

# What tools and workflows should I use to fulfil an overall goal?

Emily Perry, Eleni Christodoulou

8th October 2024



# Data security

- This training session will include data from the GEL Research Environment
- As part of your IG training you have agreed to not distribute these data in any way
- You are not allowed to:
  - Invite colleagues to watch this training with you
  - Take any screenshots or videos of the training
  - Share your webinar link (we will remove anyone who is here twice)
- We will record this training and distribute the censored video afterwards

# Presenters



Emily Perry  
Research  
Engagement  
Manager



Eleni  
Christodoulou  
Solutions  
Architect at  
Lifebit

# Questions



All your  
microphones  
are muted



Use the Zoom  
Q&A to ask  
questions



Upvote your  
favourite  
questions: if  
we are short  
on time we  
will prioritise  
those with the  
most votes

# Questions



**Miruna Carmen  
Barbu**  
Bioinformatician  
- Research  
Services



**Elena Bernabeu**  
Bioinformatician  
- Research  
Services



**Alex Ho**  
Bioinformatician  
- Research  
Services



**Charlotte  
Maughan**  
Client Manager  
- LifeBit

# Agenda

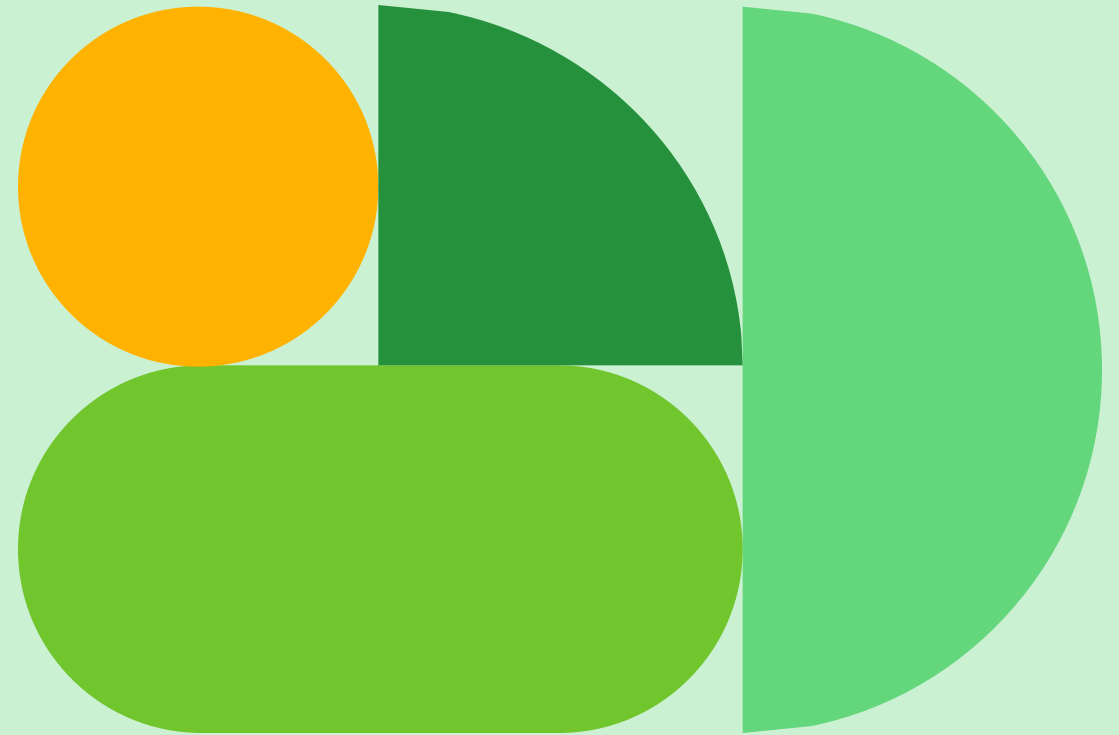
1 Introduction and admin

2 Identifying variants associated with a phenotype

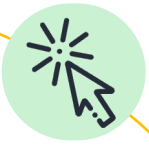
3 Identifying phenotypes associated with a gene

4 Finding diagnoses for patients who didn't get one through primary clinical interpretation

5 Help and questions



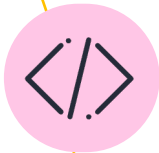
# This session



Point and click tools



Use the command line



Write your own code



Use pre-built pipelines



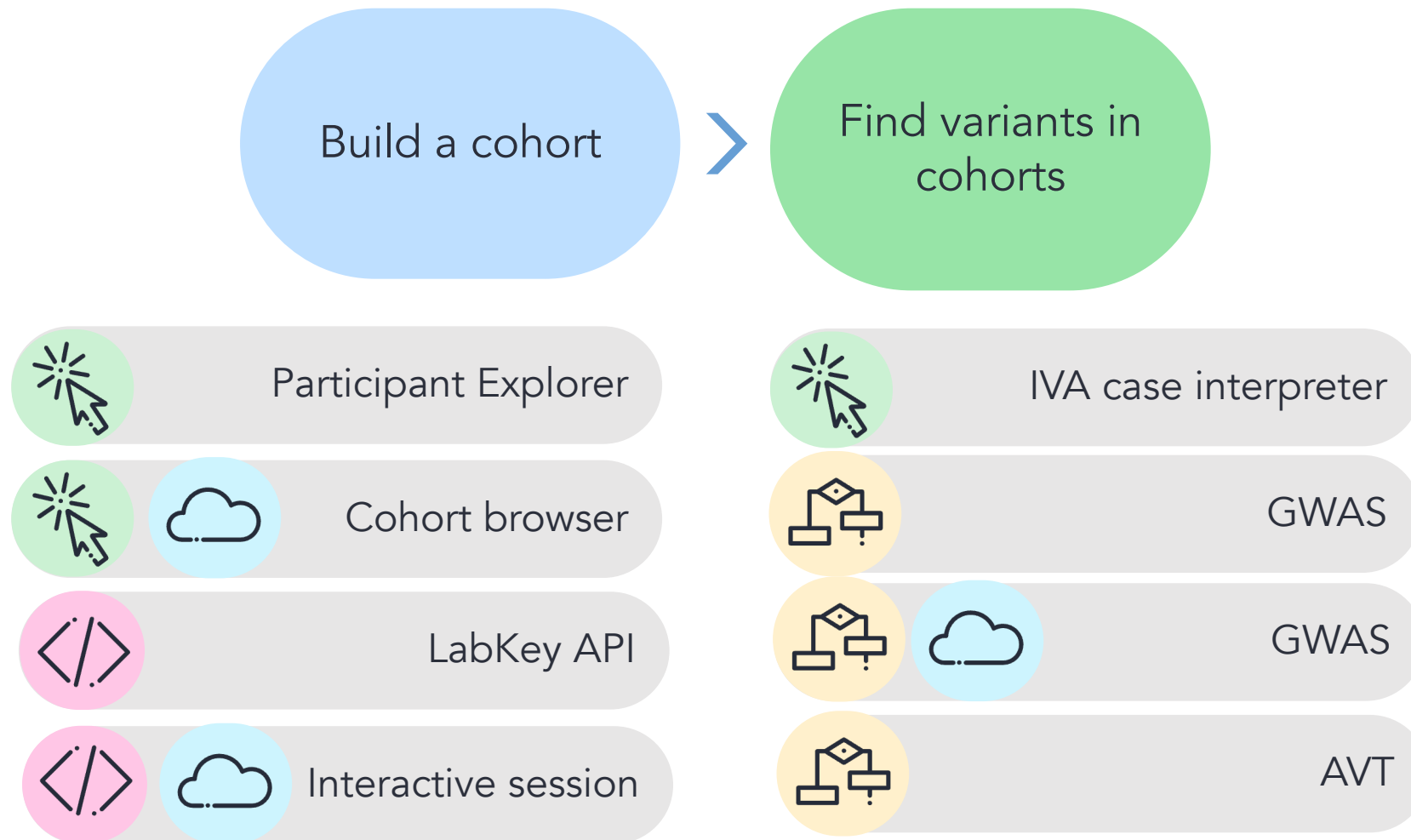
Use CloudOS

Links to more detailed online tutorials – live sessions often also available

## 2. Identifying variants associated with a phenotype



# Identifying variants associated with a phenotype





# Build a cohort – Participant Explorer



Filter participants by



Phenotypes, diagnoses



Personal details

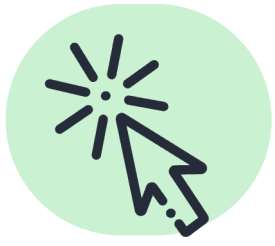


Reverse the search  
for a control cohort



Download tables  
of search results

[https://re-docs.genomicsengland.co.uk/px\\_a\\_cohorts/](https://re-docs.genomicsengland.co.uk/px_a_cohorts/)



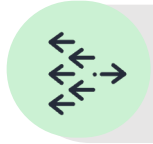
# Build a cohort – Cohort Browser



Search for participants by



Standardised OMOP tables



Structured clinical data tables

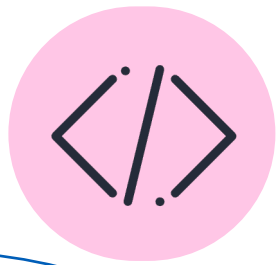


Reverse the search for a control cohort

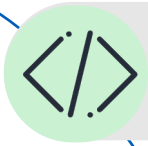


Create tables within CloudOS and download to VDI

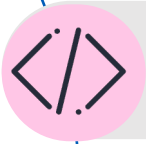
[https://re-docs.genomicsengland.co.uk/cb\\_cohorts/](https://re-docs.genomicsengland.co.uk/cb_cohorts/)



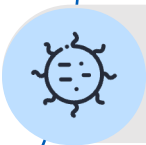
# Build a cohort – LabKey API



Use SQL queries



Tutorials in Python and R

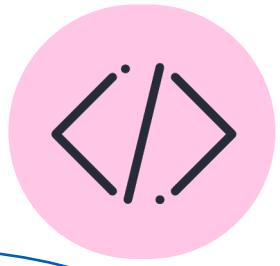


Cancer tutorial

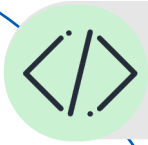


Rare disease tutorial

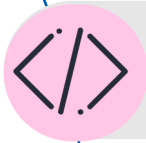
[https://re-docs.genomicsengland.co.uk/cancer\\_cohorts/](https://re-docs.genomicsengland.co.uk/cancer_cohorts/)  
[https://re-docs.genomicsengland.co.uk/rd\\_cohorts/](https://re-docs.genomicsengland.co.uk/rd_cohorts/)



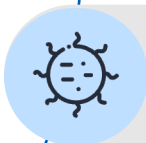
# Build a cohort – Interactive session



Use SQL queries



Tutorial in R



Cancer tutorial



Rare disease tutorial

[https://re-docs.genomicsengland.co.uk/cancer\\_cohorts/](https://re-docs.genomicsengland.co.uk/cancer_cohorts/)  
[https://re-docs.genomicsengland.co.uk/rd\\_cohorts/](https://re-docs.genomicsengland.co.uk/rd_cohorts/)

# Build a cohort demo

Chrome File Edit View History Bookmarks Profiles Tab Window Help Thu 12 Oct 09:52

Amazon WorkSpaces

Computer Text Editor Airlock Research Environment Documentation Welcome Pack

eperry's Home Data Discovery Participant Explorer report.tsv

Trash Firefox Visual Studio Code

Document Viewer IGV Browser RE Messages

IVA 2.0 R Terminal Emulator

Rocket Chat LibreOffice Panel App Research Registry

GVim Labkey Git GUI RStudio

Old Firefox Data Open Targets Emacs

LibreOffice 7.6

Applications Places System [eperry@corp.gel.ac@p... [workflows\_tr... - Jupyter... Thu Oct 12, 09:52

**Data Science**

- Data Science
- Cohorts
- Interactive Analyses
- File Explorer
- Projects
- Integrative Genome Viewer

## Dashboard

+ New

Cohort (546) [View all](#)

New Cohort

Cohort name	Owner	Date created	Date modified	Number of participants	Datasource
kidney_dysplasia_cohort	echristodoulou	10/02/2024 17:22:41	10/02/2024 17:32:27	118841	source_data_100kv17_co...
PKD1_test	echristodoulou	10/02/2024 12:17:03	10/02/2024 12:17:03	118841	source_data_100kv17_co...
PKD1_variants	echristodoulou	09/30/2024 11:17:26	09/30/2024 11:17:26	118841	source_data_100kv17_co...
mvf_strv_cohort_a	mvizueteforster	09/27/2024 13:15:07	09/27/2024 13:15:07	80502	source_data_100kv17_co...
mvf_strv_cohort	mvizueteforster	09/27/2024 13:03:46	09/27/2024 13:13:50	80502	source_data_100kv17_co...
sept_smoke_2024_005	awitulski	09/26/2024 16:15:45	09/26/2024 16:15:45	114272	source_data_100kv13_co...
sept_smoke_2024_004	awitulski	09/26/2024 16:15:20	09/26/2024 16:15:20	118841	source_data_100kv17_co...
sept_smoke_2024_003	awitulski	09/26/2024 16:14:45	09/26/2024 16:14:45	113566	source_data_100kv16_co...
sept_smoke_2024_002	awitulski	09/26/2024 16:14:20	09/26/2024 16:14:20	90177	omop_data_main_progra...
sept_smoke_2024_001	awitulski	09/26/2024 16:13:54	09/26/2024 17:42:12	54821	omop_data_100kv13_cov...


Interactive analyses (1868) [View all](#)

New Analysis


<input type="checkbox"/>	Status	Session name	Owner	Project	Created at	Total Running time	Last time saved	Cost
<input type="checkbox"/>	🔒	vlad test docker	vdembrov...	sarthak-test	10/01/2024 13:52:29	58m 28s	10/01/2024 14:52:39	\$0.3043



# Build a cohort

 Participant Explorer

  Cohort browser

 LabKey API

  Interactive session

✓		✗
use words for phenotypes	combine filters	can't save queries
OMOP available	Covid available	use codes for phenotypes
Can combine with OMICS	save queries	
GMS available	flexible output	use codes for phenotypes
easy to replicate queries		complex database schema
Covid available	flexible output	use codes for phenotypes
		complex database schema



# Find variants in cohort – IVA case interpreter



See all variants in a participant



Filter variants by



Genes, consequences, variant frequency etc



Family genotypes

[https://re-docs.genomicsengland.co.uk/iva\\_case/](https://re-docs.genomicsengland.co.uk/iva_case/)



# Find variants in cohort - GWAS



Run on the HPC



Run as a CloudOS batch job



GWAS summaries



Manhattan plots

<https://re-docs.genomicsengland.co.uk/gwas/>  
<https://lifebit.atlassian.net/wiki/spaces/CD/pages/813040563/GWAS+System+Tools>



# Find variants in cohort - AVT



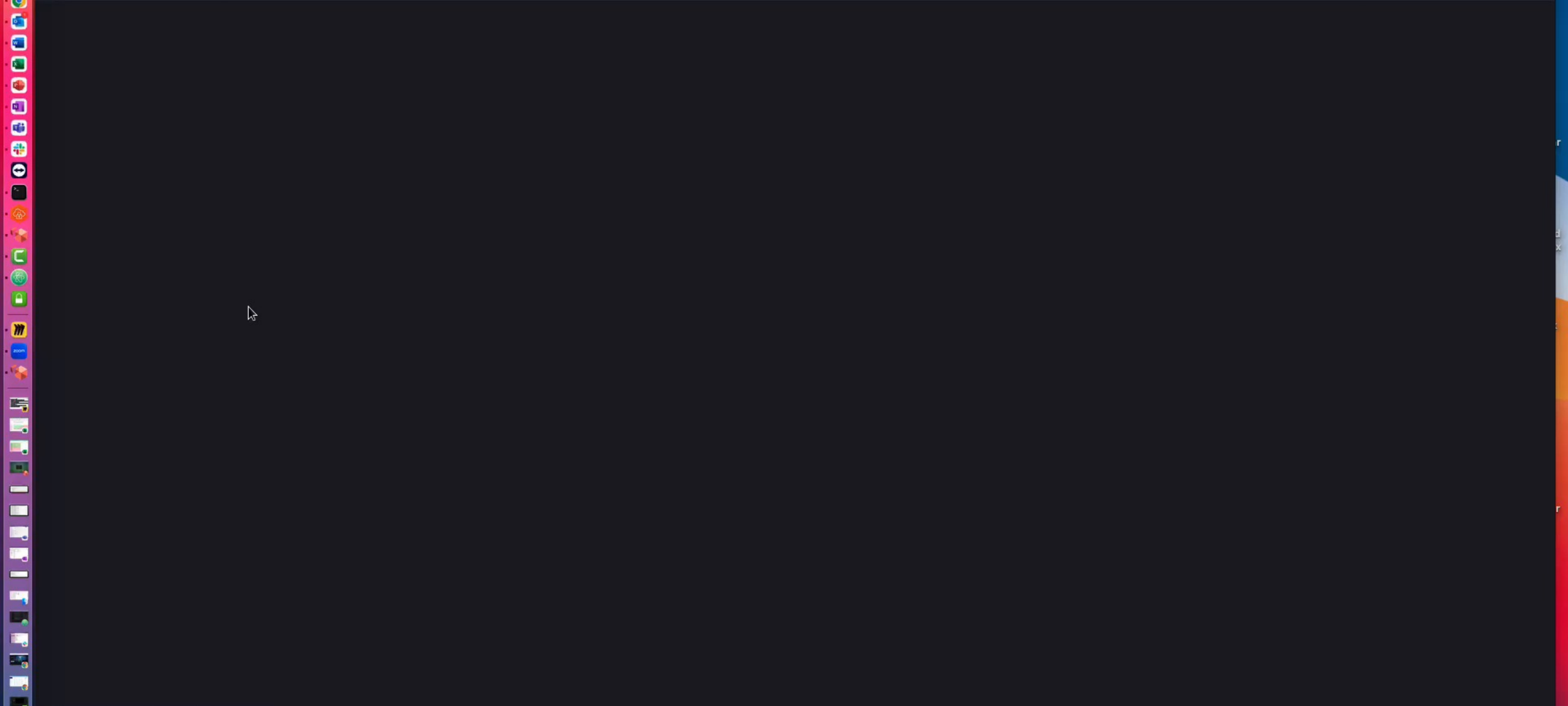
Run on the HPC



Output depends on the tools used

<https://re-docs.genomicsengland.co.uk/avt/>

Find variants in  
cohort demo



**Data Science**

- Dashboard
- Cohorts
- Interactive Analyses
- File Explorer
- Projects
- Integrative Genome Viewer

## Dashboard

New

Cohort (546) [View all](#)

New Cohort

Cohort name	Owner	Date created	Date modified	Number of participants	Datasource
polycystic_kidney_dys...	echristodoulou	10/02/2024 17:47:13	10/02/2024 17:51:51	421	source_data_100kv17_co...
PKD1_test	echristodoulou	10/02/2024 12:17:03	10/02/2024 12:17:03	118841	source_data_100kv17_co...
PKD1_variants	echristodoulou	09/30/2024 11:17:26	09/30/2024 11:17:26	118841	source_data_100kv17_co...
mvf_strv_cohort_a	mvizueteforster	09/27/2024 13:15:07	09/27/2024 13:15:07	80502	source_data_100kv17_co...
mvf_strv_cohort	mvizueteforster	09/27/2024 13:03:46	09/27/2024 13:13:50	80502	source_data_100kv17_co...
sept_smoke_2024_005	awitulski	09/26/2024 16:15:45	09/26/2024 16:15:45	114272	source_data_100kv13_co...
sept_smoke_2024_004	awitulski	09/26/2024 16:15:20	09/26/2024 16:15:20	118841	source_data_100kv17_co...
sept_smoke_2024_003	awitulski	09/26/2024 16:14:45	09/26/2024 16:14:45	113566	source_data_100kv16_co...
sept_smoke_2024_002	awitulski	09/26/2024 16:14:20	09/26/2024 16:14:20	90177	omop_data_main_progra...
sept_smoke_2024_001	awitulski	09/26/2024 16:13:54	09/26/2024 17:42:12	54821	omop_data_100kv13_cov...

Interactive analyses (1868) [View all](#)

New Analysis

<input type="checkbox"/>	Status	Session name	Owner	Project	Created at	Total Running time	Last time saved	Cost
<input type="checkbox"/>	⊖	vlad test docker	vdembrov...	sarthak-test	10/01/2024 13:52:29	58m 28s	10/01/2024 14:52:39	\$0.3043

# Find variants in cohort



IVA case interpreter



GWAS



GWAS



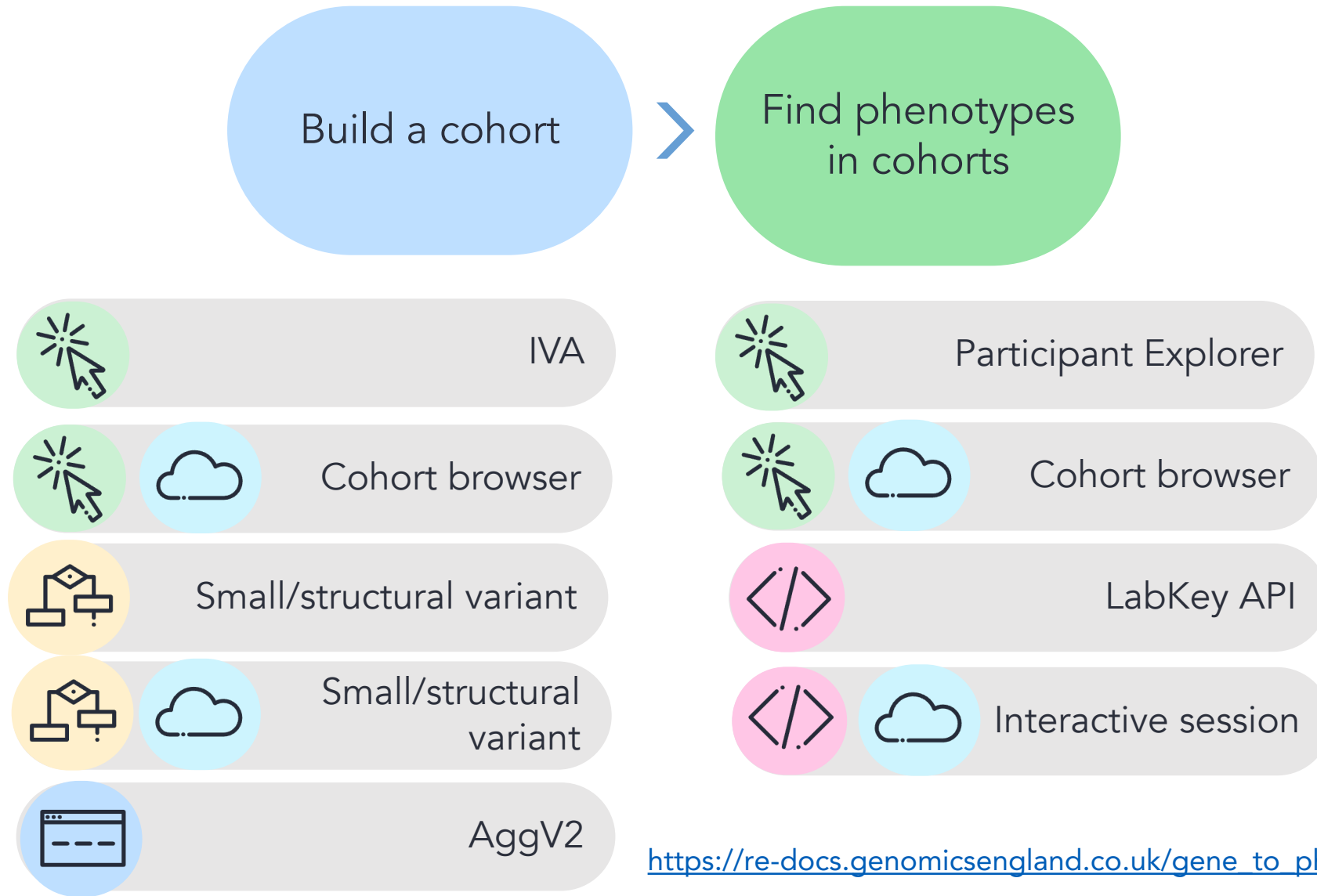
AVT

✓		✗
easy to search and interpret		one participant at a time
pre-built	common variant impact flexible options	complex to run many input files needed
pre-built	run with point and click common variant impact flexible options	many input files needed
pre-built	flexible options rare variant impact	many input files complex to interpret results



### 3. Identifying phenotypes associated with a gene

# Identifying phenotypes associated with a gene



[https://re-docs.genomicsengland.co.uk/gene\\_to\\_phenotype/](https://re-docs.genomicsengland.co.uk/gene_to_phenotype/)



# Build a cohort – IVA variant browser



See all variants



Filter variants by

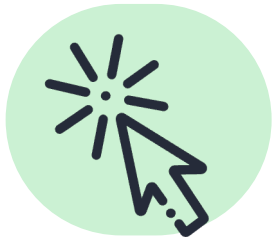


Genes, consequences,  
variant frequency etc



See all participants  
with variant

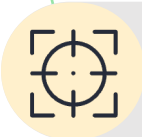
[https://re-docs.genomicsengland.co.uk/iva\\_variant/](https://re-docs.genomicsengland.co.uk/iva_variant/)



# Build a cohort – Cohort browser



See all variants



Filter variants by



Genes, consequences,  
variant frequency etc

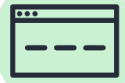


See all participants  
with variant

<https://lifebit.atlassian.net/wiki/spaces/CD/pages/813107122/Filter+cohort+by+genomic+data>



# Build a cohort – Small/structural variant workflows



Run on the HPC



Run as a CloudOS batch job



Input list of genes



List of variants in gene(s)



List of participants with variants

[https://re-docs.genomicsengland.co.uk/structural\\_variant/](https://re-docs.genomicsengland.co.uk/structural_variant/)  
[https://re-docs.genomicsengland.co.uk/small\\_variant/](https://re-docs.genomicsengland.co.uk/small_variant/)



# Build a cohort – AggV2



Aggregated VCFs  
of all variants



Participant genotypes



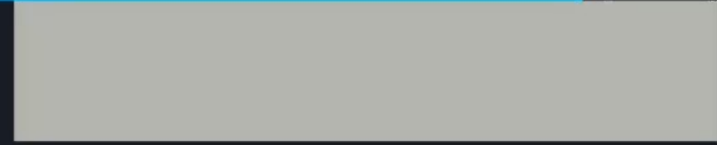
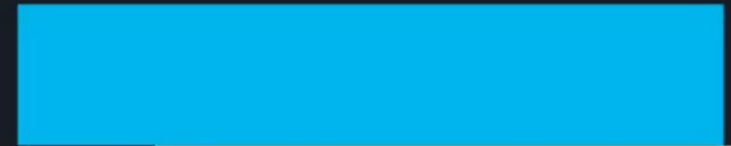
bcftools to pull  
out genotypes

<https://re-docs.genomicsengland.co.uk/aggv2>

Find participants  
with variants demo



- Computer
- Text Editor
- Airlock
- Research Environment Documentation
- Welcome Pack
- eperry's Home
- Data Discovery
- Participant Explorer
- report.tsv
- Trash
- Firefox
- Visual Studio Code
- Document Viewer
- IGV Browser
- RE Messages
- IVA 2.0
- R
- Terminal Emulator
- Rocket Chat
- LibreOffice
- Panel App
- Research Registry
- GVim
- Labkey
- Git GUI
- RStudio
- Old Firefox Data
- Open Targets
- Emacs
- LibreOffice 7.6





It looks like you haven't started Firefox in a while. Do you want to clean it up for a fresh, like-new experience? And by the way, welcome back! Refresh Firefox...



Cohort Browser / PKD1\_variants

PKD1\_variants | 118841 of 118841 participants

Run analysis

Description Add a description...

Phenotypic filter No filter applied

Genotypic filter No filter applied

Phenotypic data discovery

Omics data discovery

Overview

Cohort insights

Standard Table SQL

Phenotype

Filter data

- > aggregate\_gvcf\_sample\_stats
- > av\_imd
- > av\_patient
- > av\_rtd
- > av\_treatment
- > av\_tumour
- > cancer\_100k\_genomes\_realigned\_on\_pipeline\_2
- > cancer\_analysis
- > cancer\_care\_plan


Filter

Apply to cohort


Load query Add to Dashboard


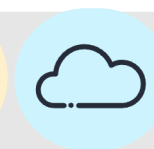
Select a phenotype


# Find participant with variants

 IVA

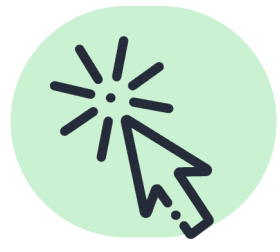
  Cohort browser

 Small/structural variant

  Small/structural variant

 AggV2

✓	✗
<p>easy to search and interpret</p>	<p>output participants one variant at a time</p>
<p>combine phenotype and omics</p> <p>save queries</p>	
<p>pre-built</p> <p>GRCh37 and GRCh38</p>	<p>CloudOS and HPC</p> <p>CloudOS user friendly</p> <p>extra input files for CloudOS</p>
<p>use BCFtools</p>	<p>command line familiarity</p> <p>subset participants</p>



# Find phenotypes in cohorts – Participant Explorer



Search for participant(s) by ID(s)

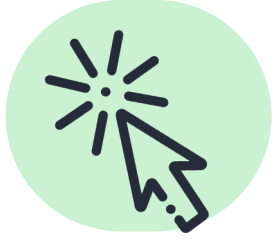


See medical history for a participant



Compare medical history between participants

[https://re-docs.genomicsengland.co.uk/mehist\\_pxa/](https://re-docs.genomicsengland.co.uk/mehist_pxa/)



# Find phenotypes in cohorts – Cohort browser



OMOP standardised format

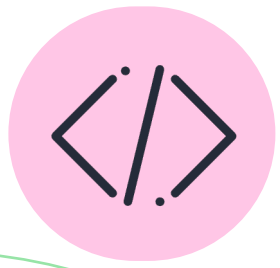


Source 100kGP clinical tables




Plots of phenotype frequencies


<https://lifebit.atlassian.net/wiki/spaces/CD/pages/813107011/Get+insights+on+your+cohort>




# Find phenotypes in cohorts – LabKey API



Use SQL queries

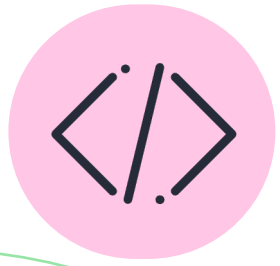


Tutorials in Python and R




Detailed medical history tables


[https://re-docs.genomicsengland.co.uk/mehist\\_api/](https://re-docs.genomicsengland.co.uk/mehist_api/)




# Find phenotypes in cohorts – Interactive session



Use SQL queries



Tutorial in R



Detailed medical  
history tables

[https://re-docs.genomicsengland.co.uk/mehist\\_api/](https://re-docs.genomicsengland.co.uk/mehist_api/)

Find phenotypes in  
cohorts demo



Computer Text Editor Airlock Research Environment Documentation Welcome Pack

eperry's Home Data Discovery Participant Explorer report.tsv

Trash Firefox Visual Studio Code

Document Viewer IGV Browser RE Messages

IVA 2.0 R Terminal Emulator

Rocket Chat LibreOffice

GVim Labkey

Old Firefox Data Open Targets

LibreOffice 7.6







Cohort Browser / polycystic\_kidney\_dysplasia\_cohort



▼ polycystic\_kidney\_dysplasia\_cohort | 421 of 118841 participants

Run analysis



Description Add a description...



Phenotypic filter **hpo\_term** IS **POLYCYSTIC KIDNEY DYSPLASIA** AND **case\_solved\_family** IS **NO** × Remove



Genotypic filter No filter applied



Phenotypic data discovery

Omics data discovery

Overview

Cohort insights



Standard Table SQL

## Phenotype

Filter data

- ▼ registered\_at\_ldp\_organisation\_name
- ▼ registered\_at\_ldp\_site\_name
- ▼ registration\_date
- ▼ reproductive\_additional\_findings
- ▼ secondary\_data\_received\_until\_year
- ▼ total\_full\_brothers
- ▼ total\_full\_sisters
- ▼ withdrawal\_form

## Filter

Apply to cohort

**hpo\_term** IS **POLYCYSTIC KIDNEY DYSPLASIA** × AND × **case\_solved\_family** IS **NO** × +

Query ▼ + Add to Dashboard

## year\_of\_birth

Database table participant

Database field year\_of\_birth


Description year\_of\_birth



# Find phenotypes in cohorts

 Participant Explorer

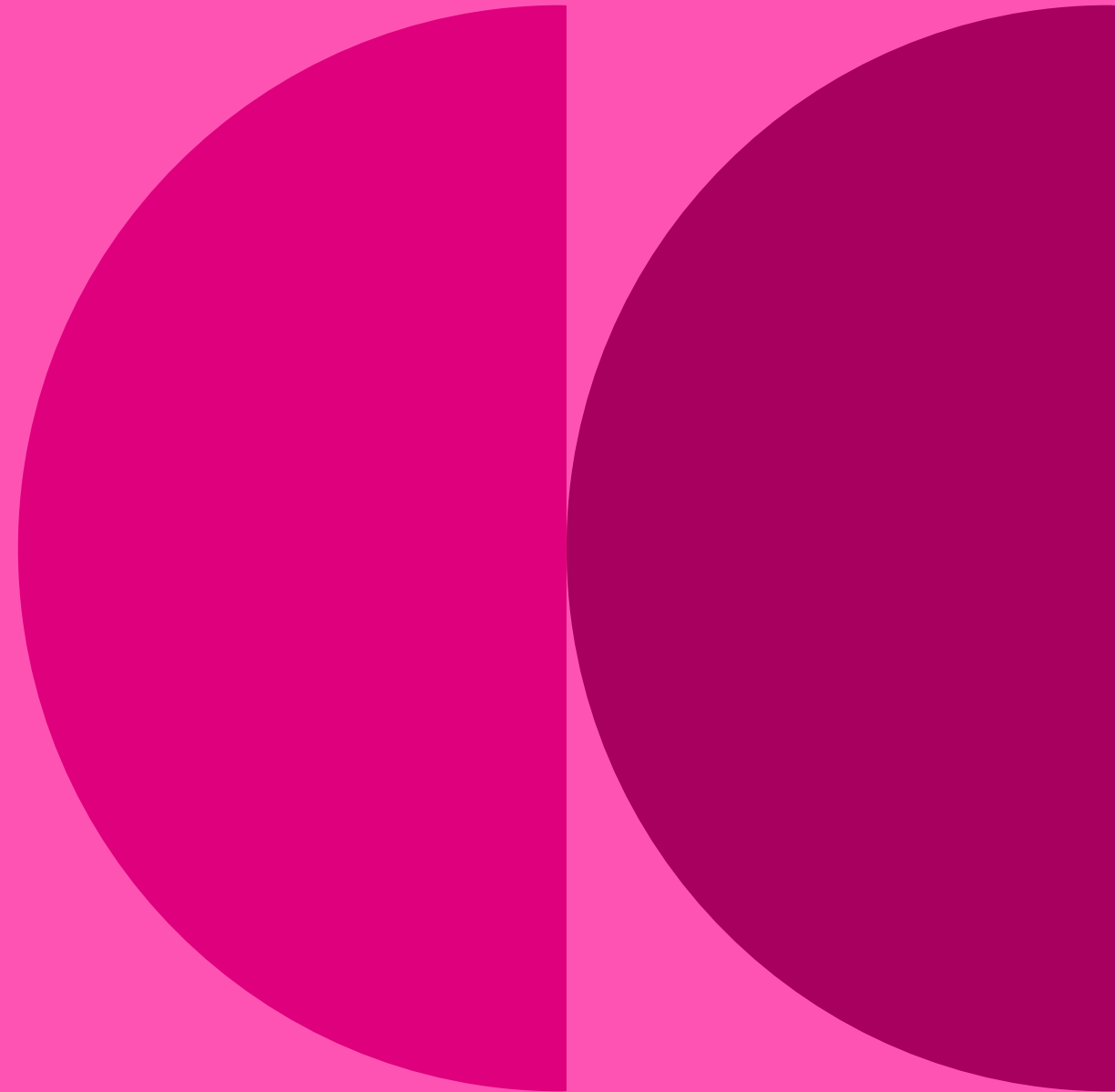
  Cohort browser

 LabKey API

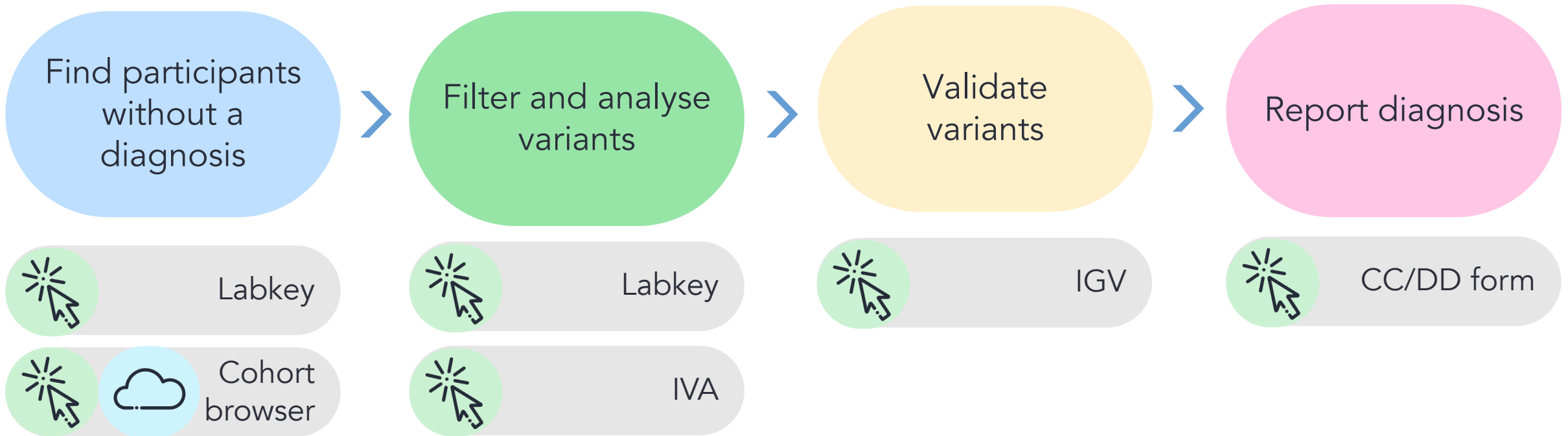
  Interactive session

✓	✗
easy to search and interpret phenotypes as words	limited scale can't save queries
graphical output of phenotypes save queries build and analyse in one tool	phenotypes as codes
flexible output	phenotypes as codes

4. Finding diagnoses for patients who didn't get one through primary clinical interpretation



# Finding diagnoses for patients who didn't get one through primary clinical interpretation





# Find participants without a diagnosis - Labkey

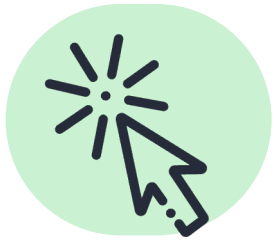


Search for participants without solved cases



See unapproved diagnoses

[https://re-docs.genomicsengland.co.uk/exist\\_questionnaire/](https://re-docs.genomicsengland.co.uk/exist_questionnaire/)



# Find participants without a diagnosis – Cohort Browser



Search for participants without solved cases



See unapproved diagnoses

[https://re-docs.genomicsengland.co.uk/exist\\_questionnaire/](https://re-docs.genomicsengland.co.uk/exist_questionnaire/)



# Filter and analyse variants - Labkey



See variants prioritised by tiering and exomiser



Look at panels used

<https://re-docs.genomicsengland.co.uk/tiering/>  
<https://re-docs.genomicsengland.co.uk/exomiser/>



# Filter and analyse variants – IVA case interpreter



See all variants in a participant



Filter variants by



Genes, consequences, variant frequency etc



Family genotypes

[https://re-docs.genomicsengland.co.uk/iva\\_case/](https://re-docs.genomicsengland.co.uk/iva_case/)





# Validate variants – IGV



Identify family BAM file locations



Visualise in IGV

<https://re-docs.genomicsengland.co.uk/igv/>



# Report diagnosis – CI/DD form



Request to contact  
clinician for:



Consent to publish



More samples or  
phenotype data



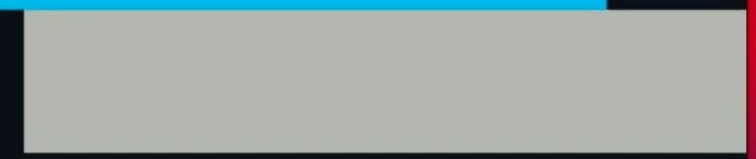
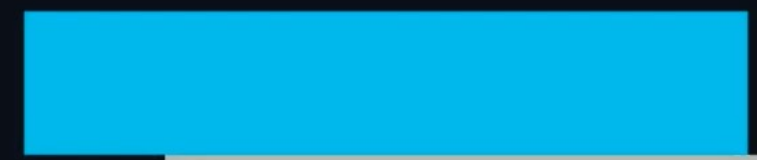
Report diagnosis to GEL

<https://re-docs.genomicsengland.co.uk/cri/>

# Diagnostic discovery demo



- Computer
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- Open Targets
- Emacs
- LibreOffice 7.6



# 5. Help and questions

# Getting help



Check our documentation:  
<https://re-docs.genomicsengland.co.uk/>  
Click on the documentation icon in the environment



Contact our Service Desk:  
<https://jiraservicedesk.extge.co.uk/plugins/servlet/desk>

# Questions



All your  
microphones  
are muted



Use the Zoom  
Q&A to ask  
questions



Upvote your  
favourite  
questions: if  
we are short  
on time we  
will prioritise  
those with the  
most votes

# Training sessions 2024

12/11

Running workflows on the HPC and  
Cloud

10/12

Introduction to the RE



Materials  
from past  
training all  
online



# Training sessions 2025

3<sup>rd</sup> Tuesday every  
month

Introduction to the RE

21/1

18/2

18/3

15/4

20/5

17/6



Materials  
from past  
training all  
online

# Training sessions 2025

14/1

Using the Research Environment for  
clinical diagnostic discovery

11/2

Importing data and tools to use in  
the RE

11/3

Working with R in the RE

8/4

Working with python in the RE

13/5

Building cancer cohorts and survival  
analysis

10/6

Building rare disease cohorts with  
matching controls



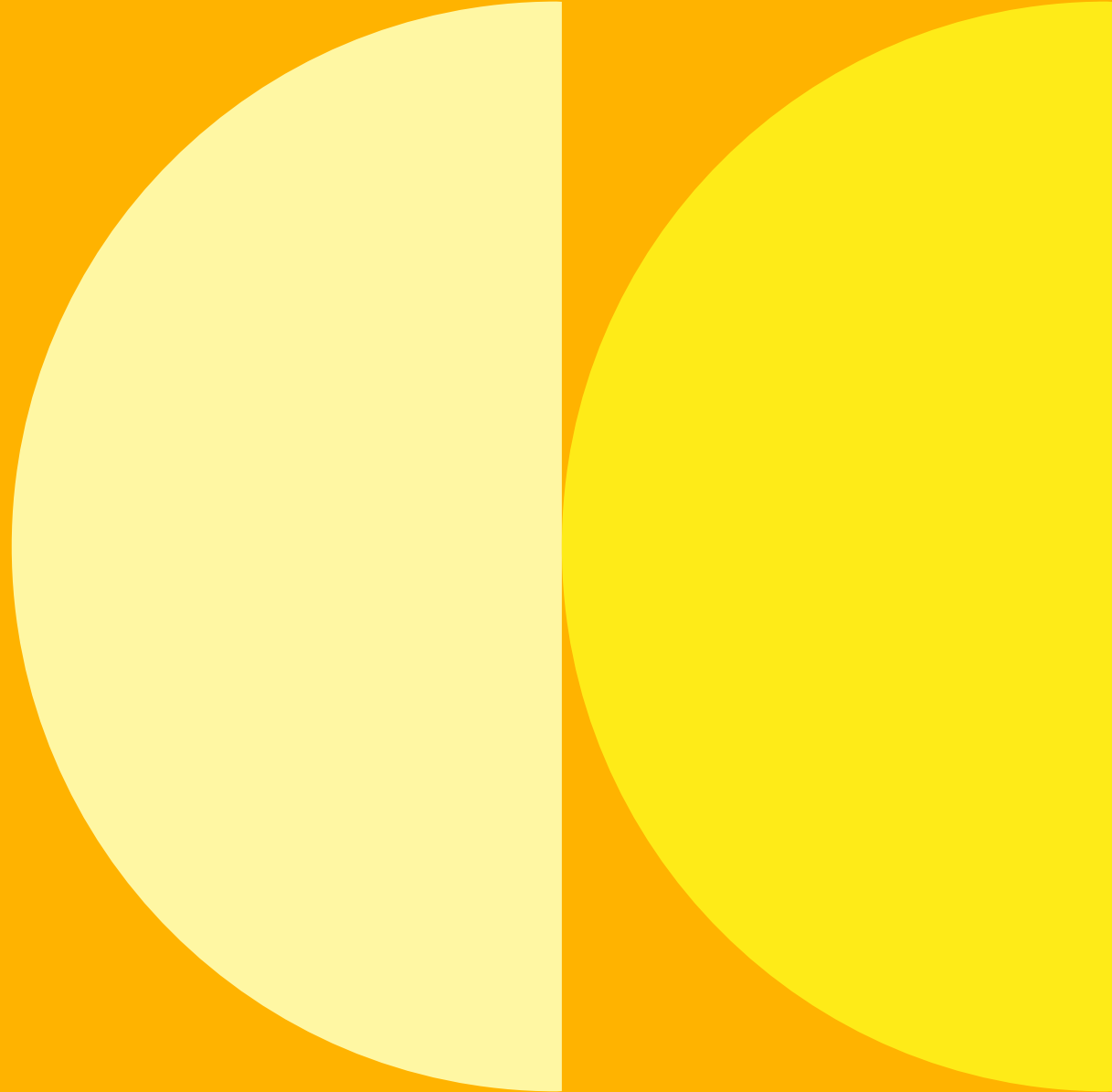
Materials  
from past  
training all  
online

# In-person training day

- For any registered RE users
- 20<sup>th</sup> November 2024
- Held in our offices at Canary Wharf
- Hybrid attendance
- Hands-on practicals and exercises



# Feedback



# Thank you

Visit: <https://re-docs.genomicsengland.co.uk/>