Genomics England

Using genomic data to build cohorts

Emily Perry

9th June 2026

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

Questions

All your microphones are muted

Use the Zoom Q&A to ask questions

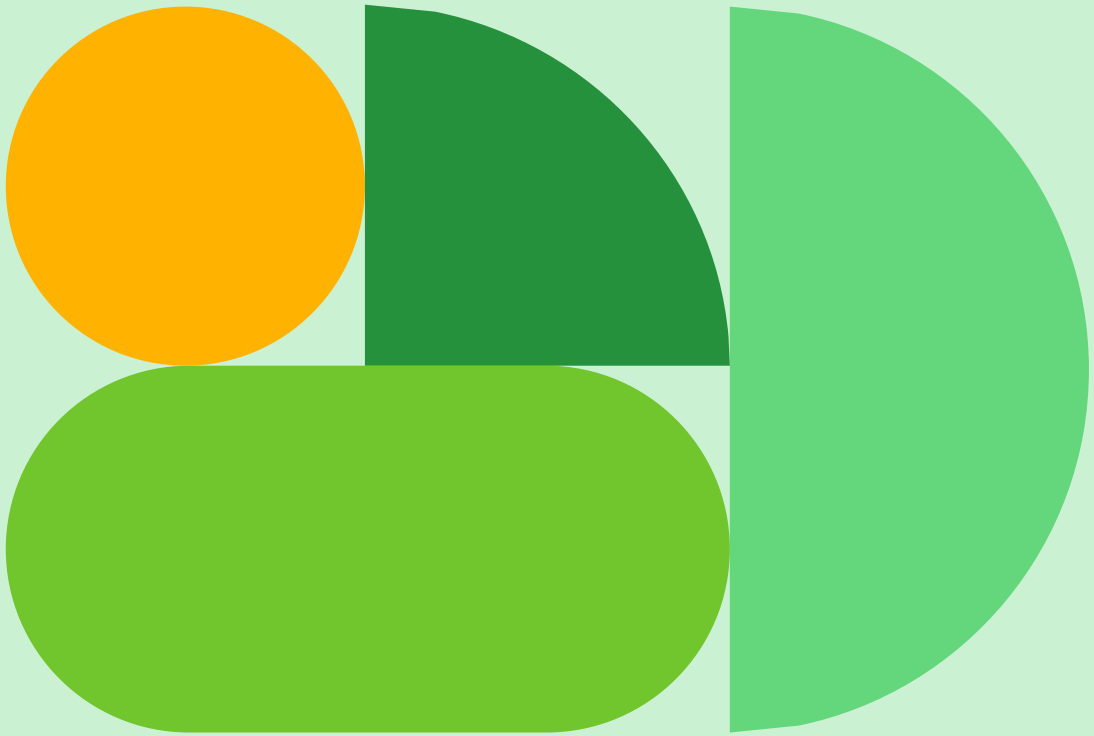
Upvote your favourite questions: if we are short on time we will prioritise those with the most votes

Questions

Matthieu Vizuete-Forster
Learning designer

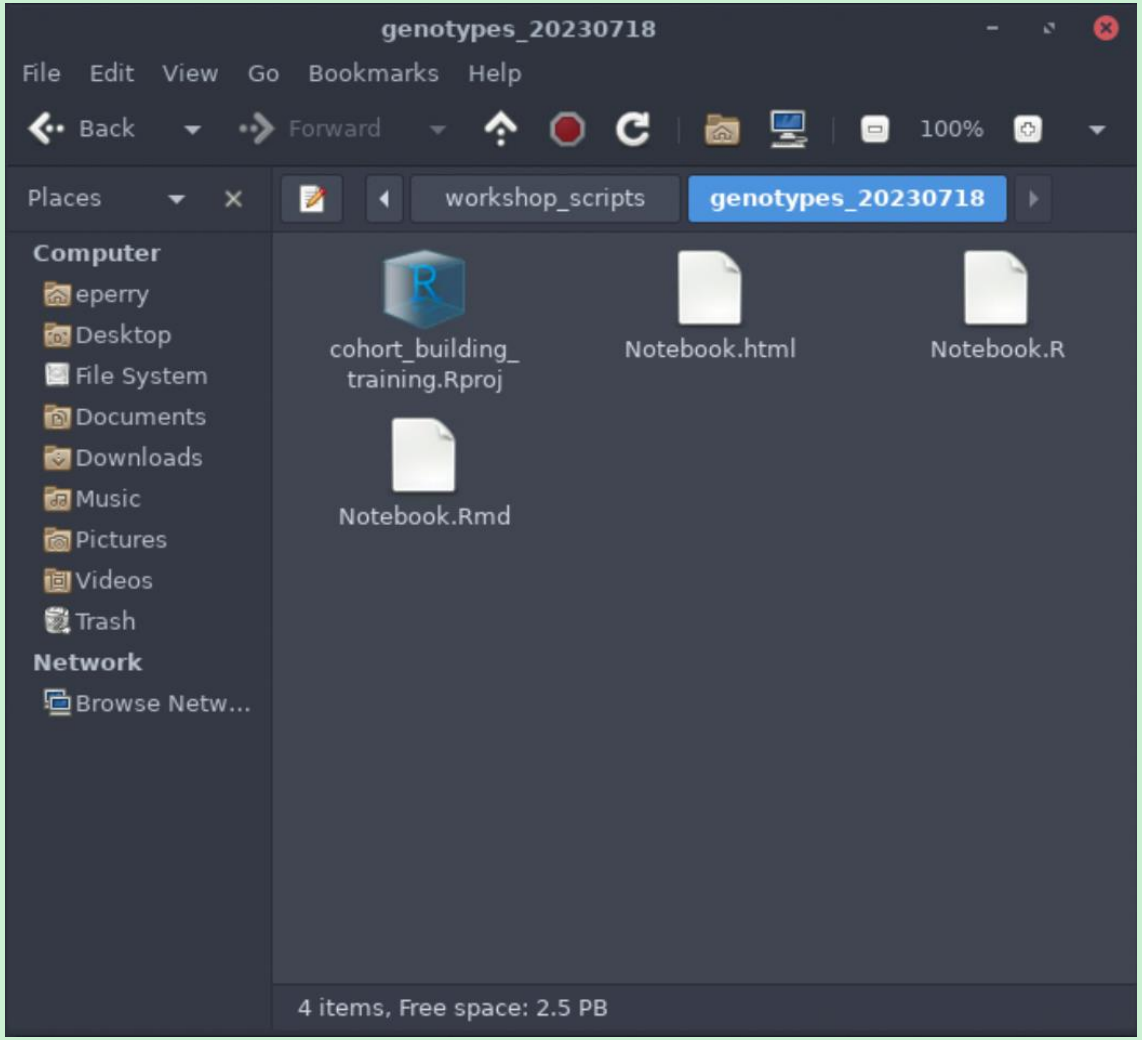
Agenda

1. Introduction and admin
2. Genome assembly
3. LabKey tables of variant genotypes
4. Finding genotypes with IVA and Cohort Browser
5. The Small Variant and Structural Variant workflows
6. Aggregated variant files
7. When/why you would use each method
8. Help and questions



Materials

- Slides and video will be sent out to you after the session
- Scripts available in `/gel_data_resources/example_scripts/workshop_scripts/genotypes_2026`



2. Genome Assembly

100,000 Genomes Project

Rare disease

GRCh37 (hg19)
GRCh38 (hg38)

Cancer

Germline GRCh37 (hg19)
Somatic GRCh37 (hg19)
Germline GRCh38 (hg38)
Somatic GRCh38 (hg38)

100,000 Genomes Project

Rare disease

GRCh37 (hg19)

GRCh38 (hg38)

Cancer

~~Germline GRCh37 (hg19)~~

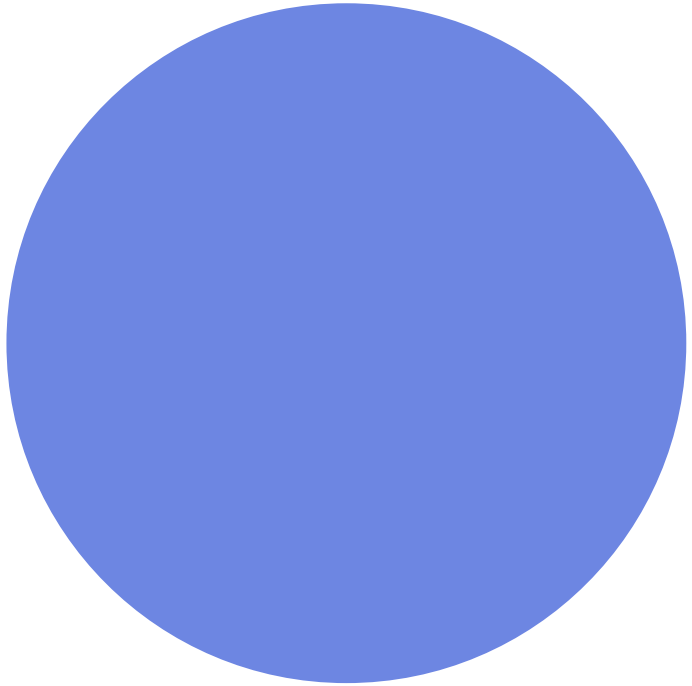
~~Somatic GRCh37 (hg19)~~

Germline GRCh38 (hg38)

Somatic GRCh38 (hg38)

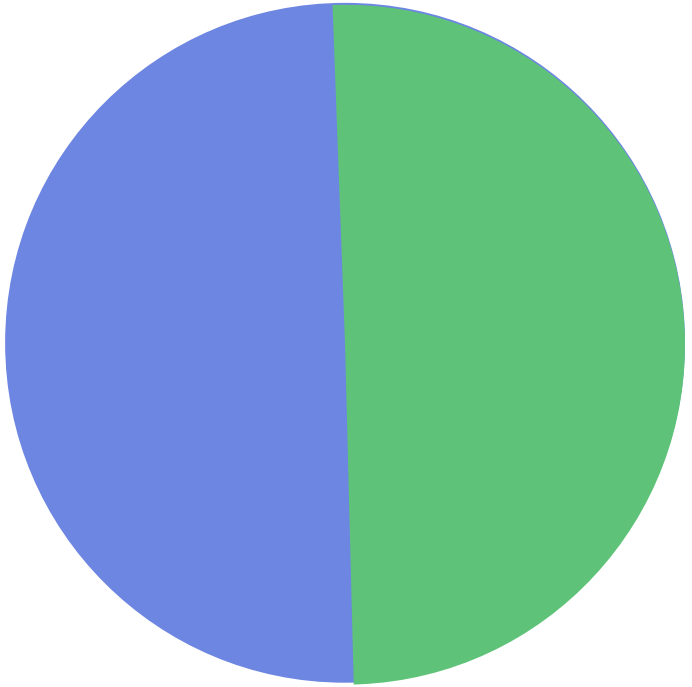
NHS GMS

Rare disease



GRCh38 (hg38)

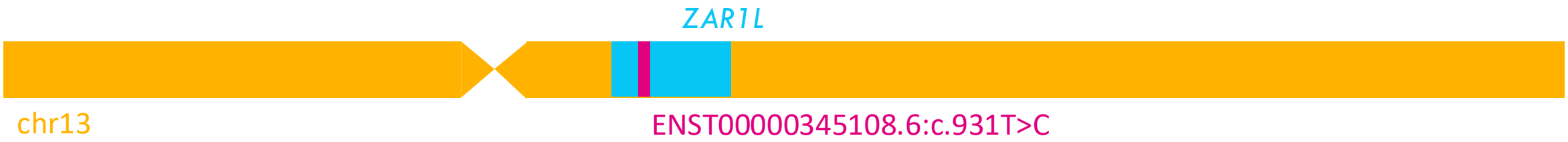
Cancer



Germline GRCh38 (hg38)

Somatic GRCh38 (hg38)

Genome assembly coordinates



	GRCh37 (hg19)	GRCh38 (hg38)
ZAR1L	13:32,877,837-32,889,481	chr13:32,303,699- 32,315,363
ENST00000345108.6:c.931T>C	13:32,878,051	chr13:32,303,914

Converting between assemblies

Inside the RE

- Liftover tool on HPC
- Chain files in `public_data_resources`

Outside the RE

- Ensembl Assembly converter
- UCSC Liftover

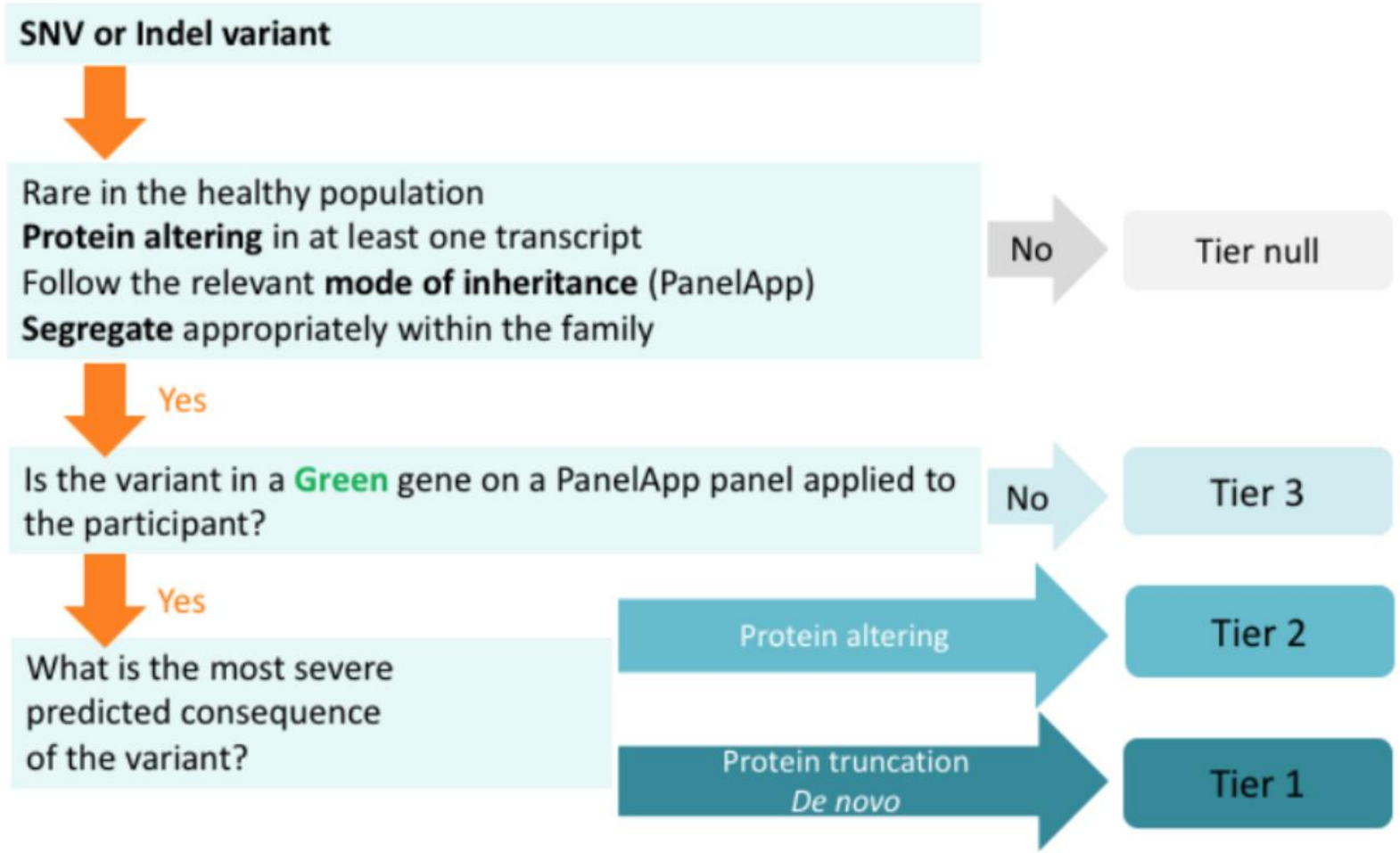
3. LabKey tables of variant genotypes

LabKey

- Participant details and family relationships
- Sample details
- Genomic file locations
- Clinical data
- Bioinformatics analysis results
  - Rare disease tiering
  - Cancer tiering
  - Exomiser

https://re-docs.genomicsengland.co.uk/labkey/

Rare disease tiering



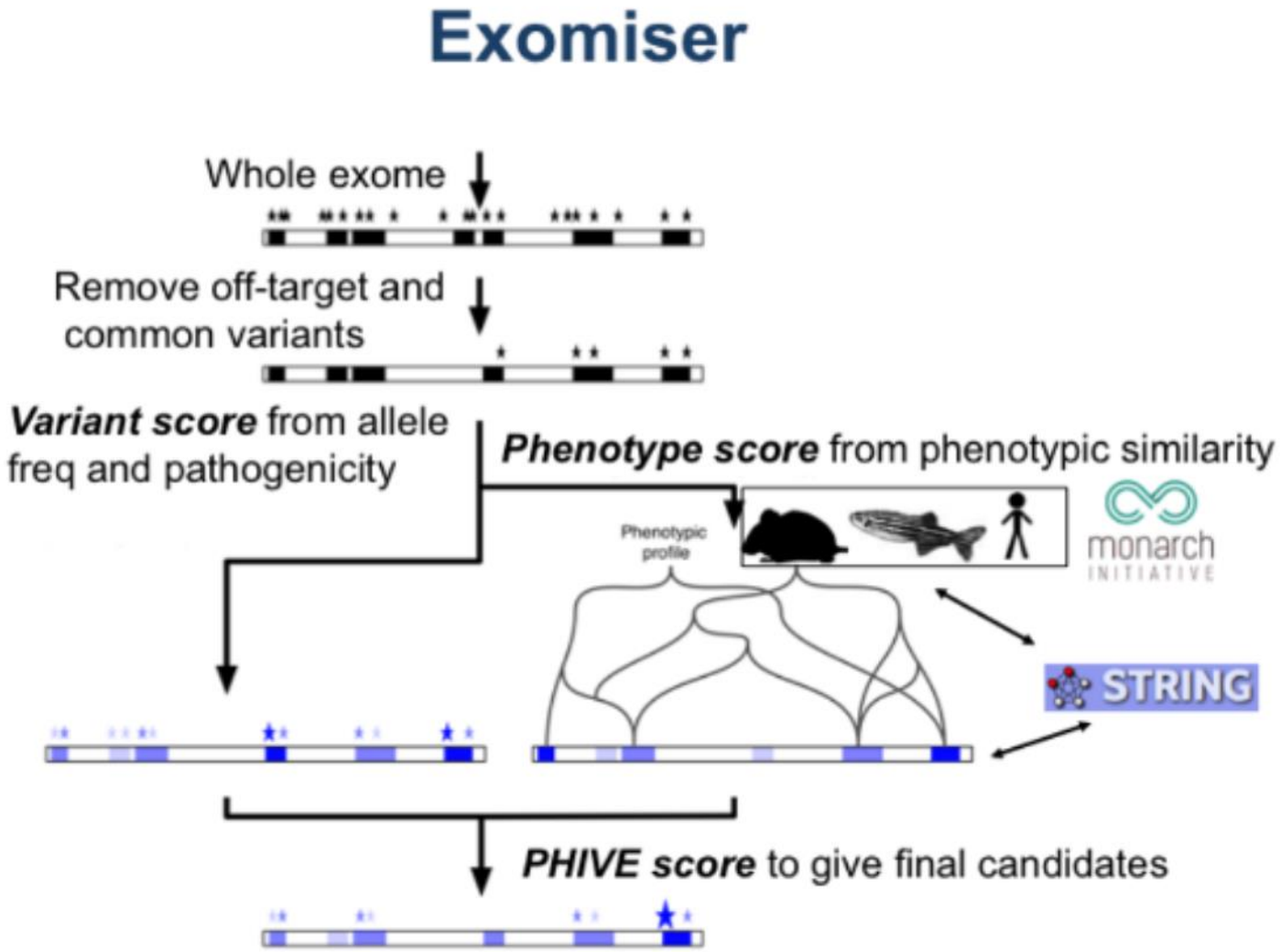
https://re-docs.genomicsengland.co.uk/tiering/

Rare disease tiering based on PanelApp genes

List	Entity	Reviews	Mode of inheritance	Details
Filter Entities				8 Entities
Green	ATP1A3	1 review 1 green	MONOALLELIC, autosomal or pseudoautosomal, NOT imprinted	**Sources** • Expert Review • Expert Review Green **Phenotypes** • 601338 • 614820 **Tags**
Green	DFNB59	2 reviews 1 green	BIALLELIC, autosomal or pseudoautosomal	**Sources** • Expert Review • Expert Review Green **Phenotypes** • 610219 **Tags** new-gene-name
Green	OPA1	2 reviews 1 green	MONOALLELIC, autosomal or pseudoautosomal, NOT imprinted	**Sources** • Eligibility statement prior genetic testing • Expert Review Green **Phenotypes** • Optic atrophy 1, OMIM:165500 • Optic atrophy plus syndrome, OMIM:125250 **Tags**
Green	OTOF	1 review 1 green	BIALLELIC, autosomal or pseudoautosomal	**Sources** • Expert Review Green • Radboud University Medical Center, Nijmegen **Phenotypes** • 601071 **Tags**
Amber	DIAPH3	3 reviews 1 red	BOTH monoallelic and biallelic, autosomal or pseudoautosomal	**Sources** • Expert Review Amber • Radboud University Medical Center, Nijmegen **Phenotypes** • Auditory neuropathy, autosomal dominant, 1, 609129 **Tags**

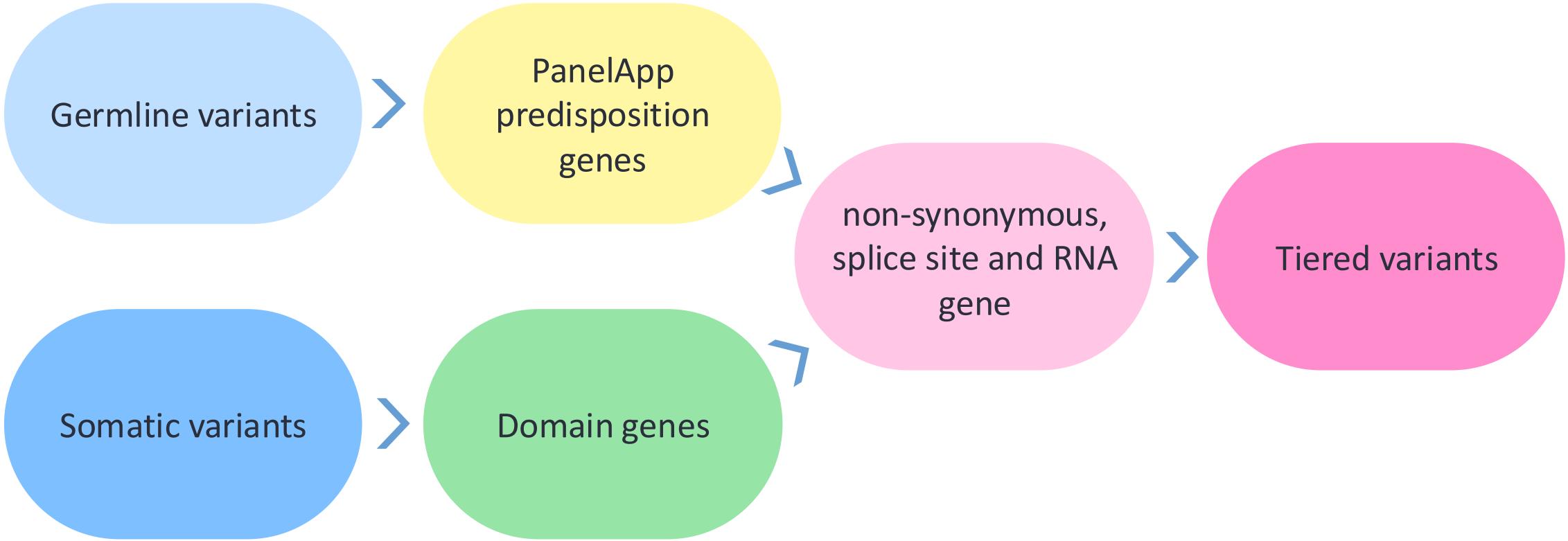
https://re-docs.genomicsengland.co.uk/panelapp/

Rare disease Exomiser



https://re-docs.genomicsengland.co.uk/exomiser/

Cancer tiering



https://re-docs.genomicsengland.co.uk/cancer_tiering/

100k tiering

Rare disease

GRCh37 (hg19)

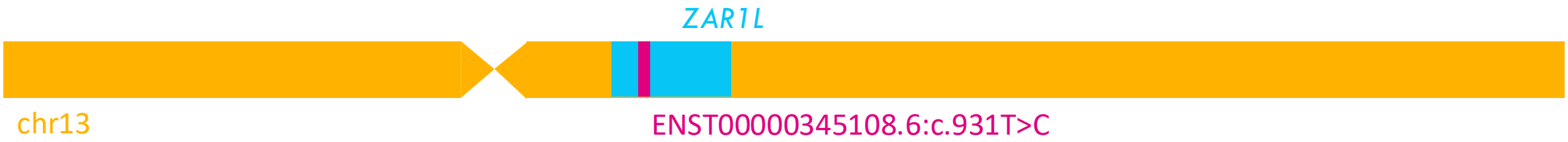
GRCh38 (hg38)

Cancer

Germline GRCh38 (hg38)

Somatic GRCh38 (hg38)

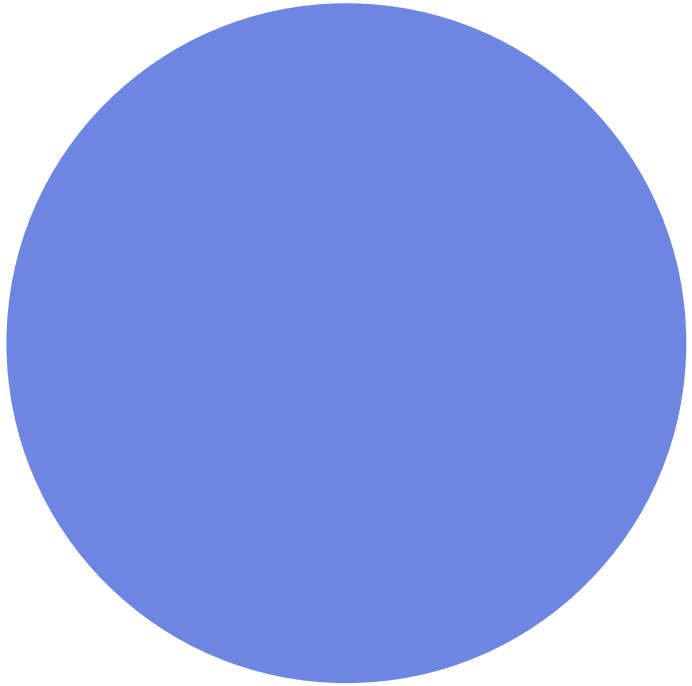
Tiering tables genome assembly – 100k



Search by	
gene	Should find all filter-passing variants in the gene on either assembly
coordinate	You must also specify the genome assembly
HGVS (exomiser only)	Should find all filter-passing variants that match your string on either assembly

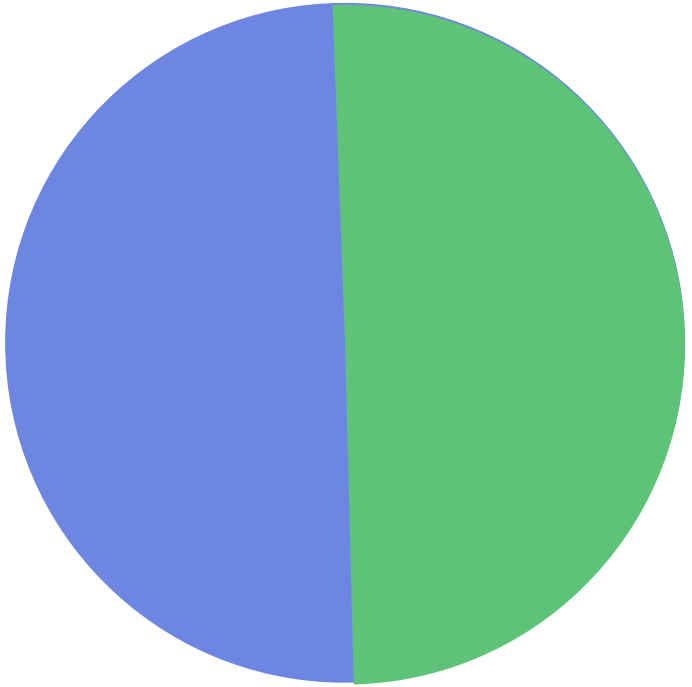
NHS GMS tiering

Rare disease



GRCh38 (hg38)

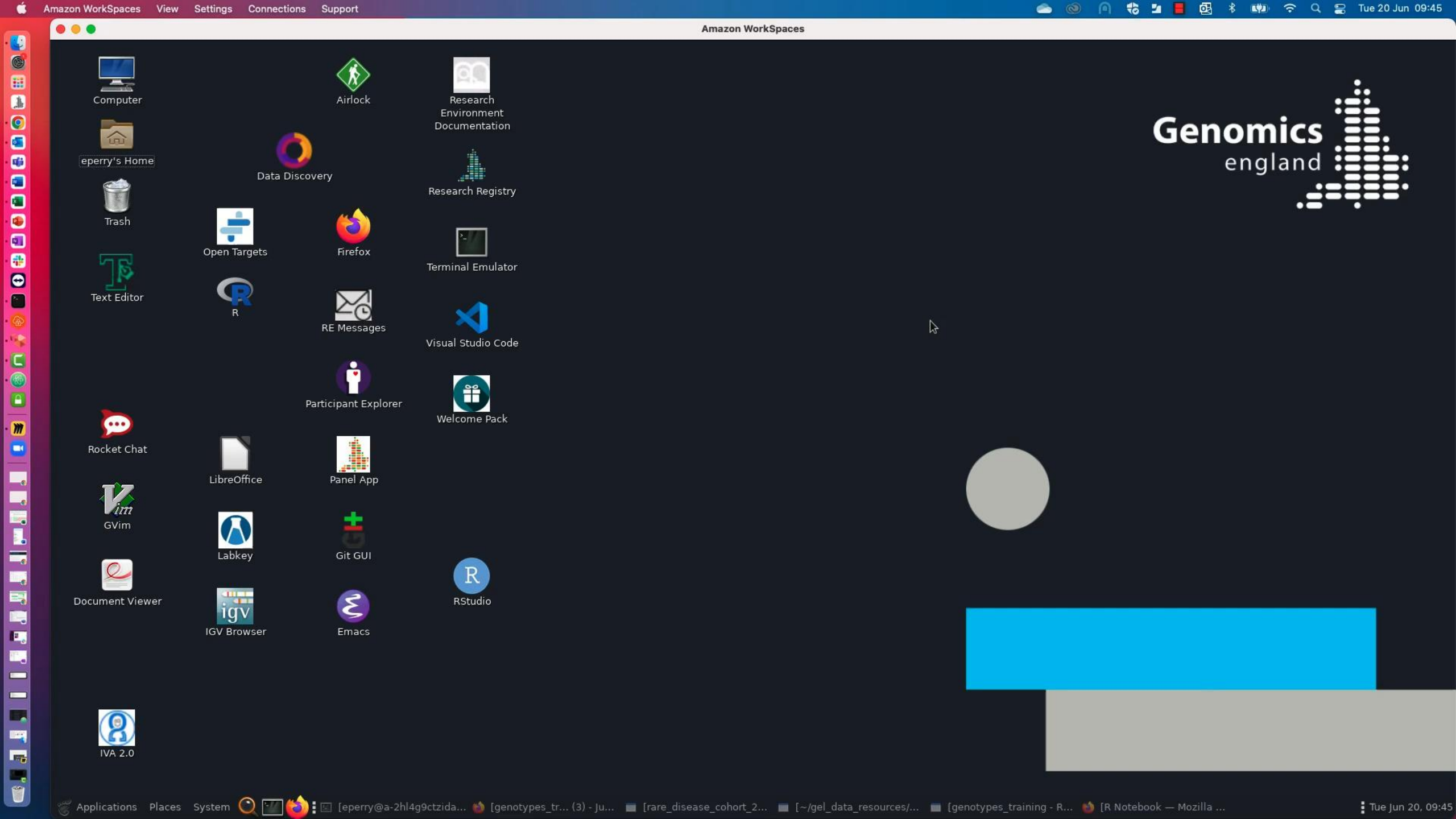
Cancer



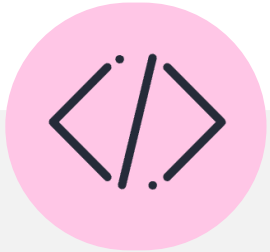
Germline GRCh38 (hg38)

Somatic GRCh38 (hg38)

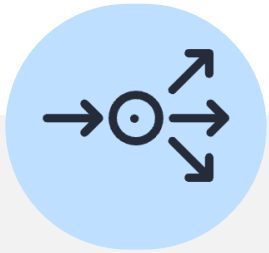
Variant data in LabKey demo


Amazon WorkSpaces
View
Settings
Connections
Support
Tue 20 Jun 09:45
Amazon WorkSpaces
Computer
Airlock
Research Environment Documentation
eperry's Home
Data Discovery
Research Registry
Trash
Open Targets
Firefox
Terminal Emulator
Text Editor
R
RE Messages
Visual Studio Code
Participant Explorer
Welcome Pack
Rocket Chat
LibreOffice
Panel App
GVim
Labkey
Git GUI
Document Viewer
RStudio
IGV Browser
Emacs
IVA 2.0
Genomics england
Applications
Places
System
[eperry@a-2hl4g9ctzida...
[genotypes_tr... (3) - Ju...
[rare_disease_cohort_2...
[~/gel_data_resources/...
[genotypes_training - R...
[R Notebook — Mozilla ...
Tue Jun 20, 09:45

LabKey API



Work in a variety of programming languages (support for Python and R) using SQL queries



Combine queries between tables

Replicate queries between releases and analyses

Work locally and on the HPC

https://re-docs.genomicsengland.co.uk/labkey_api/

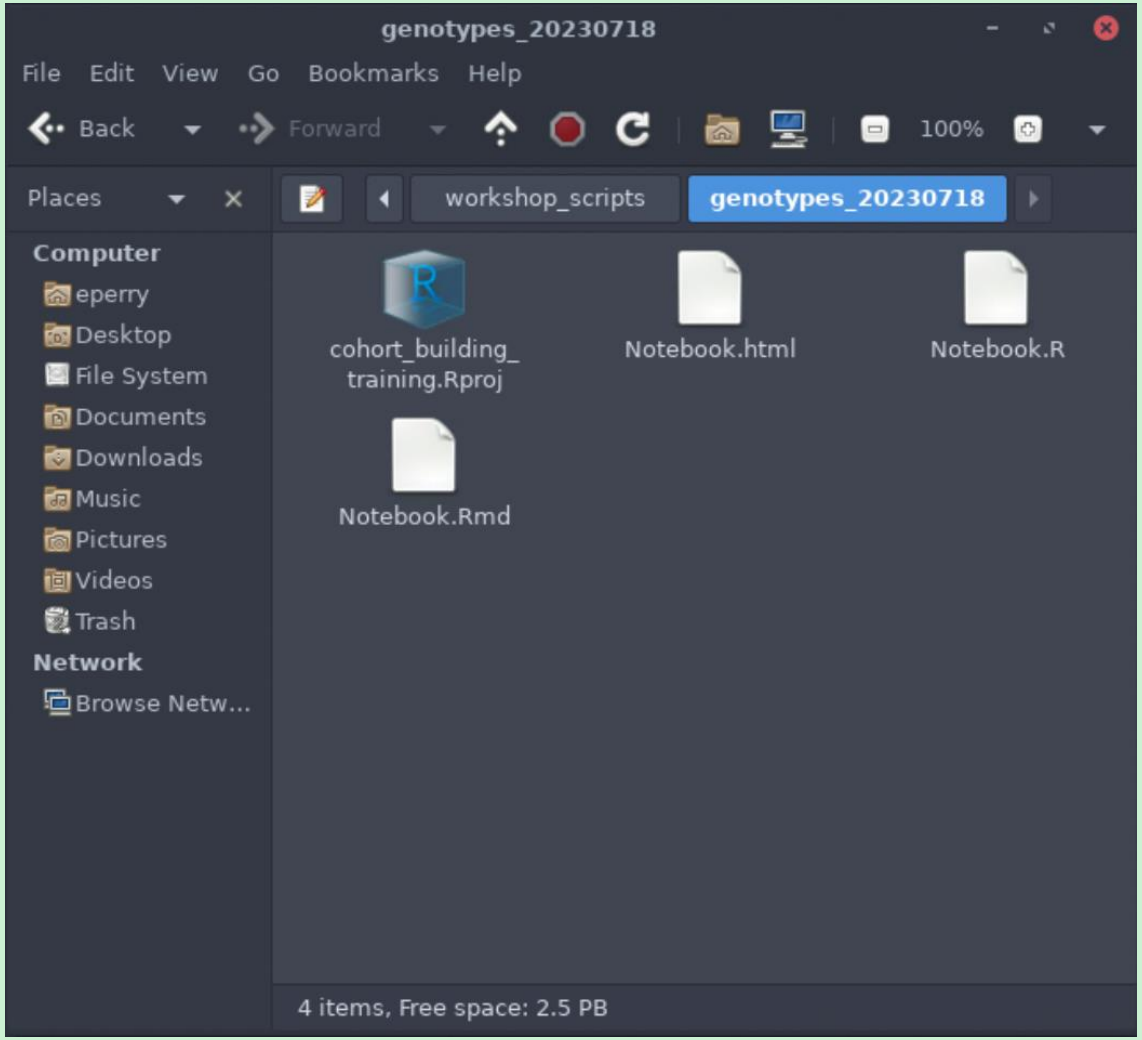
LabKey .netrc

- You can access the same data via the LabKey API as you can through other means
- You will need to configure access to the LabKey API with your username and password
    - In your home directory
    - On the HPC
- You do this by editing a file called .netrc

https://re-docs.genomicsengland.co.uk/labkey_api/

Materials

- Slides and video will be sent out to you after the session
- Scripts available in `/gel_data_resources/example_scripts/workshop_scripts/genotypes_2026`



Variant data in LabKey API demo

Amazon WorkSpaces View Settings Connections Support Tue 20 Jun 09:57

Amazon WorkSpaces

genotypes_tr... (3) - JupyterLab — Mozilla Firefox

Jupyter Lab on Helix - Ge | R Notebook | genotypes_tr... (3) - Jupy

127.0.0.1:9537/lab/tree/genotypes_training.ipynb

File Edit View Run Kernel Tabs Settings Help

GENOTYPES_TRAINING.IPYNB

rd_cohort_building_trainir | genotypes_training.ipynb | cohort_building_training.ip

Markdown | Python 3 (ipykernel)

Finding participants by genotypes in Python

This notebook will walk you through finding participants by genotypes. You are welcome to copy/paste any code from this notebook for your own scripts/notebooks.

Contents:

Use the LabKey API

Import Python modules you need

[32]:
```
import numpy as np
import functools
import labkey
import pandas as pd
```

Helper function to access the LabKey API with

Simple 0 3 Python 3 (ipykernel) | Idle Mode: Command Ln 1, Col 1 genotypes_training.ipynb

R Notebook — Mozilla Firefox

R Notebook

file:///nas/weka.gel.zone/pgen_int_work/BRS/emily/genotypes_2023/genotyp

R Notebook

Finding participants by genotypes in R

This notebook will walk you through finding participants by genotypes. You are welcome to copy/paste any code from this notebook for your own scripts/notebooks.

Contents:

Use the LabKey API

Import R libraries you need

```
library(tidyverse)
```

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.1.2     ✔ readr     2.1.4
## ✔ forcats   1.0.0     ✔ stringr   1.5.0
## ✔ ggplot2   3.4.2     ✔ tibble    3.2.1
## ✔ lubridate 1.9.2     ✔ tidyr     1.3.0
## ✔ purrr     1.0.1
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(Rlabkey)
```

Applications Places System [eperry@a-2hl4g9c... | genotypes_tr... (3) ... | [rare_disease_coho... | [~/gel_data_resour... | [genotypes_trainin... | R Notebook — Mozi... | [exomiser: /nhs-g... | [workshop_scripts] Tue Jun 20, 09:57

4. Finding genotypes with IVA and Cohort Browser

Interactive variant analysis (IVA)

- Point-and-click interface to explore variants
- Filter by loci, consequences, population frequencies and inheritance
- Find participant genotypes

https://re-docs.genomicsengland.co.uk/iva/

100k in IVA

Rare disease

GRCh37 (hg19)

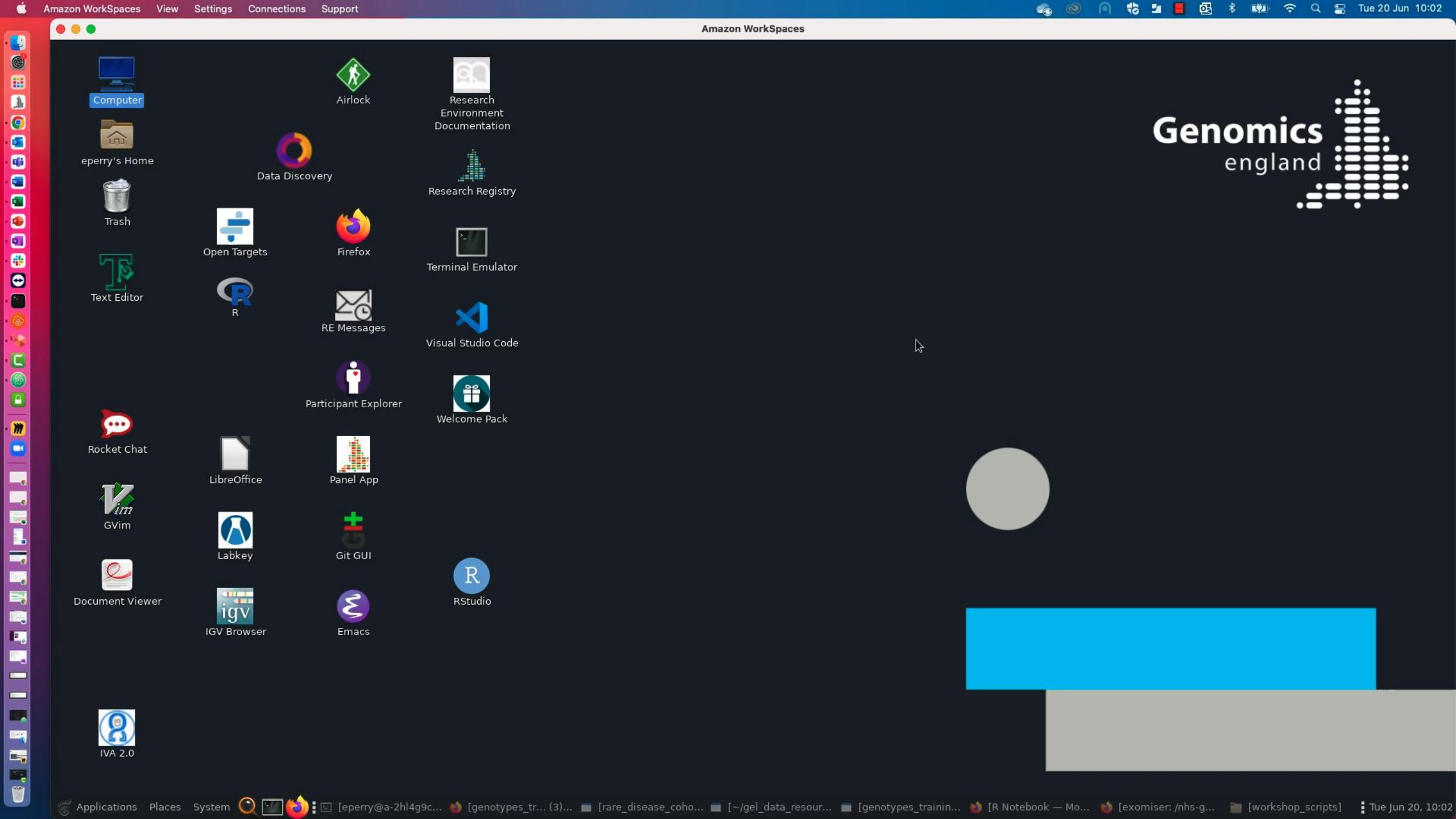
GRCh38 (hg38)

Cancer

Germline GRCh38 (hg38)

Somatic GRCh38 (hg38)

IVA demo


Amazon WorkSpaces View Settings Connections Support
Tue 20 Jun 10:02
Amazon WorkSpaces
Computer
Airlock
Research Environment Documentation
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Data Discovery
Research Registry
Trash
Open Targets
Firefox
Terminal Emulator
Text Editor
R
RE Messages
Visual Studio Code
Participant Explorer
Welcome Pack
Rocket Chat
LibreOffice
Panel App
GVim
Labkey
Git GUI
Document Viewer
RStudio
IGV Browser
Emacs
IVA 2.0
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[genotypes_tr... (3)...
[rare_disease_coho...
[~/gel_data_resour...
[genotypes_trainin...
[R Notebook — Mo...
[exomiser: /nhs-g...
[workshop_scripts]
Tue Jun 20, 10:02

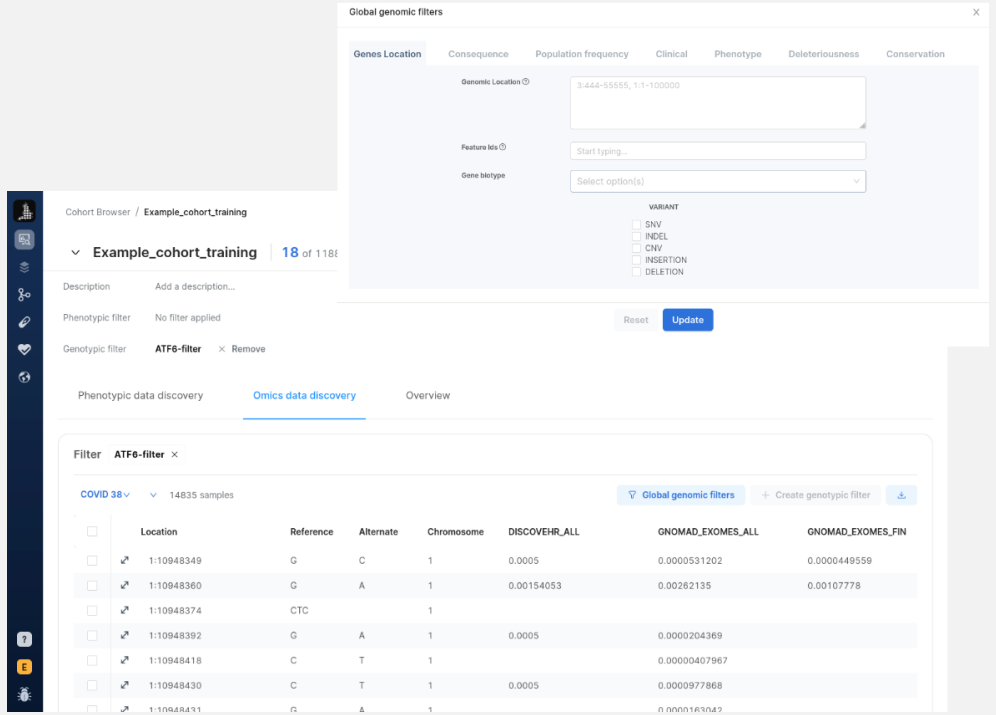
CloudOS Cohort Browser – genotypes

Filter genotypes and phenotypes in one interface

Point-and-click interface to explore variants

Filter by loci, consequences, population frequencies and inheritance.

Find participant genotypes.



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

CloudOS omics demo

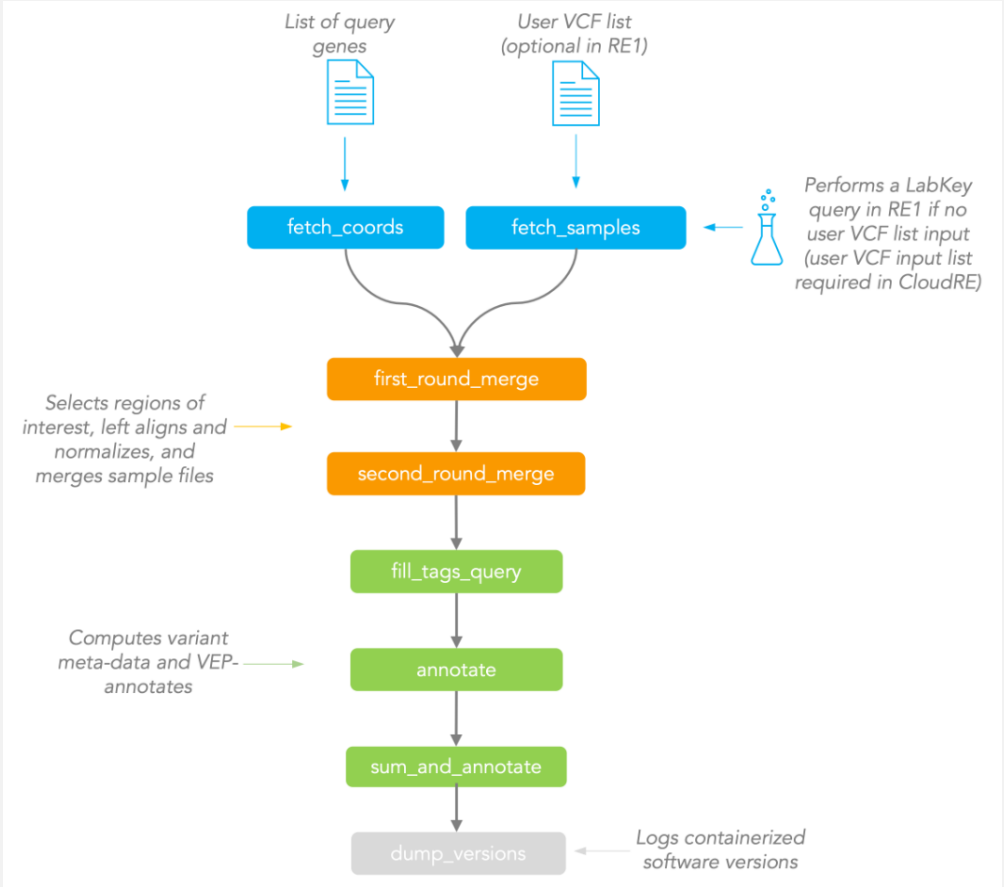
5. The Small Variant and Structural Variant workflows

Small variant workflow

Submit a list of genes

Find all short variants in these genes

Get 100k participants with these variants



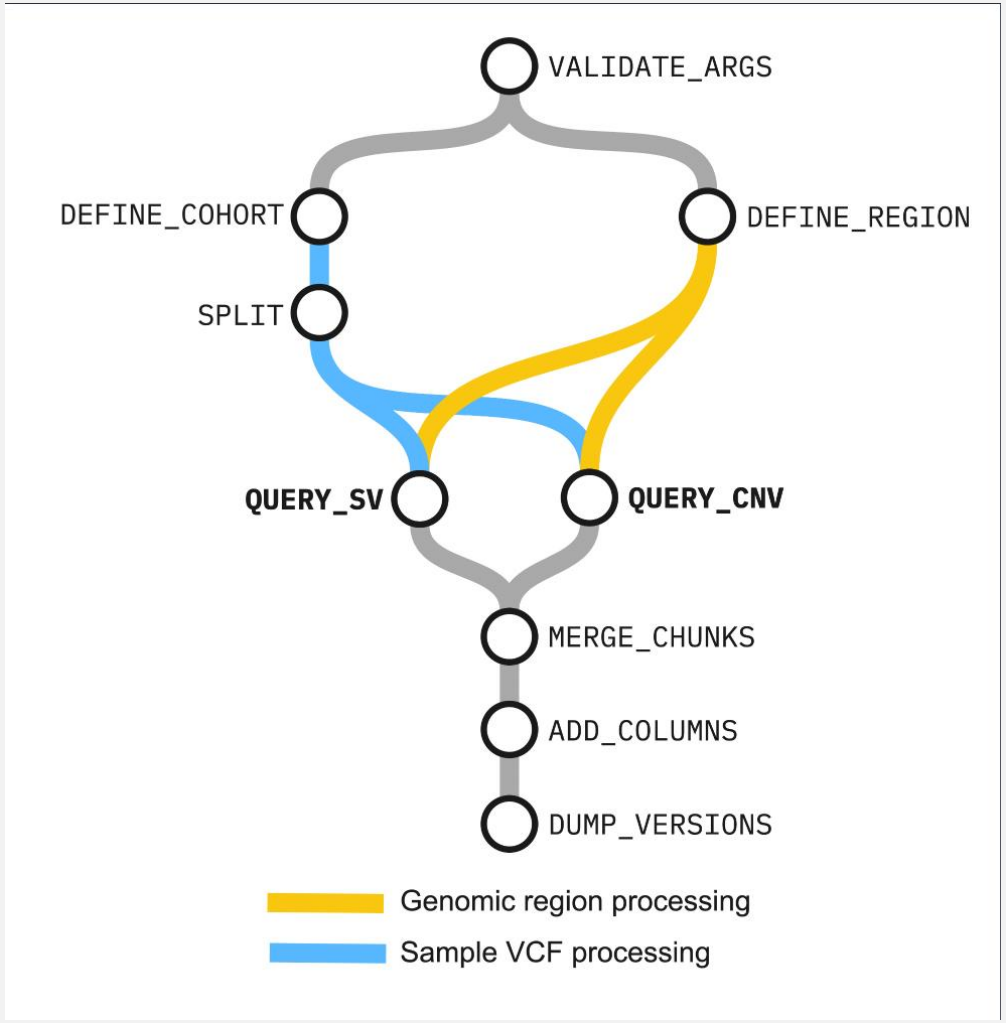
https://re-docs.genomicsengland.co.uk/small_variant/

Structural variant workflow

Submit a list of genes or regions

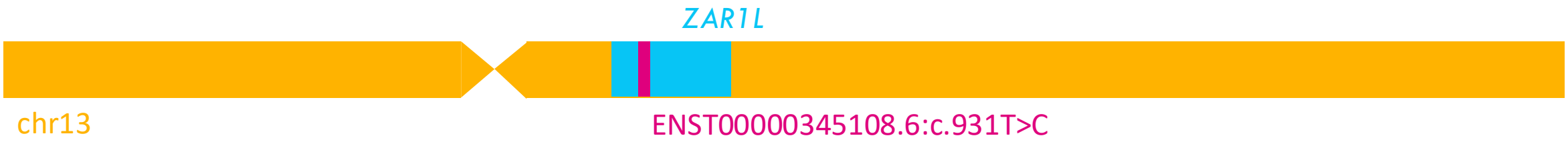
Find all structural variants overlapping these genes

Get 100k participants with these variants



https://re-docs.genomicsengland.co.uk/structural_variant/

Workflows genome assembly – 100k



Search by	
gene	Should find all variants in the gene(s) on either assembly
coordinates (structural only)	You must also specify the genome assembly

Running workflows on the HPC demo

Amazon WorkSpaces View Settings Connections Support

Wed 24 Apr 10:47

Amazon WorkSpaces

genotypes_tr... - JupyterLab — Mozilla Firefox

genotypes_tr... - Jupyter

127.0.0.1:8387/lab/tree/genotypes_training.ipynb

File Edit View Run Kernel Tabs Settings Help

Launcher | genotypes_training.ipynb

Markdown | Python 3 (ipykernel)

Filter files by name

/

Name	Last Modified
small_variant	2 days ago
structural_...	2 days ago
cohort_buil...	2 days ago
genotypes...	a day ago
Notebook....	20 hours ago
Notebook.R	2 years ago
Notebook....	20 hours ago

604 rows × 7 columns

Running workflows on the HPC

Small variant workflow

- `ssh` to the HPC with your usual login credentials
- `cd` into your working directory
- Make and cd into your working directory
  `mkdir small_variant_demo`
  `cd small_variant_demo`
- Copy the Small Variant workflow submission script into your folder
  `cp /pgen_int_data_resources/workflows/rdp_small_variant/main/submit.sh .`
- Make the file `gene_list.txt` and add your list of genes to it
  `vi gene_list.txt`
  Add `SMC3` to the file
  `Esc :wq`
- Edit the submission script:
  `vi submit.sh`
  Change the `project_code` to your code Change the `gene_input` to `gene_list.txt`
  `Esc :wq`
- Run the workflow
  `bsub < submit.sh`
- Find your results when the job is finished

[18]:
```
small_variant_results = pd.read_csv('small_variant/results/GRCh38_
small_variant_results
```

```
/resources/conda/miniconda3/envs/2022_base/lib/python3.7/site-pac
kages/IPython/core/interactiveshell.py:3186: DtypeWarning: Column
s (101) have mixed types.Specify dtype option on import or set lo
w_memory=False.
  interactivity=interactivity, compiler=compiler, result=result)
```

Simple 0 1 Python 3 (ipykernel) | Idle Mode: Command Ln 1

eperry@a-avtl60awn8z7:~

/nas/weka.gel.zone/pgen_int_work/BRS/emily/genotypes_2024/Notebook.html

Notebook.html | Open in Browser | Find | Publish

Running workflows on the HPC

Small variant workflow

- `ssh` to the HPC with your usual login credentials
- `cd` into your working directory
- Make and cd into your working directory `mkdir small_variant_demo` `cd small_variant_demo`
- Copy the Small Variant workflow submission script into your folder `cp /pgen_int_data_resources/workflows/rdp_small_variant/main/submit.sh .`
- Make the file `gene_list.txt` and add your list of genes to it `vi gene_list.txt` Add `SMC3` to the file `Esc :wq`
- Edit the submission script: `vi submit.sh` Change the `project_code` to your code Change the `gene_input` to `gene_list.txt` `Esc :wq`
- Run the workflow `bsub < submit.sh`
- Find your results when the job is finished

```
small_variant_results <- readr::read_tsv('small_variant/results/GRCh38_SMC3_ENSG00000108055_annotated_variants.tsv')
```

```
## Rows: 58169 Columns: 102
## ── Column specification ────────────────────────────────────────────────────
## Delimiter: "\t"
## chr (91): CHROM_variant, ID_variant, REF_variant, ALT_variant, Location_anno...
## dbl (11): POS_variant, AN_variant, AC_variant, AC_Hom_variant, AC_Het_varian...
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
head(small_variant_results)
```

CHROM_variant <chr>	POS_variant <dbl>	ID_variant <chr>	REF_variant <chr>	ALT_variant <chr>	AN_variant <dbl>	AC_variant <dbl>
chr10	110567687	chr10_110567687_1	G	A	242	121
chr10	110567687	chr10_110567687_1	G	A	242	121
chr10	110567687	chr10_110567687_1	G	A	242	121
chr10	110567687	chr10_110567687_1	G	A	242	121
chr10	110567687	chr10_110567687_1	G	A	242	121
chr10	110567687	chr10_110567687_1	G	A	242	121

6 rows | 1-7 of 102 columns

Applications Places System [genotypes_2024] [workshop_scripts] [eperry@a-avtl60awn8... [genotypes_2024 - RSt... genotypes_tr... - Jupyte... /nas/weka.gel.zone/pge... [Homepage - Genomic... Wed Apr 24, 10:47

6. Aggregate variant files

Aggregate VCFs

Combined gVCFs

Quality metrics

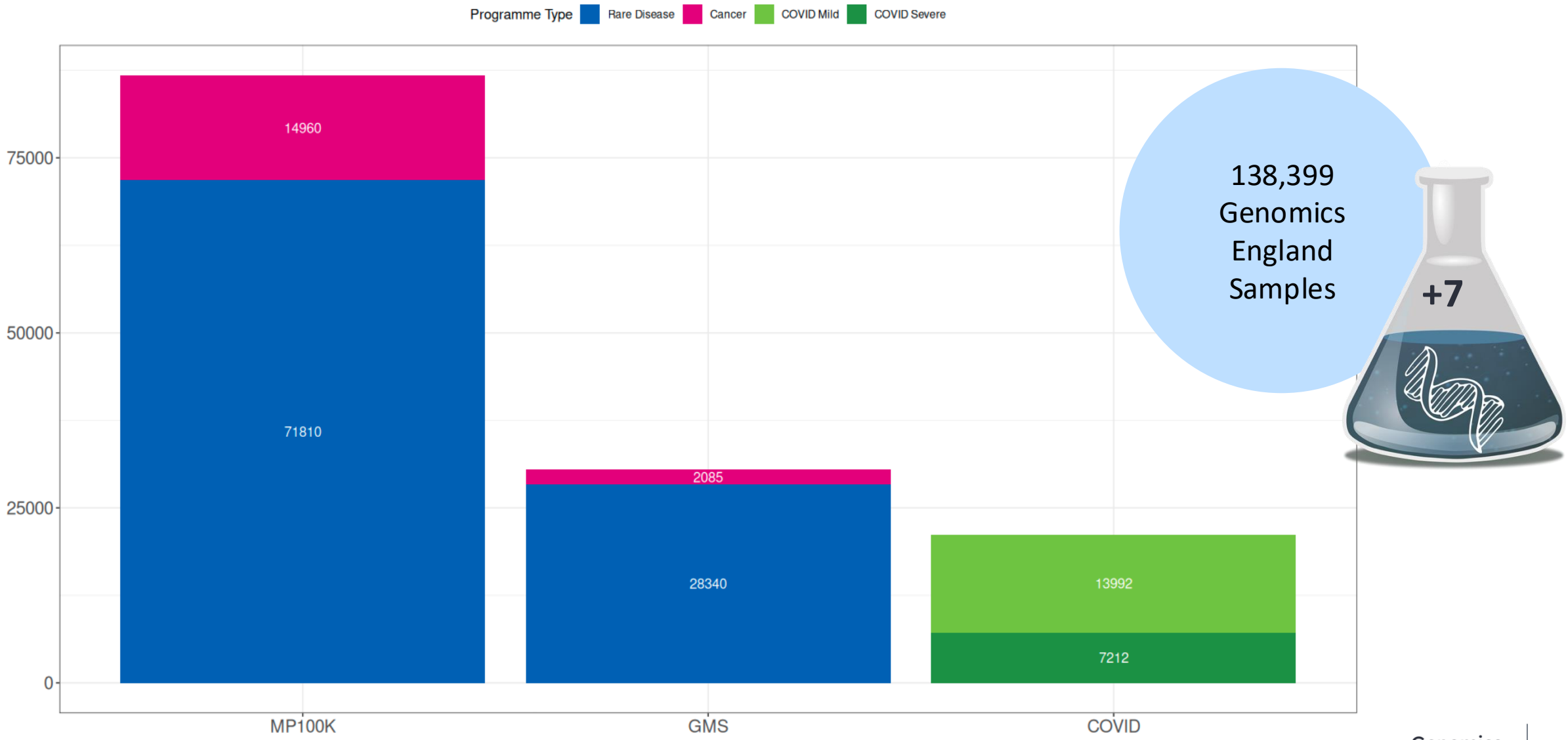
Functional annotation files

Genotype files – platekeys

Chunks/ shards

https://re-docs.genomicsengland.co.uk/aggv3/ https://re-docs.genomicsengland.co.uk/aggv2/ https://re-docs.genomicsengland.co.uk/somAgg/

AggV3 – germline samples



https://re-docs.genomicsengland.co.uk/aggv3_samples/

AggV2 – germline samples

Rare disease

GRCh37 (hg19)

GRCh38 (hg38)

Cancer

Germline GRCh38 (hg38)

Somatic GRCh38 (hg38)

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

somAgg

Rare disease

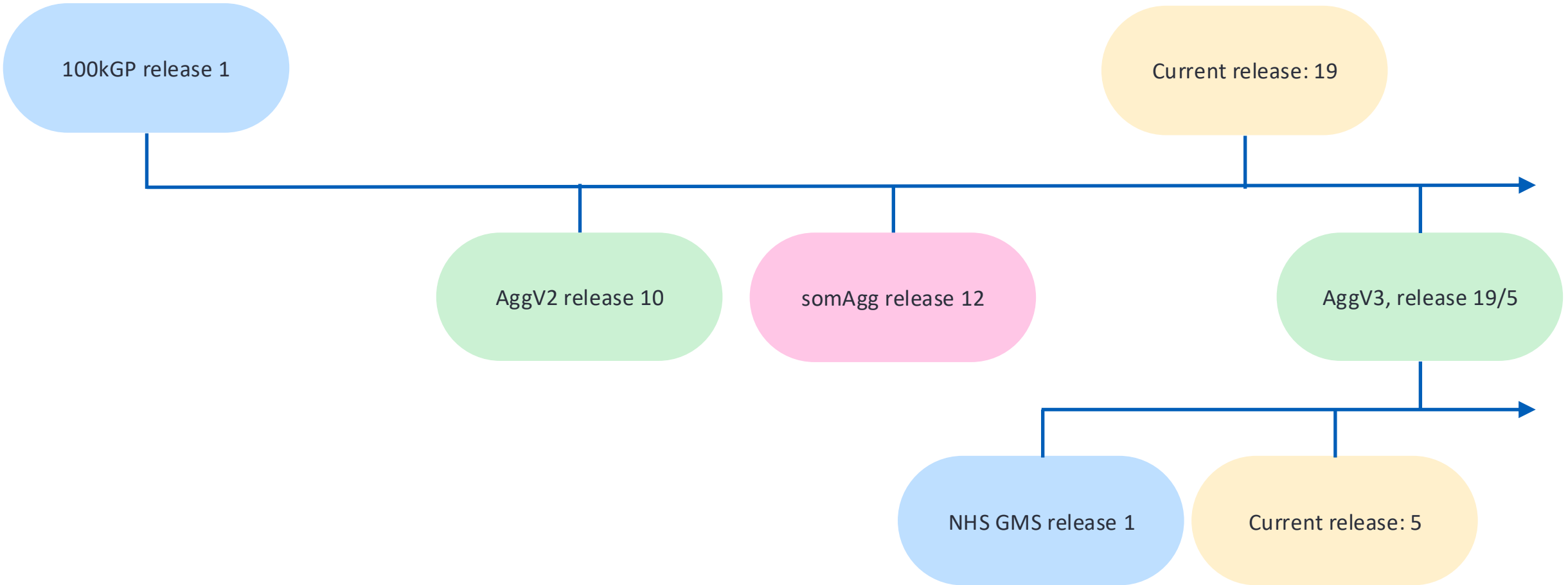
Cancer

GRCh37 (hg19)
GRCh38 (hg38)

Germline GRCh38 (hg38)
Somatic GRCh38 (hg38)

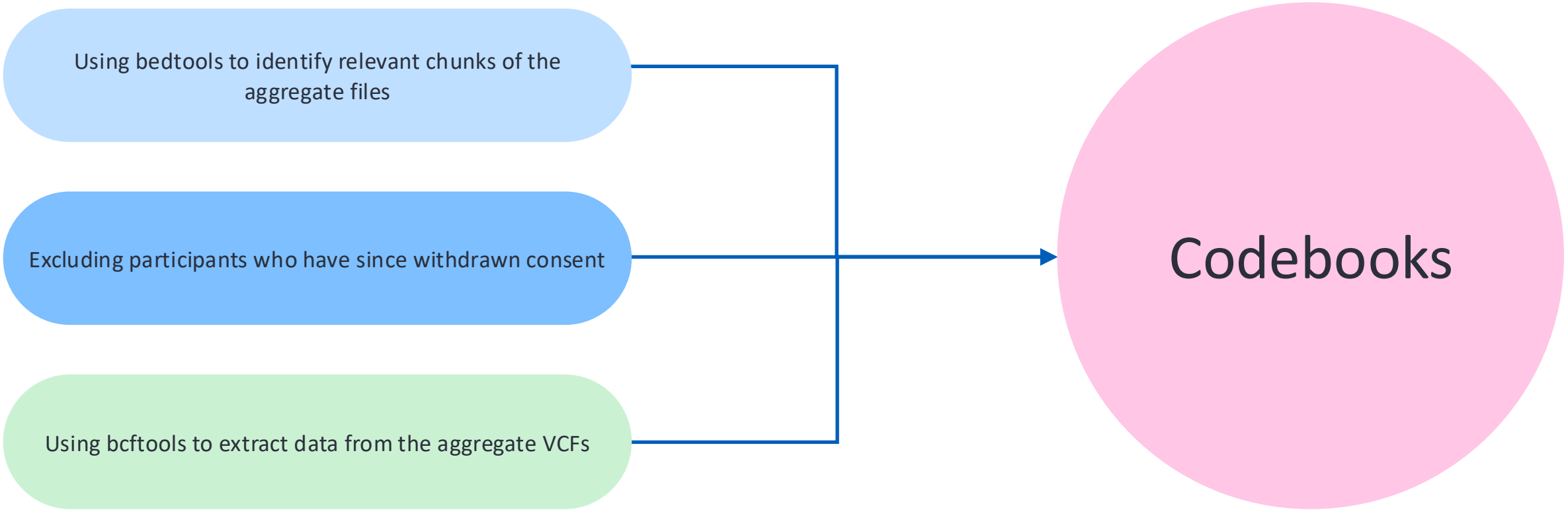
https://re-docs.genomicsengland.co.uk/somAgg/

Aggregate VCFs



https://re-docs.genomicsengland.co.uk/aggv3/ https://re-docs.genomicsengland.co.uk/aggv2/ https://re-docs.genomicsengland.co.uk/somAgg/

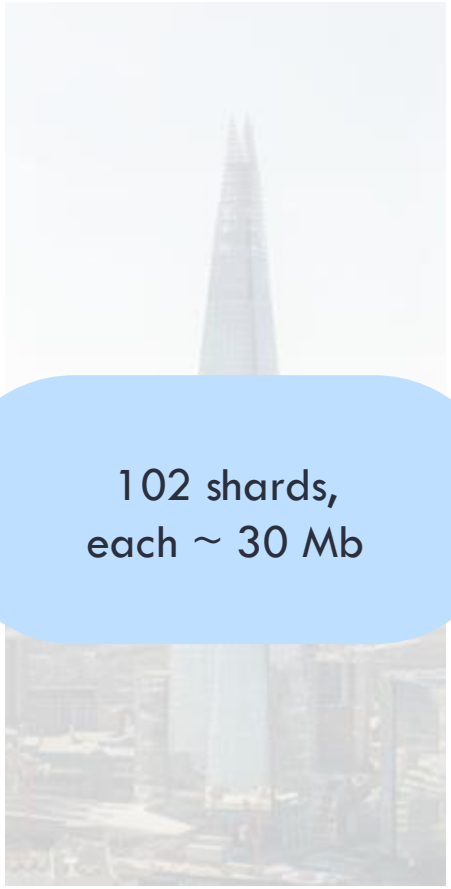
Aggregate VCFs



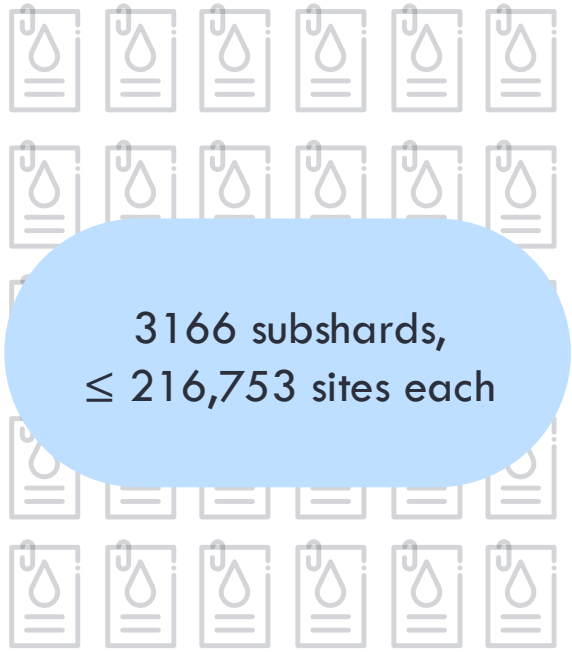
https://re-docs.genomicsengland.co.uk/aggv2_code_book/ https://re-docs.genomicsengland.co.uk/somAgg_code_book/

AggV3 shards

22 autosomes, two sex chromosomes and mitochrondrion



102 shards, each ~ 30 Mb



3166 subshards, ≤ 216,753 sites each

Same shards used across the genotype, functional annotation and site QC VCFs

https://re-docs.genomicsengland.co.uk/aggv3_data_overview/#sharding

AggV2/somAgg VCF chunks

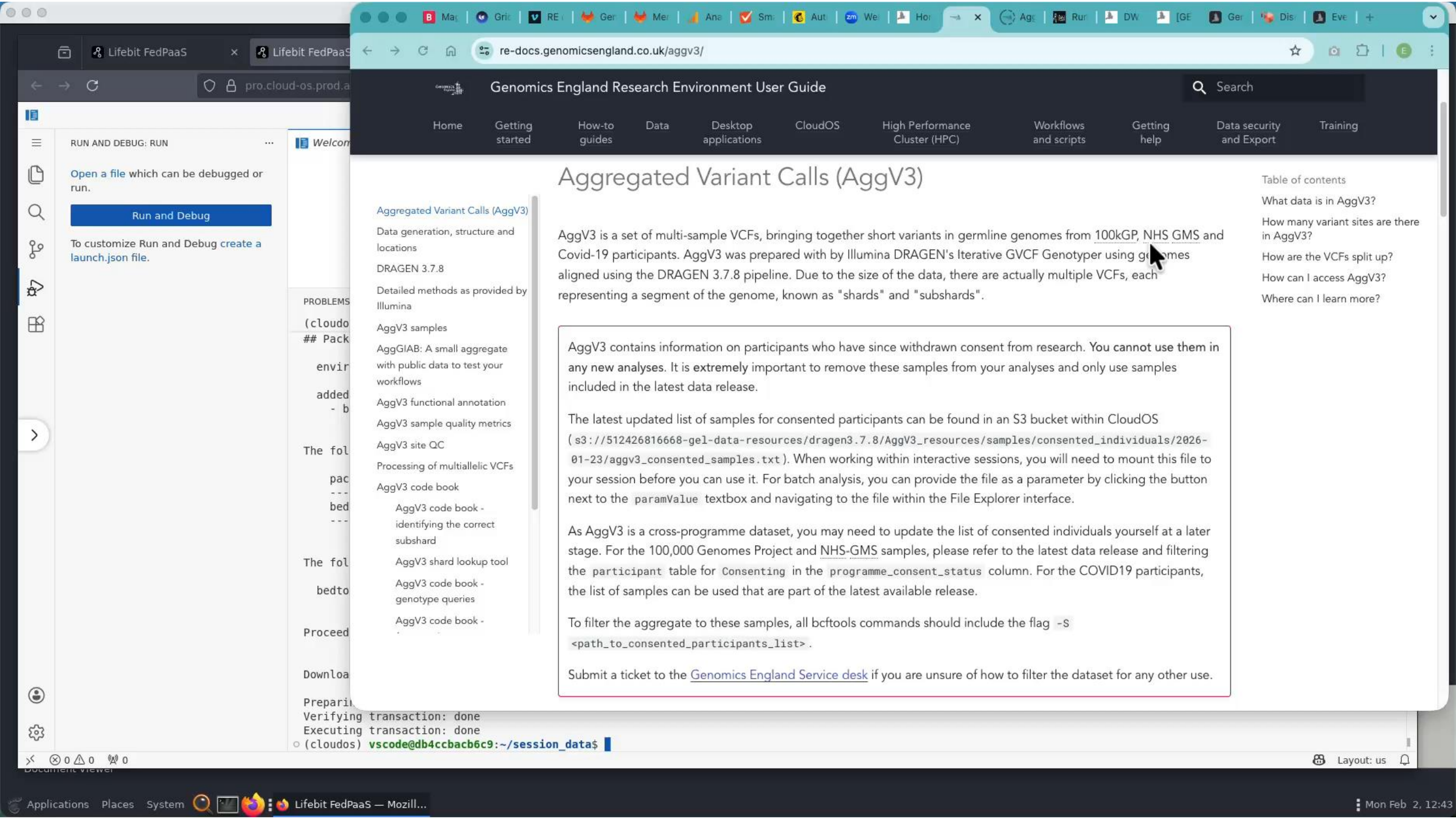
- Locus-based queries must query the correct chunk file
- BED file of chunks available
- Create a sorted BED file of your own regions
- Intersect with BEDtools
- Code books with more information
- Also available in Plink2 format

https://re-docs.genomicsengland.co.uk/aggv2_code_book/ https://re-docs.genomicsengland.co.uk/somAgg_code_book/

AggV3 vs AggV2

- More samples — 138,399 compared to 78,195, including 100kGP, NHS GMS and COVID-19
- Chunks vs shards — Consistent sizing of shards means it's easier to estimate compute needs of large tasks/pipelines
- CloudOS — AggV3 only available on CloudOS with no plans to change. Time to get ready for the future Cloud-based RE
- Iterative build — We can add more genomes to it as we receive them (>40k at a time to make it viable).
- DRAGEN 3.7.8 — All genomes aligned and called using the same pipeline - better comparison within RE and to other similar projects
- AggGIAB — Smaller aggregate for testing your workflows

Using bcftools demo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Lifebit FedPaaS
pro.cloud-os.prod.a
RUN AND DEBUG: RUN
Open a file which can be debugged or run.
Run and Debug
To customize Run and Debug create a launch.json file.
PROBLEMS
(cloudo
Pack
envir
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bed

The fol
bedto
Proceed
Downloa
Preparii
Verifying transaction: done
Executing transaction: done
(cloudos) vscode@db4ccbacb6c9:~/session_data$
re-docs.genomicsengland.co.uk/aggv3/
Genomics England Research Environment User Guide
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Aggregated Variant Calls (AggV3)
Data generation, structure and locations
DRAGEN 3.7.8
Detailed methods as provided by Illumina
AggV3 samples
AggGIAB: A small aggregate with public data to test your workflows
AggV3 functional annotation
AggV3 sample quality metrics
AggV3 site QC
Processing of multiallelic VCFs
AggV3 code book
AggV3 code book - identifying the correct subshard
AggV3 shard lookup tool
AggV3 code book - genotype queries
AggV3 code book -
AggV3 is a set of multi-sample VCFs, bringing together short variants in germline genomes from 100kGP, NHS GMS and Covid-19 participants. AggV3 was prepared with by Illumina DRAGEN's Iterative GVCF Genotyper using genomes aligned using the DRAGEN 3.7.8 pipeline. Due to the size of the data, there are actually multiple VCFs, each representing a segment of the genome, known as "shards" and "subshards".
AggV3 contains information on participants who have since withdrawn consent from research. You cannot use them in any new analyses. It is extremely important to remove these samples from your analyses and only use samples included in the latest data release.
The latest updated list of samples for consented participants can be found in an S3 bucket within CloudOS (s3://512426816668-gel-data-resources/dragen3.7.8/AggV3_resources/samples/consented_individuals/2026-01-23/aggv3_consented_samples.txt). When working within interactive sessions, you will need to mount this file to your session before you can use it. For batch analysis, you can provide the file as a parameter by clicking the button next to the paramValue textbox and navigating to the file within the File Explorer interface.
As AggV3 is a cross-programme dataset, you may need to update the list of consented individuals yourself at a later stage. For the 100,000 Genomes Project and NHS-GMS samples, please refer to the latest data release and filtering the participant table for Consenting in the programme_consent_status column. For the COVID19 participants, the list of samples can be used that are part of the latest available release.
To filter the aggregate to these samples, all bcftools commands should include the flag -S <path_to_consented_participants_list>.
Submit a ticket to the Genomics England Service desk if you are unsure of how to filter the dataset for any other use.
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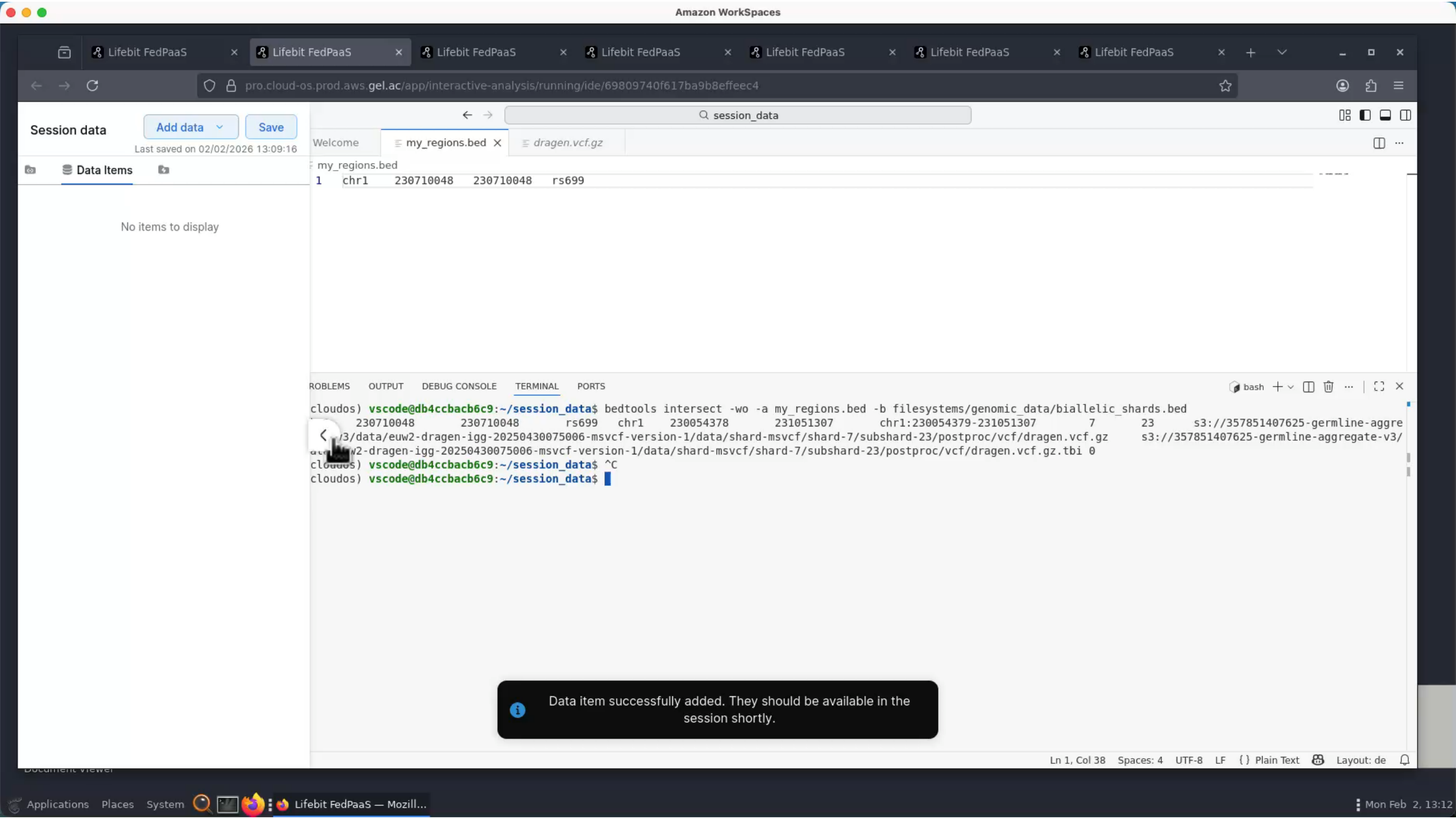

Amazon WorkSpaces
Lifebit FedPaaS
pro.cloud-os.prod.aws.gel.ac/app/interactive-analysis/running/ide/69809740f617ba9b8effeec4
Session data
Add data
Save
Last saved on 02/02/2026 13:09:16
Data Items
No items to display
session_data
Welcome
my_regions.bed
dragen.vcf.gz
my_regions.bed
1 chr1 230710048 230710048 rs699
ROBLEMS OUTPUT DEBUG CONSOLE TERMINAL PORTS
bash
cloudos) vscode@db4ccbacb6c9:~/session_data$ bedtools intersect -wo -a my_regions.bed -b filesystems/genomic_data/biallelic_shards.bed
230710048 230710048 rs699 chr1 230054378 231051307 chr1:230054379-231051307 7 23 s3://357851407625-germline-aggre
/3/data/euw2-dragen-igg-20250430075006-msvcf-version-1/data/shard-msvcf/shard-7/subshard-23/postproc/vcf/dragen.vcf.gz s3://357851407625-germline-aggregate-v3/
w2-dragen-igg-20250430075006-msvcf-version-1/data/shard-msvcf/shard-7/subshard-23/postproc/vcf/dragen.vcf.gz.tbi 0
cloudos) vscode@db4ccbacb6c9:~/session_data$ ^C
cloudos) vscode@db4ccbacb6c9:~/session_data$
Data item successfully added. They should be available in the session shortly.
Ln 1, Col 38 Spaces: 4 UTF-8 LF Plain Text Layout: de
Applications Places System
Lifebit FedPaaS — Mozill...
Mon Feb 2, 13:12

7. When/why you would use each method

Platform

Tiering and exomiser tables

LabKey®

IVA

INTERACTIVE VARIANT ANALYSIS

Small/ Structural variant workflows

Querying the aggregates

Search by

Tiering and exomiser tables

HGVS HUMAN GENOME VARIATION SOCIETY

IVA

dbSNP Short Genetic Variations

Small/ Structural variant workflows

Querying the aggregates

Variants included

Tiering and exomiser tables

Variants that have passed filters

IVA

All

Small/ Structural variant workflows

All

Querying the aggregates

AggV3 – all variants
AggV2 – from GRCh38-aligned genomes from release 12
somAgg – from GRCh38-aligned genomes from release 8

Datasets

Tiering and exomiser tables

100k and NHS GMS

IVA and Cohort browser omics

100k

Small/ Structural variant workflows

100k

Querying the aggregates

AggV2 and somAgg: 100k
AggV3: 100k, NHS GMS and Covid

Genome assembly

Tiering and exomiser tables

GRCh37 and GRCh38
Assembly as a separate column

IVA

GRCh37 and GRCh38 in separate databases

Small/ Structural variant workflows

GRCh37 and GRCh38 queries simultaneously

Querying the aggregates

AggV3: genomes realigned to GRCh38
AggV2 and somAgg: GRCh38 only

Underlying VCFs

Tiering and exomiser tables

Rare disease: Platypus
Cancer: Strelka

IVA

Rare disease: Platypus
Cancer: Strelka

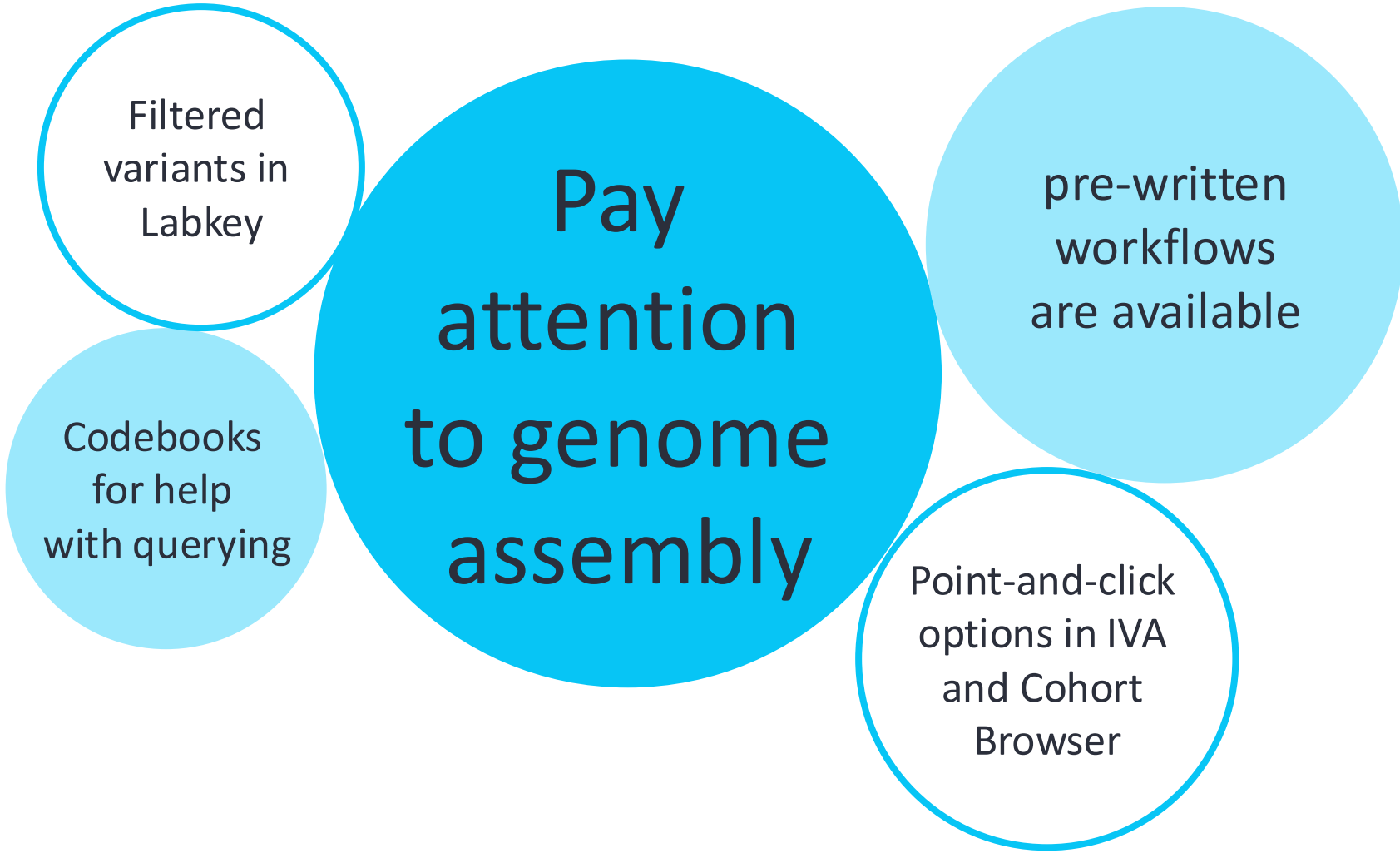
Small/ Structural variant workflows

Strelka

Querying the aggregates

AggV3: Dragen 3.7.8
AggV2 and somAgg: Strelka

Key takeways



8. 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

Feedback

Thank you

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