

# Genomic data - improving discovery and access management

Wednesday 14 June 2023

 [biocommons.org.au](https://biocommons.org.au)  [AustralianBioCommons](https://www.youtube.com/AustralianBioCommons)  [@AusBiocommons](https://twitter.com/AusBiocommons)

# Acknowledgement of Country

We acknowledge the Traditional Owners and their custodianship of the lands on which we meet today.

We pay our respects to their Ancestors and their descendants, who continue cultural and spiritual connections to Country.

We recognise their valuable contributions to Australian and global society.



# Australian **BioCommons**

Actively supporting Australian life sciences research through  
bioinformatics and bioscience data infrastructure

[biocommons.org.au](https://biocommons.org.au)



[AustralianBioCommonsChannel](#)



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# Introductions



Jess Holliday  
Australian BioCommons



Mustafa Syed  
Children's Cancer Institute



Dr Andrew Patterson  
University of Melbourne



A/Prof Sarah Kummerfeld  
Garvan Institute of Medical  
Research

Images from LinkedIn and organisation webpages

# Australian Context



# Current state in Australia

- Huge amounts of human genomic data being generated
- No national solution for genomic data archiving, querying & sharing
- Data siloed within institutions and not discoverable
- Some data sent to European Genome-Phenome Archive (EGA) but:
  - It is challenging
  - Contextual metadata is lacking

<https://www.biocommons.org.au/human-genome-informatics-initiative>



images from <https://www.australiansilcarttrail.com/>

Human  
Genomes  
Platform  
Project



# The Human Genomes Platform Project

## ❓ THE OPPORTUNITY:

- Enhance capability for **securely, responsibly & FAIRly sharing** human genomics research data nationally and internationally
- Ensure **maximum value** can be derived from Australian research outputs

## 💡 THE SOLUTION:

- HGPP
- Nationally-funded **collaborative** project
- Running from Jan 2021- Nov 2023
- Deliver a **services toolbox** based on emerging **global standards**

<https://www.biocommons.org.au/hgpp>



HUMAN GENOMES  
PLATFORM PROJECT



Virtual Cohorts



DAC Automation



Federated Identity & Access Management



Data & Metadata Archiving



Communications, Documentation & Training

Project Partners





# What's in our toolbox?

## virtual cohorts



## DAC approval



## Identity & access



## Data archives



## Documentation & training



## Principles:

- open source
- global standards
- build on what exists
- document



**Global Alliance**  
for Genomics & Health  
Collaborate. Innovate. Accelerate.



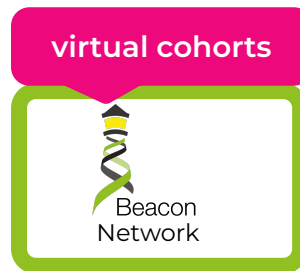
# Outputs so far...

- Knowledge discovery reports and documentation published to Zenodo, GitHub
- Posters and oral presentations delivered at multiple national and international conferences
- Prototype implementations of Beacon, Beacon network, CILogon, REMS, LocalEGA
- Connections established to international initiatives - ELIXIR, GA4GH, EGA, CILogon
- Relationships built between major players in human genomics and beyond
- Foundation for future national-scale projects and initiatives

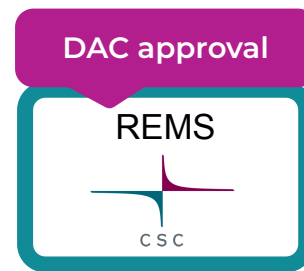
# Today's webinar



Andrew Patterson



Mustafa Syed



Sarah Kummerfeld

# IAM (Identity Access Management)

Identity management a key infrastructure plank in any federation of systems (i.e. cross institute)

There is a broadly agreed base technology set that achieves this

- Open ID Connect (OIDC)
- OAuth
- SAML
- (and to some extent GA4GH Passports/Visas on top)

# IAM (Identity Access Management)

TLDR; What all this means is that users can use their own institute credentials to login to collaborative websites.

The same technology as “login via Google” / “login via Github”.

But across all Australian universities and a lot of research institutes.

The “user” has a consistent identifier across the entire network.

# IAM in Practice

In practice then, what were the goals of the IAM stream of HGPP?

- Demonstrate the technology in practice
- Investigate gaps and recommend solutions to address these gaps
- Pilot solutions

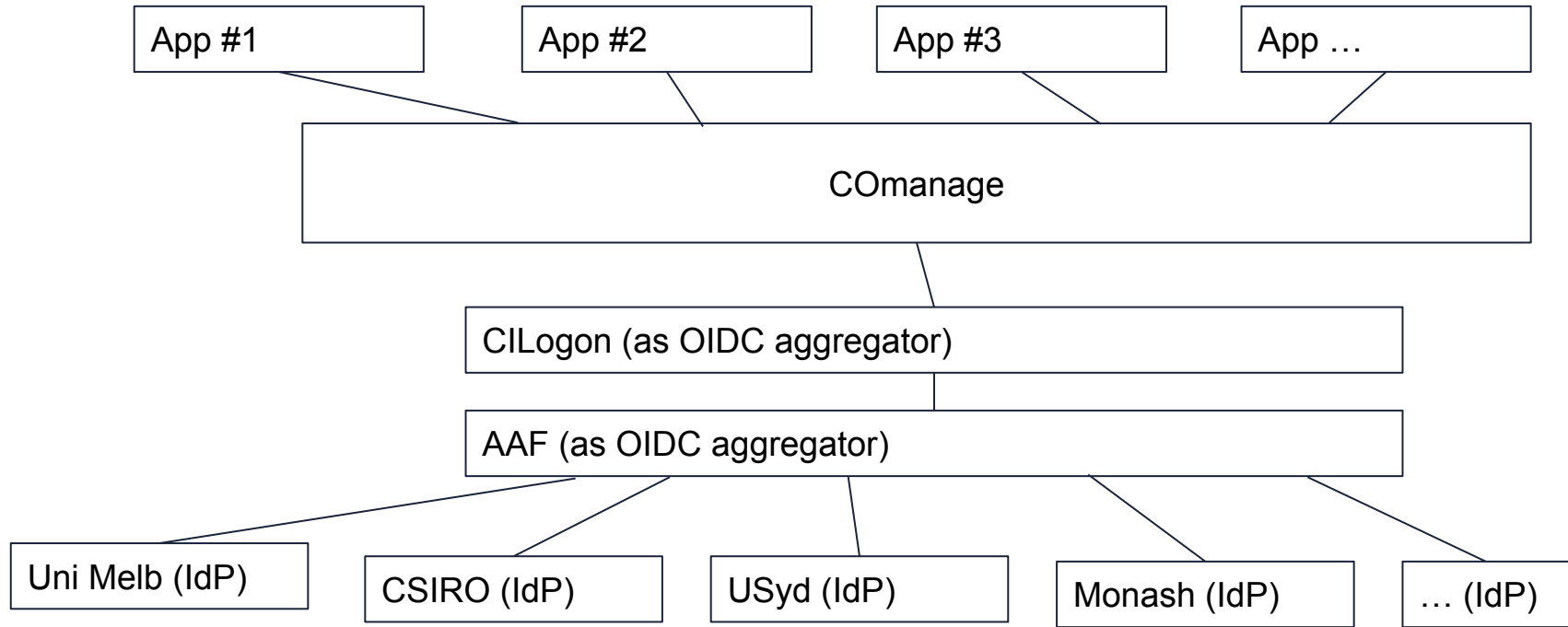
# IAM in Practice

Main gap identified in the base technology is “Community Management”  
- the ability of groups of users to self organise into communities and control rights etc

After some scans of products - chose CILogon from University of Illinois  
- National Center for Supercomputing Applications  
(<https://www.cilogon.org/>)



# CILogon / CManage



# CILogon / CManage

- Home
- Human Genomics
- My Population
- Human Genomics People
- Filter
- a b c d e f g h i j k l m n o p q r s t u v w x y z
- Name
- Status
- Roles
- Actions
- Andrew Patterson
- andrew@patto.net
- Andrew Patterson
- andrew.patterson@umccr.org
- Andrew Patterson
- andrew.patterson@unimelb.edu.au
- Display 25 records GO

Home > Human Genomics > My Population

## Human Genomics People

Sort By: [▲ Name](#) [Status](#) [Created](#) [Modified](#)

Filter

a b c d e f g h i j k l m n o p q r s t u v w x y z

Name	Status	Roles	Actions
<a href="#">Andrew Patterson</a> andrew@patto.net	Active	No Title Active	<a href="#">Edit</a>
<a href="#">Andrew Patterson</a> andrew.patterson@umccr.org	Active	No Title Active, UMCCR grp moderator, Member	<a href="#">Edit</a>
<a href="#">Andrew Patterson</a> andrew.patterson@unimelb.edu.au	Active	No Title Active	<a href="#">Edit</a>
<a href="#">Andrew Patterson</a> andrew.patterson@unimelb.edu.au	Active	No Title Active, University of Melbourne Centre for Cancer Research, Member	<a href="#">Edit</a>

Display 25 records GO

Page 1 of 1, Viewing 1-3 of 3

The Australian BioCommons is supported by Bioplatforms Australia. Bioplatforms Australia is enabled by NCRIS.

# CILogon / COmanage

Australian BioCommons



0 Andrew Patterson

[Home](#) > [Human Genomics](#) > [Groups](#) > [Edit Group](#)

## Edit HGPP Researcher by Organisation

[PROPERTIES](#)

[MEMBERS](#)

[NESTED GROUPS](#)

[PROVISIONED SERVICES](#)

[EMAIL LISTS](#)

### Source Groups

Members of each Source Group become indirect members of HGPP Researcher by Organisation

[+ Add Source Gr](#)

Name	Actions
CO:COU:Zero Childhood Cancer:members:active	<a href="#">✕ Remove</a>
CO:COU:University of Melbourne Centre for Cancer Research :members:active	<a href="#">✕ Remove</a>

### Target Groups

Members of HGPP Researcher by Organisation become indirect members of each Target Group

Name	Actions
No target groups	

The Australian BioCommons is supported by Bioplatforms Australia. Bioplatforms Australia is enabled by f

# CILogon / COmanage

PROPERTIES

MEMBERS

NESTED GROUPS

PROVISIONED SERVICES

EMAIL LISTS

## Manage Group Memberships

Add member:

ADD

Filter

Members

Owners

CLEAR FILTERS

Name	Roles	CO Person Status	Permissions
William Intan	Member via <i>CO:COU:University of Melbourne Centre for Cancer Research :members:active nested group</i>	Active	<input checked="" type="checkbox"/> Member <input type="checkbox"/> Owner
Marko Malenic	Member via <i>CO:COU:University of Melbourne Centre for Cancer Research :members:active nested group</i>	Active	<input checked="" type="checkbox"/> Member <input type="checkbox"/> Owner
Andrew UniMelb Patterson Snr	Member via <i>CO:COU:University of Melbourne Centre for Cancer Research :members:active nested group</i>	Active	<input checked="" type="checkbox"/> Member <input type="checkbox"/> Owner

# IAM in Practice (app #1)

We used CILogon in a particularly boring way - as a gateway into logging in to an application (Elsa Data)

The “group” was the blocker to being able to login (only users in the group could do that).

# IAM in Practice (app #2)

In a more sophisticated usage - we wanted to establish the concept of a “bona fide researcher”. A bona fide researcher was similarly someone who was registered in a group signifying their trust within a community - but this information needed to be passed out to the Beacon network federation.

We will now hand over to Mustafa for a demonstration of Beacon network. The CILogon IAM underpins the authentication in this cross institute system.

# Mustafa

Demo

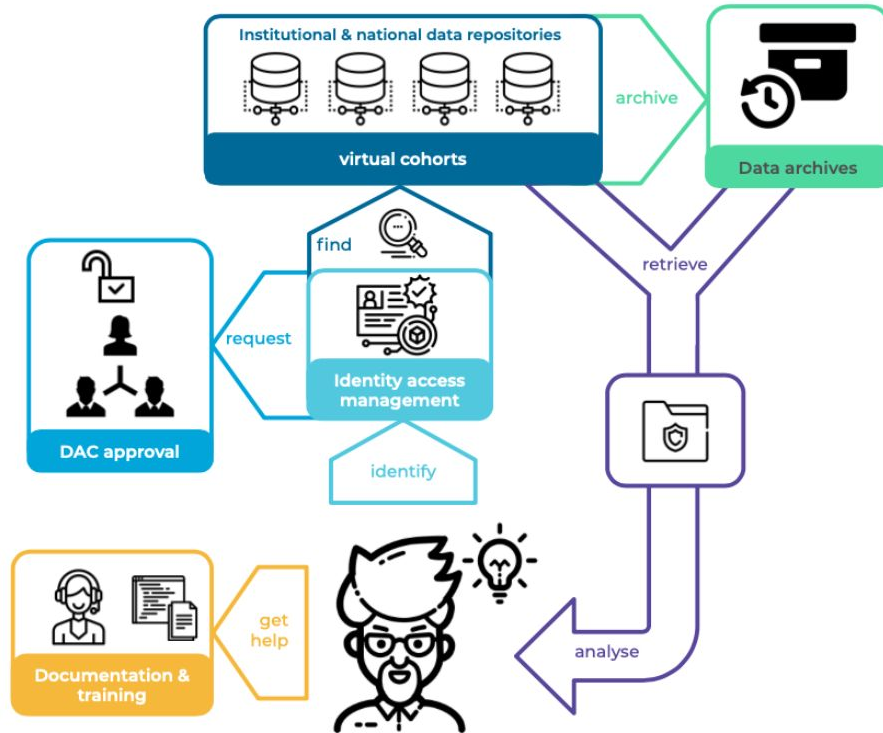
# Goal



Enhance capability for securely and responsibly sharing human genomics research data nationally



# Concept



# Current State

- ❖ We have identify set of problems that need to be addressed
- ❖ The current state of cross-institutional human genomic data querying in Australia
- ❖ The current state of processes and tools for virtual cohort querying
- ❖ Recommendations on preferred technology and proposed implementation architecture
- ❖ Candidate solutions to enable cross-institutional virtual cohort querying

# Requirements

- ❖ Common data description (ontology) to annotate data from different sources
- ❖ A minimal common data model
- ❖ Implementation of distributed search/query protocol or framework
- ❖ User interface - browse, search data, request access, download data
- ❖ Integration with other sub-project - IAM, DAC, Data Metadata Arhieve

# User Stories

## Data Model

Rank	QIMR Berghofer MRI	Garvan	NCI (JCSMR)	UMCCR	ZERO
U.S.1	<p><b>As a research user:</b> I want to know who holds sequencing data for PDAC cases <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a research user:</b> I want to identify all individuals with a particular set of clinical characteristics and obtain primary data <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a research user:</b> I have an interest in research topic X. What datasets have the required consents for me to use to address research topic X? <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a curator:</b> I want to find variant information for cancer samples of a given subtype <b>So that:</b> We can assess a novel variant</p>	<p><b>As a research user:</b> I want to find all medulloblastoma samples get access and download them <b>So that:</b> We can utilise them for research</p>
U.S.2	<p><b>As a research user:</b> I want to know who holds sequencing data for PDAC cases, from fresh-frozen tissue <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a research user:</b> I want to identify all individuals with a particular set of variants and/or clinical characteristics and obtain primary data <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a research user:</b> I want to know what restrictions I have on the use of data? <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a research user:</b> I want to find primary / read level data for published cancer cohorts stored in Australia <b>So that:</b> So I can re-process / harmonise data</p>	<p><b>As a research user:</b> I don't have access to large datasets where can I run my analyses on samples <b>So that:</b> I can perform my analyses on a cohort</p>
U.S.3	<p><b>As a research user:</b> I want to know who holds sequencing data for PDAC cases, from fresh-frozen tissue, with survival timepoints <b>So that:</b> We can build a virtual cohort of cases for discovery</p>	<p><b>As a research user:</b> I want to run analyses on my virtual cohorts in situ (i.e. bringing compute to the data) <b>So that:</b> We can analyse the data in the virtual cohort</p>	<p><b>As a research user:</b> Can I download the data and share it with my collaborators in Australia and/or overseas? <b>So that:</b> We can establish allowed uses of the data</p>	<p><b>As a research user:</b> I want to find primary / read level data for published cancer cohorts stored in Australia of a given phenotype / with minimal metadata requirements <b>So that:</b> So I can re-process / harmonise data</p>	<p><b>As a research user:</b> How can I find all paediatric (&lt; 21 yrs) <b>So that:</b> I can consolidate my data with other cohorts</p>
U.S.4	<p><b>As a research user:</b> I want to know how frequently a particular germline variant occurs in cases of healthy normal/never diagnosed <b>So that:</b> We can better understand variant distribution in the Australian population</p>	<p><b>As a research user:</b> I want to share data and analyses on my virtual cohorts in situ (i.e. bringing compute to the data) <b>So that:</b> We can analyse the data in the virtual cohort</p>	<p><b>As a research user:</b> Where can I perform computation on data once I have identified all required samples to comply with DAC requirements? <b>So that:</b> We can analyse the data in the virtual cohort</p>	<p><b>As a research user:</b> I want to find primary / read level data for published cancer cohorts stored in Australia of a given phenotype / with minimal metadata requirements and with data access control requirements matching my research plan <b>So that:</b> So I can re-process / harmonise data</p>	<p><b>As a research user:</b> I want to be able to access various cohorts and studies <b>So that:</b> I know how to normalise my data with the virtual cohort(s)</p>
U.S.5	<p><b>As a clinician researcher user:</b> I want to know who holds clinical data including treatment regime and survival timepoints, for PDAC cases with KRAS G12D mutation <b>So that:</b> We can build a virtual cohort of cases for analysis</p>	<p><b>As a research user:</b> I want to identify samples with a particular set of clinical characteristics and/or variants that have available tissue for follow up studies <b>So that:</b> We can perform follow up research</p>	<p><b>As a research user:</b> [How] can I reconnect with participants for follow up sample, additional information, or return results of incidental findings? <b>So that:</b> We can perform follow-up research and potentially return results</p>	<p><b>As a research user:</b> I want to share primary / read level and secondary / variant level data for our own research cohorts alongside agreed-upon phenotype and minimal metadata annotation restricted by DUO codes <b>So that:</b> others can use our data</p>	<p><b>As a clinician researcher:</b> I want to build a cohort where after last follow-up the patient has status <b>So that:</b> I can build a virtual cohort for analysis</p>
U.S.6	<p><b>As a data custodian:</b> I want to limit which users can view which information — e.g. public access for catalogue type data (what do we hold) plus possibly somatic variants <b>So that:</b> Access to data is restricted or exposed as appropriate</p>				<p><b>As a research user:</b> I want to identify all Neuroblastoma patients with ALK fusions, with disease status at most recent timepoint <b>So that:</b> I can determine the prognostic impact of this driver mutation (SNPs and AMP are well established biomarkers in this disease).</p>

**Sample types:** blood, fresh frozen, nail, skin biopsies

**Sequencing Data types:** primary, secondary, WGS

**Phenotype:** cancer diagnosis, or a patient's genetic disorder

**Mutations:** SNVs, indels, and gene fusions

**Data Access:** Consent, data location, data use requirements

**Clinical metadata:** survival time, age, follow-up, disease status

**Cohort level data:** Number of patients of a certain type

# Candidate Solutions



CINECA - GECKO



GA4GH - Data Connect



GA4GH - Phenopacket

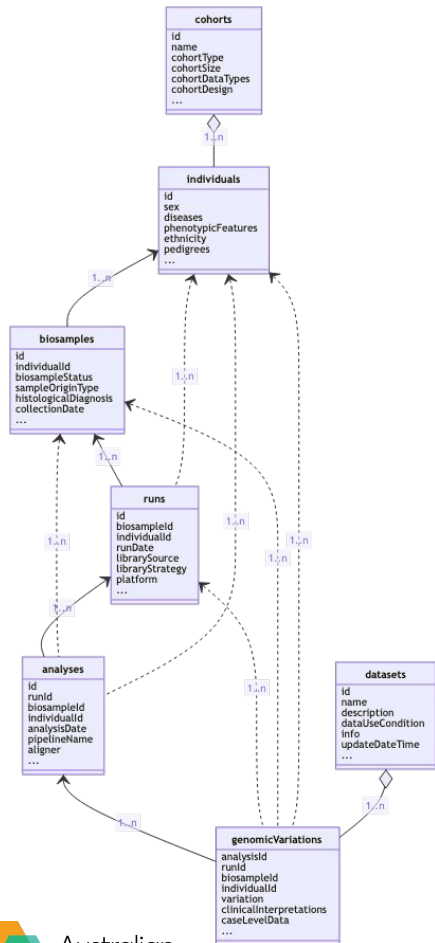
**GEN3**  
Data Commons



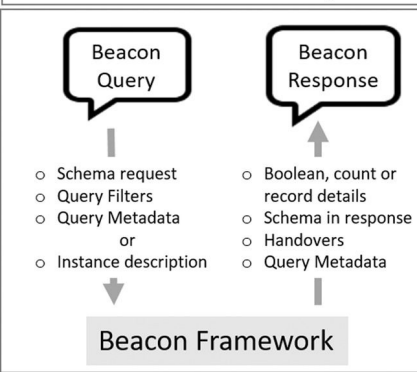
OMOP - CDM

  
**Beacon v2**

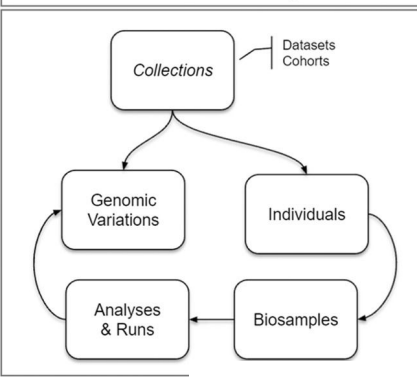
# Beacon v2



## Beacon Framework: How to Query ?



## Beacon Model: What to Query ?



### SIMPLE

Beacons can be implemented on top of any underlying variant or variant annotation datastore



### FEDERATED

Beacons can be lit and maintained by individual organizations, and assembled into a distributed network



### AGGREGATIVE

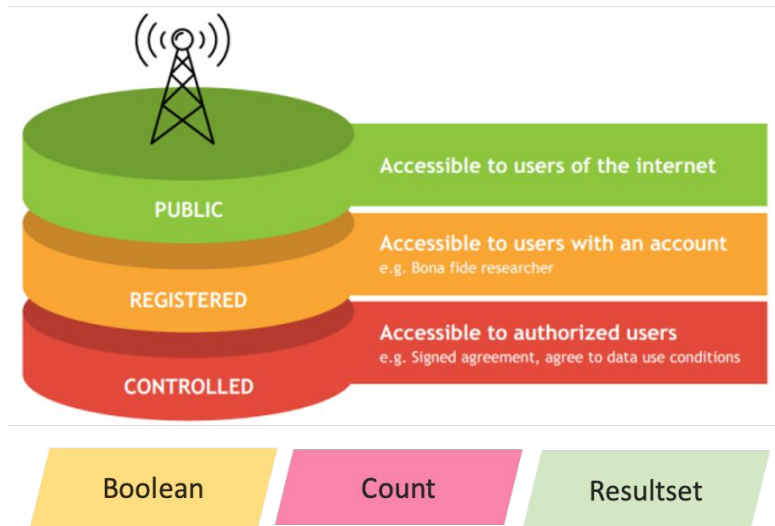
Beacon results can be aggregated across an entire populations to support de-identification.



### SECURABLE

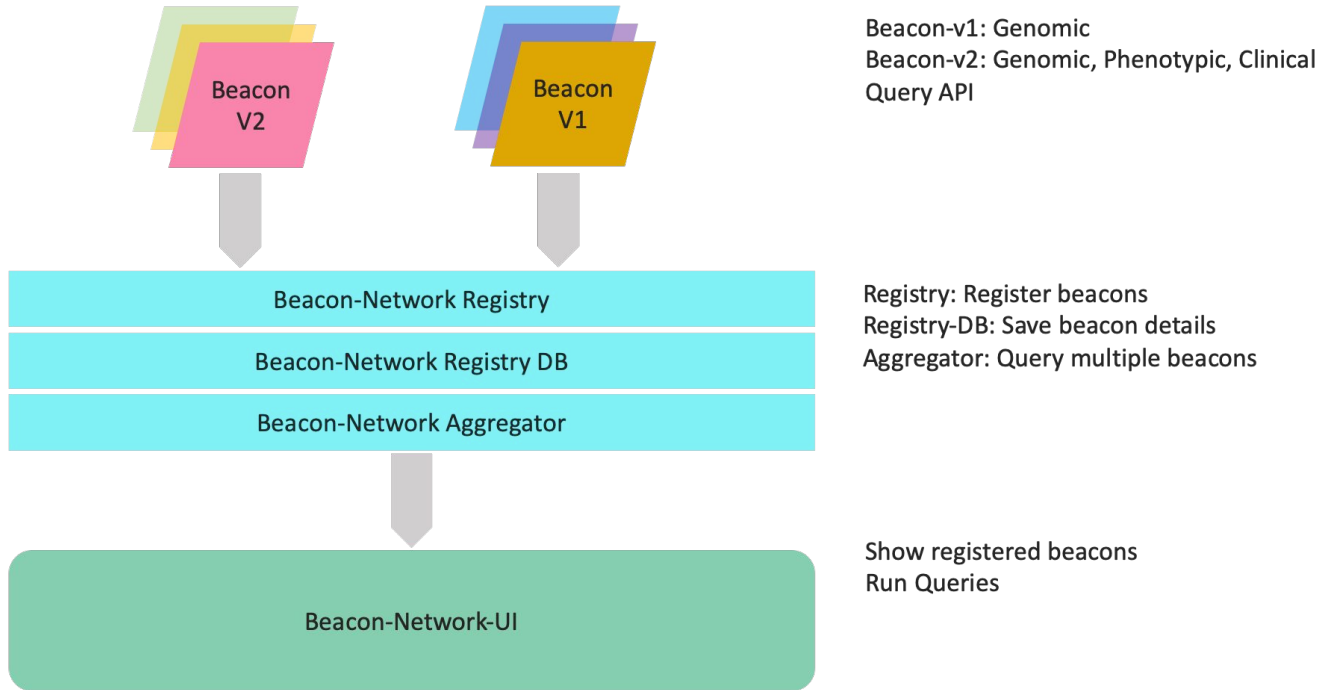
Beacon access can be restricted using institutional security protocols, and authorization schemes can be implemented to respect consent conditions.

# Data Access Control



```
"datasets": [  
  {  
    "id": "urn:hg:1000genome",  
    "name": "1000 genome",  
    "externalUrl": "ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/",  
    "description": "Data from the 1000 Genomes Project. The 1000 Genomes Project ran between 2008 and 2015 the Wellcome Trust to maintain and expand the resource.",  
    "assemblyId": "GRCh38",  
    "variantCount": 4242,  
    "callCount": 3892,  
    "sampleCount": 2504,  
    "version": "v0.4",  
    "info": {  
      "accessType": "PUBLIC"  
    },  
    "createDateTime": "2013-05-02T12:00:00Z",  
    "updateDateTime": "2013-05-02T12:00:00Z"  
  },  
  {  
    "id": "urn:hg:example-controlled",  
    "name": "Example CONTROLLED dataset",  
    "externalUrl": null,  
    "description": "Example dataset to showcase CONTROLLED access level.",  
    "assemblyId": "GRCh38",  
    "variantCount": 1,  
    "callCount": 2,  
    "sampleCount": 1,  
    "version": "1.0.0",  
    "createDateTime": null,  
    "updateDateTime": null,  
    "info": {  
      "accessType": "CONTROLLED"  
    },  
  },  
  {  
    "id": "urn:hg:example-registered",  
    "name": "Example REGISTERED dataset",  
    "externalUrl": null,  
    "description": "Example dataset to showcase REGISTERED access level for ELIXIR Bona Fide status.",  
    "assemblyId": "GRCh38",  
    "variantCount": 1,  
    "callCount": 2,  
    "sampleCount": 1,  
    "version": "1.0.0",  
    "createDateTime": null,  
    "updateDateTime": null,  
    "info": {  
      "accessType": "REGISTERED"  
    },  
  },  
],
```

# Architecture Diagram





# Beacon Network v2 UI



We have designed and implemented a UI to support Beacon v2.

The purpose of the UI is to enable querying the full catalogue of data by all members of the Beacon network.

Demo: <https://beacon-network.dev.umccr.org/>

# Demo

# Powered by **9000** Beacons enabling secure genomic data sharing and analysis

[Explore our data](#)

Don't have an account?  
[Request to register.](#)

**7209**

Individuals

**4050**

Beacons Worldwide

**4050**

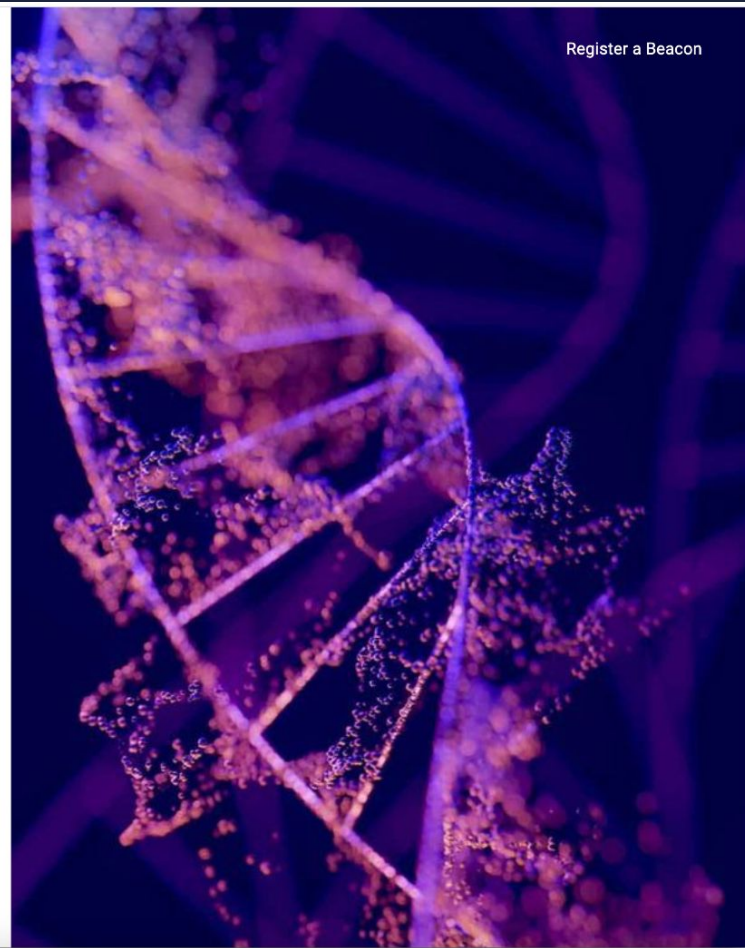
Analyses

**36**

Countries

**30000**

Biosamples



### Filter and analyse data sets

+ Add Filter

3004 records retrieved

Summary

Tab

Institution

org.umccr.demo.beacon

au.org.ccia.beacon

org.umccr.demo.beacon

au.org.ccia.beacon

org.umccr.demo.beacon

filter Individuals



with Disease

THYROIDITIS | x Select



and Sex

MALE | x Select



+ and

Cancel

Clear all

Apply

ographic Origin

and

HG00097

British

female

England

HG00099

Asian or Asian British

female

Wales

Rows per page: 5

1-5 of 3004



# Filter and analyse data sets



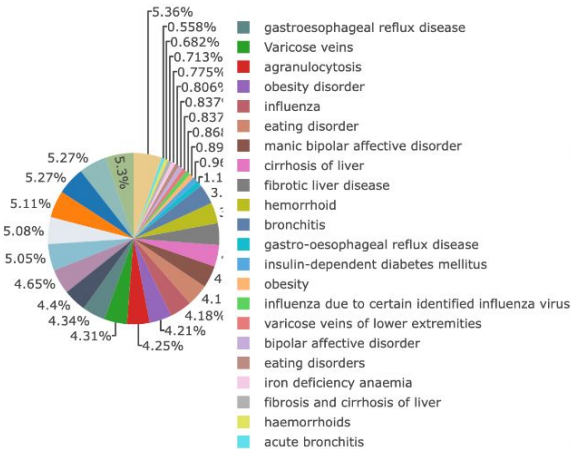
+ Add Filter

3004 records retrieved

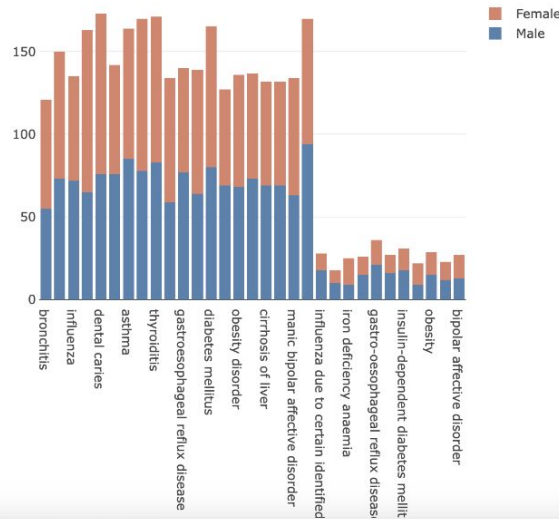
Summary

Table

### Disease distribution



### Sex distribution across diseases



Australian BioCommons [Explore](#) [About Us](#) AL

Filter and analyse data sets


+ Add Filter

3004 records retrieved

Summary **Table**

Please sign in to view the detailed results of the Beacon network

Login via CILogon

 **CILogon**

[Consent to Attribute Release](#)

Beacon UMCCR Patis (deployed dev) requests access to the following information. If you do not approve this request, do not proceed.

- Your CILogon user identifier
- Your name
- Your email address

Select an Identity Provider

Google

Remember this selection

**Log On**

By selecting "Log On", you agree to the [privacy policy](#).

For questions about this site, please see the [FAQs](#) or send email to [help@cilogon.org](mailto:help@cilogon.org).  
Know your responsibilities for using the CILogon Service.  
See acknowledgements of support for this site.

## Filter and analyse data sets

 + Add Filter

3004 records retrieved

Summary

Table

Institution	Id ↑	Disease	Ethnicity	Sex	Geographic Origin
org.umccr.demo.beacon	HG00096		African	male	-
au.org.ccia.beacon	HG00096		African	male	-
org.umccr.demo.beacon	HG00097		British	female	England
au.org.ccia.beacon	HG00097		British	female	England
org.umccr.demo.beacon	HG00099		Asian or Asian British	female	Wales

Rows per page: 5 ▾

1-5 of 3004



## Filter and analyse data sets



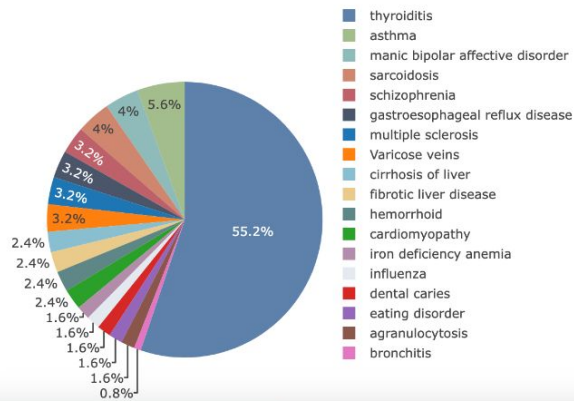
+ Add Filter

69 records retrieved

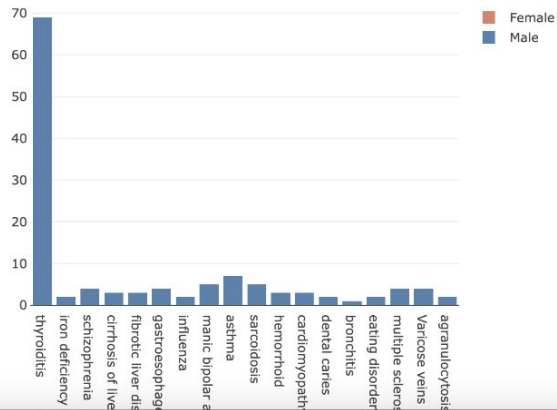
Summary

Table

### Disease distribution



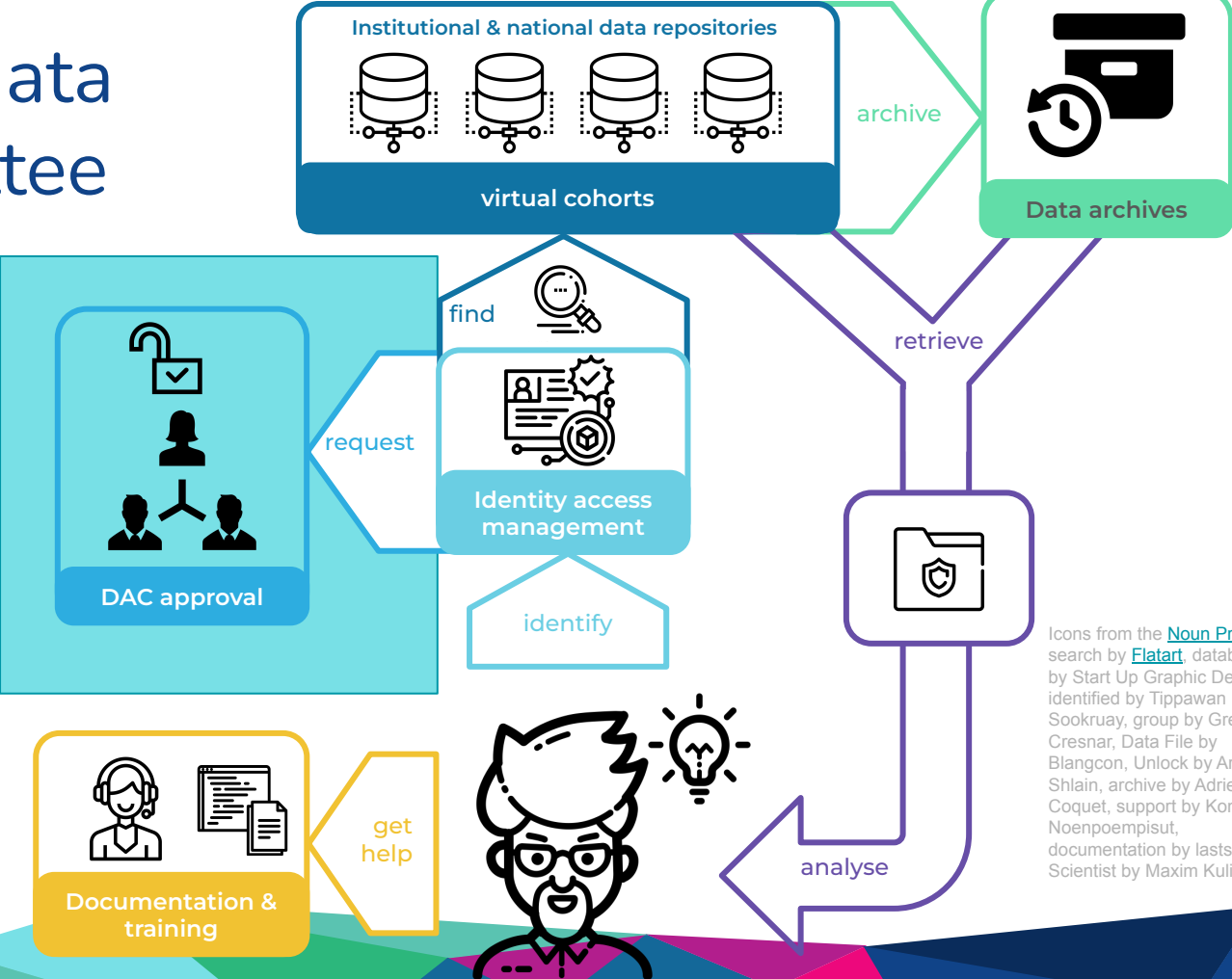
### Sex distribution across diseases





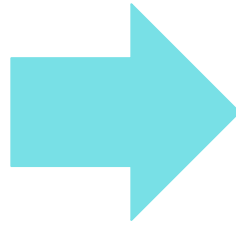
# Data Access Committee Automation

# Streamlining data access committee management



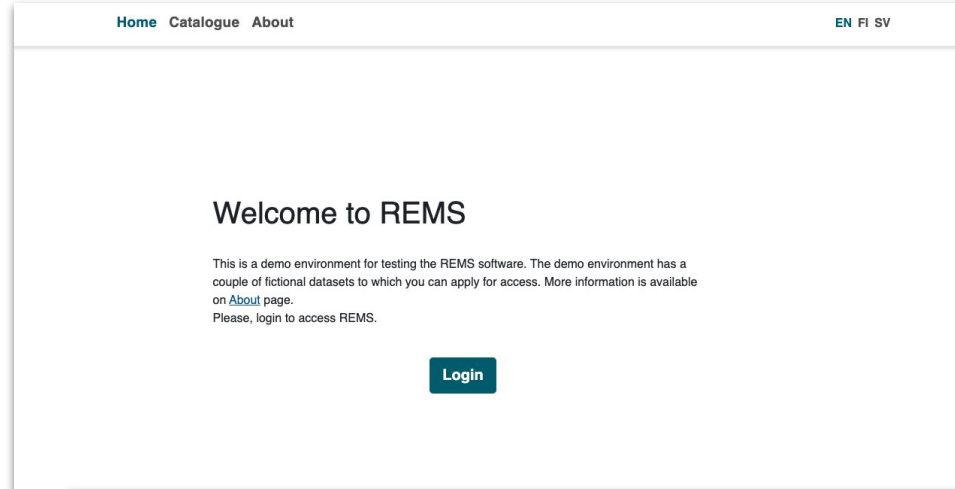
Icons from the [Noun Project](#): search by [Flatart](#), database by Start Up Graphic Design, identified by Tippawan Sookruay, group by Gregor Cresnar, Data File by Blangcon, Unlock by Arthur Shlain, archive by Adrien Coquet, support by Komkrit Noenpoempisut, documentation by lastspark, Scientist by Maxim Kullikov.

# Data Access Committee Support



# Subproject process

- ❖ Compile user stories
- ❖ Document requirements and test scenarios
- ❖ Identify candidate solutions: REMS and DUOS
- ❖ REMS installed at Garvan and UMCCR
- ❖ Business analysis of REMS
- ❖ Interaction with REMS team in Finland to add features (allow use of AWS email servers) was quick and effective
- ❖ Assess REMS against requirements using test scenarios




Home Catalogue About EN FI SV

## Welcome to REMS

This is a demo environment for testing the REMS software. The demo environment has a couple of fictional datasets to which you can apply for access. More information is available on [About](#) page.  
Please, login to access REMS.

Login



DUOS About FAQs Contact Us Sign-in/Register

## DUOS

### Data Use Oversight System

Expediting compliant data sharing, by facilitating data submissions and access requests for researchers and data access committees

#### What is DUOS and how does it work?

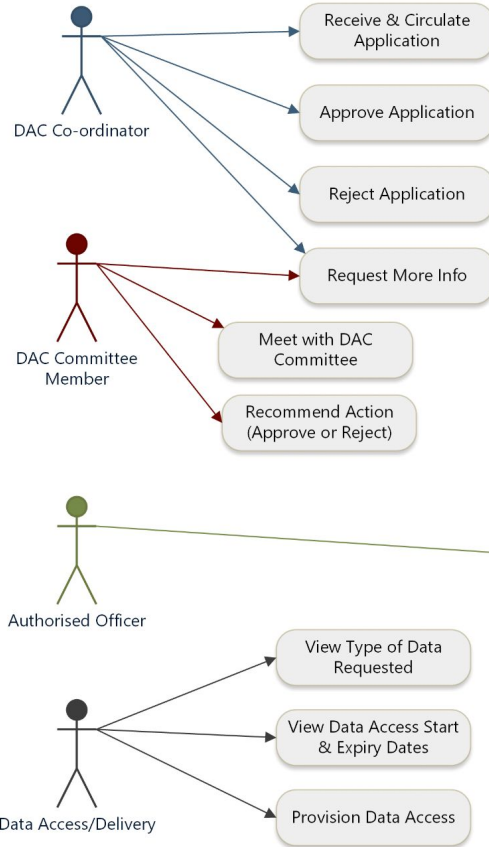
DUOS is a multi-sided data sharing platform bringing together researchers submitting and requesting data, and data access committees and institutional officials overseeing the use of the data.

Data Registration → Matching Algorithm → Data Access Request Review → Data Access Request Application

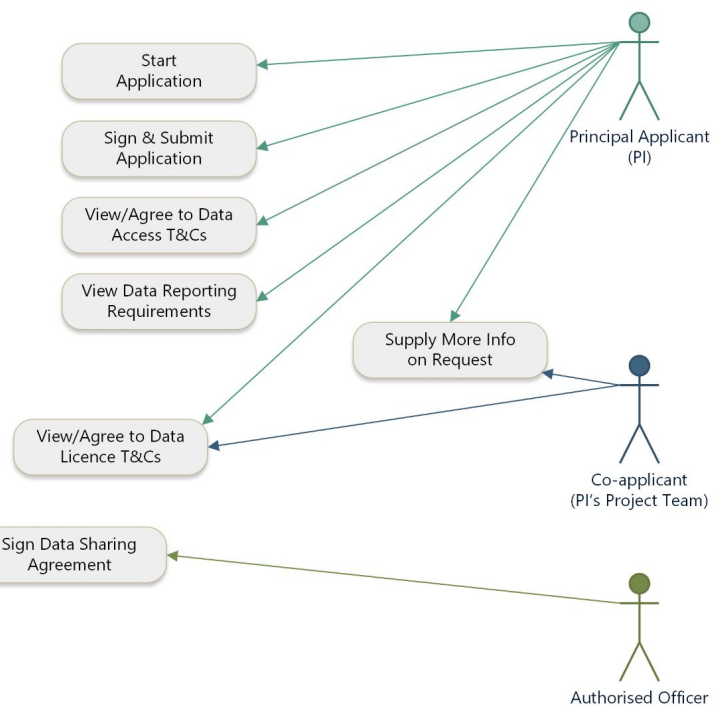
DATA REGISTRATION → MATCHING ALGORITHM → DATA ACCESS COMMITTEE (DAC) → DATA REQUESTORS

# System Use Cases | Submit Data Access Application and Approve, Reject, Sign, Provision

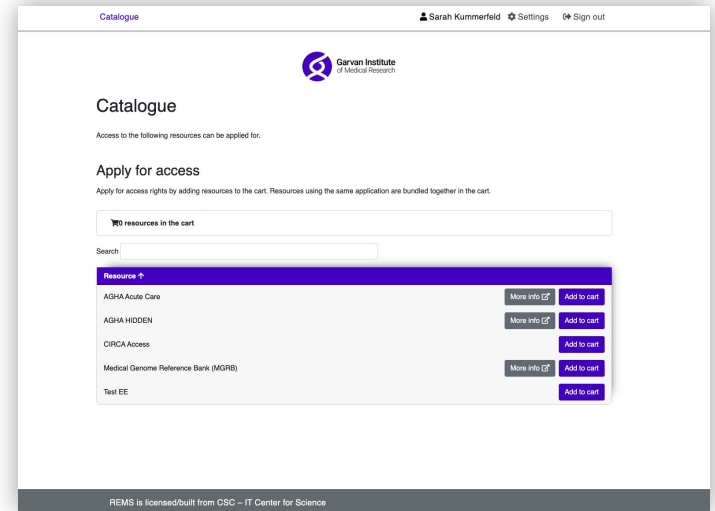
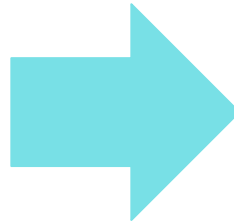
Holding Organisation - Granting Access to Data



Receiving Organisation - Receiving Data



# Case Study: Garvan Data Access Committee Automation with REMS



# Streamlining data access

- ❖ High value, access controlled datasets
- ❖ Each cohort has a separate data access committee
- ❖ Users from around the world request access
- ❖ Garvan's data science platform are the data custodians

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## Catalogue items

Create catalogue item Change form

Disabling hides an item from applicants. Archiving also hides it in the administration view.  Display archived

Search

<input type="checkbox"/>	Organization	Resource ↑	Resource	Form	Workflow	Created	Active	
<input type="checkbox"/>	default	AGHA Acute Care	[Acute Care]9da80d63-c29e-48bd-8cbb-a725f662df05	AGHA - RedCap PDF Form	Australian Genomics Health Alliance - Single Handler	2020-06-17 16:38	<input checked="" type="checkbox"/>	<a href="#">View</a> <a href="#">Edit</a> <a href="#">Disable</a> <a href="#">Archive</a>
<input type="checkbox"/>	default	AGHA HIDDEN	[HIDDEN]f387cbd4-006d-4253-9b80-70176cf2bcc6	HIDDEN Application Form	HIDDEN Workflow	2020-03-27 12:58	<input checked="" type="checkbox"/>	<a href="#">View</a> <a href="#">Edit</a> <a href="#">Disable</a> <a href="#">Archive</a>
<input type="checkbox"/>	default	CIRCA Access	[CIRCA]e95ab684-6153-4ea2-888f-8fca8644b43e	Cohort access demo	Test workflow	2020-03-20 10:33	<input checked="" type="checkbox"/>	<a href="#">View</a> <a href="#">Edit</a> <a href="#">Disable</a> <a href="#">Archive</a>
<input type="checkbox"/>	default	Medical Genome Reference Bank (MGRB)	[MGRB]741a6235-f98b-4890-842b-641d1e7ae5a1	MGRB 1.4 Form	MGRB 1.4 Workflow	2020-05-07 22:40	<input checked="" type="checkbox"/>	<a href="#">View</a> <a href="#">Edit</a> <a href="#">Disable</a> <a href="#">Archive</a>
<input type="checkbox"/>	default	Test EE	[Epileptic Encephalopathies]01ed6f6d-78d9-4da4-9f8d-80a87d73dd89	cohort access form with PDF	Test Workflow 2	2020-05-19 09:50	<input checked="" type="checkbox"/>	<a href="#">View</a> <a href="#">Edit</a> <a href="#">Disable</a> <a href="#">Archive</a>



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## Catalogue item

### Medical Genome Reference Bank (MGRB)

Organization	default
Title (EN)	Medical Genome Reference Bank (MGRB)
More info (EN)	<a href="https://sgc.garvan.org.au/">https://sgc.garvan.org.au/</a>
Resource	[MGRB]741a6235-f98b-4890-842b-641d1e7ae5a1
Workflow	MGRB 1.4 Workflow
Form	MGRB 1.4 Form
Start	2020-05-07 22:40
End	
Active	<input checked="" type="checkbox"/>

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## Actions

### Open applications

Search

Id	Title	Resource	Applicant	Handlers	Action needed	Sent	Last activity ↓
2021/7		Medical Genome Reference Bank (MGRB)		j.coply@garvan.org.au, mgb@garvan.org.au	All requests have been responded to		<a href="#">View</a>
2020/63		Medical Genome Reference Bank (MGRB)			New application		<a href="#">View</a>
2020/62		Medical Genome Reference Bank (MGRB)			New application		<a href="#">View</a>

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### Processed applications

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### Processed applications

Search

Id	Title	Resource	Applicant	Handlers	State	Last activity ↓	View
2020/66	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		m.hobbs@garvan.org.au	Approved	2023-05-04 14:28	View
2022/27	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		m.hobbs@garvan.org.au	Approved	2023-02-21 09:05	View
2022/19	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		m.hobbs@garvan.org.au	Rejected	2022-12-22 07:22	View
2022/16	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		m.hobbs@garvan.org.au	Rejected	2022-12-22 07:21	View
2022/22	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		m.hobbs@garvan.org.au	Rejected	2022-11-17 22:47	View
2022/14	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		j.coply@garvan.org.au, m.hobbs@garvan.org.au	Approved	2022-10-18 16:05	View
2022/17	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		j.coply@garvan.org.au, m.hobbs@garvan.org.au	Approved	2022-10-18 16:04	View
2022/7	Medical Genome Reference Bank (MGRB)	Medical Genome Reference Bank (MGRB)		j.coply@garvan.org.au, m.hobbs@garvan.org.au	Approved	2022-10-07 09:30	View
2022/7	Medical	Medical					

# Opportunities

- ❖ Expanded reporting (in discussion with REMS team)
- ❖ After applications are approved: Data access automation
- ❖ REMS as a service

# Acknowledgements



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# Thanks!

Any questions?

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# Questions?

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## ***International Congress of Genetics***

16-21 July 2023, Melbourne Convention and Exhibition Centre

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<https://www.biocommons.org.au/webinars-workshops>



# Thanks for joining us!

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