation has been set up for the Ehlers Danlos Syndrome Consortium to allow the controlled discovery of EDS patients and variants without revealing detailed information that might compromise the research value of the data.

Individual research/clinical groups can deposit data in this installation and control access to their data. The access-control levels range from fully open and immediately available, to fully controlled and only available upon request.

At present, none of the data in this installation can be accessed by any person outside of the EDS Consortium.

View current source statistics [here](#).



<http://eds.cafevariome.org>

# COL3A1: Six Data-match Discoveries

- Two examples:
- c.812G>A p.(Arg271Gln)
  - Site #1: two EDS entries: both “Probably Pathogenic”
  - Site #2: (no phenotype specified) VUS
- c.3938A>G p.(Lys1313Arg)
  - Site #1: two EDS entries: one “Pathogenic” & the other “Probably Pathogenic”
  - Site #2: (no phenotype specified) VUS
  - Site #3: “Pathogenic”

## List of Café Variome adopters (July2016)

- **Café EDS**                      **EDS Mendelian mutations**                      **private network**
- **Café HCV**                      **HCV bio-samples**                      **[public]**
- **PREPAD**                      **population & dementia cohorts**                      **private network**
- **Café REQUITE**                      **Radiotherapy toxicity data**                      **[public]**
- **Café Cardiokit**                      **CVD mutation frequencies**                      **public**
- **LCBRU Biobank**                      **CVD Biobank + Omics data**                      **[public]**
- **Café eTOX**                      **Drug company toxicity data**                      **[public]**
- **Café IPSI**                      **GP Clinic data**                      **private**

# SUMMARY

- **DATA POSSESSION  $\neq$  DATA CONTROL**
- **EXPLOIT THIS INSIGHTS, e.g.,**
  - **Stress synergistic/collaborative use of data**
  - **Share alternative forms of data**
  - **Make greater use of encrypted data**
  - **Metadata standards, e.g., for data use conditions (ADA-M)**
  - **Public ledger of data sharing deals & terms (Blockchain, fees)**
  - **Create a universal 'Data Discovery Lattice'**

*[stress interoperability standards, e.g., query API, metadata, consents]*

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- ❖ *The community of Café Variome adopters*

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- Raymond Dalgleish**

- Owen Lancaster**
- Robert Hastings**
- Robert Free**



innovative  
medicines  
initiative



Tissue Directory and  
Coordination Centre