

User



BioData Catalyst

Documentation:

- [Open access GWAS tutorial](#)
- [Terra Authorization Domain](#)
- [Search data in Gen3 and export](#)
- [TOPMed harmonized & unharmonized phenotypes](#)
- [Launch Dockstore workflows with Terra](#)
- Frequently asked questions (coming soon)

Gen3 Windmill

Search TOPMed projects and export harmonized traits, metadata, & WGS data

"Bring Your Own Data"

Dockstore

[WDL](#)
[Docker](#)

json (coming soon)

Terra Featured Workspace "GWAS in BioData Catalyst"

Dashboard

5

Data

Notebook:
0-terra_data_util

Notebook:
1-GWAS_preliminary_analysis

Workflows

Notebook:
2-GWAS_summary

1. Overview of DataSTAGE/BioCatalyst platform
2. GWAS tutorial using Gen3 formatted TOPMed data

[Fiss API](#)

Gen3 graph structure as Terra data model

Graph structured data consolidation and reformatting

Explore phenotype distributions & covariates >> phenotypes CSV
Population genetics ([Hail using Spark](#)) to explore linkage disequilibrium, genetic stratification, kinship >> Genetic Relatedness Matrix (GRM)
Filter genotypes ([Hail using Spark](#)) >> VCF

1. Convert VCF to Genomic Data Structure (GDS) for use in R-based Genesis workflows
2. Generate null model using phenotypes CSV, GRM, GDS
3. Association tests using phenotypes CSV, GRM, GDS, null model
4. Summary CSV of association tests

Interactive summarization of results of summary CSV file