

EUROPEAN GWAS ANALYSIS RUN

Quality Control Code

PLINK v2.00a3.3LM 64-bit Intel (3 Jun 2022)

Options in effect:

--pfile eur_merge_albumia
--geno 0.01
--mind 0.05
--hwe 1e-6
--maf 0.01
--make-bed
--out eur_gwas_albumia_cohort

GWAS analysis test

PLINK v2.00a3.3LM 64-bit Intel (3 Jun 2022)

Options in effect:

--bfile eur_gwas_albumia_cohort
--covar PC_corrected_allpop.txt
--covar-variance-standardize
--glm hide-covar omit-ref log10
--out eur_gwas_albumia
--pheno albumin_corrected_WGR.txt

Hostname: fl-n-1-9

Working directory: /frazer01/home/wgonzalezrivera/med264_project/EUR

Random number seed: 1669768907

128663 MiB RAM detected; reserving 64331 MiB for main workspace.

Using up to 32 threads (change this with --threads).

317 samples (169 females, 148 males; 317 founders) loaded from
eur_gwas_albumia_cohort.fam.

6627492 variants loaded from eur_gwas_albumia_cohort.bim.

1 quantitative phenotype loaded (317 values).

12 covariates loaded from PC_corrected_allpop.txt.

--covar-variance-standardize: 12 covariates transformed.

--glm linear regression on phenotype 'ALBUMIN': done.

Results written to eur_gwas_albumia.ALBUMIN.glm.linear .

AFRICAN GWAS ANALYSIS RUN

Quality Control Code

PLINK v2.00a3.3LM 64-bit Intel (3 Jun 2022)

Options in effect:

--bfile afr_train_cohort

--geno 0.01

--mind 0.05

--hwe 1e-6

--maf 0.01

--make-bed

--out afr_albumin_cohort_qc

GWAS analysis test

PLINK v2.00a3.3LM 64-bit Intel (3 Jun 2022)

Options in effect:

--bfile afr_gwas_albumia_cohort

--covar PC_corrected_allpop.txt

--covar-variance-standardize

--glm hide-covar omit-ref log10

--out afr_gwas_cohort_gwas_albumin

--pheno albumin_gwas_corrected_wgr.txt

Hostname: fl-n-1-9

Working directory: /frazer01/home/wgonzalezrivera/med264_project/AFR

Random number seed: 1669768534

128663 MiB RAM detected; reserving 64331 MiB for main workspace.

Using up to 32 threads (change this with --threads).

312 samples (174 females, 138 males; 312 founders) loaded from
afr_gwas_albumia_cohort.fam.

3527091 variants loaded from afr_gwas_albumia_cohort.bim.

1 quantitative phenotype loaded (285 values).

12 covariates loaded from PC_corrected_allpop.txt.

--covar-variance-standardize: 12 covariates transformed.

--glm linear regression on phenotype 'ALBUMIN': done.

Results written to afr_gwas_cohort_gwas_albumin.ALBUMIN.glm.linear .