

EDGE-GWAS Full Function Test (sample data)

2026-02-10 16:35

Summary

All sections passed.

Functions exercised

all exports: import OK
load_plink_data: OK
prepare_phenotype_data: OK
stratified_train_test_split: OK
filter_variants_by_maf: OK
filter_variants_by_missing: OK
filter_samples_by_call_rate: OK
calculate_hwe_pvalues: OK
filter_variants_by_hwe: OK
calculate_genomic_inflation: OK
get_pc_covariate_list: OK
calculate_pca_sklearn: OK
attach_pcs_to_phenotype: OK
EDGEAnalysis.calculate_alpha: OK
EDGEAnalysis.apply_alpha: OK

save_results: OK

load_alpha_values: OK

format_gwas_output: OK

create_summary_report: OK

manhattan_plot: OK

qq_plot: OK

plot_alpha_distribution: OK

load_vcf_data: OK

download_test_files: OK

load_pgen_data: SKIP (no data): pgenlib is required to load PGEN files. Install wi...

load_bgen_data: SKIP (no data): bgen_reader is required to load BGEN files. Instal...

calculate_pca_plink: OK

calculate_pca_pcair: OK

calculate_grm_gcta: OK

load_grm_gcta: SKIP (no .grm files)

identify_related_samples: OK

filter_related_samples: OK

Testing all exported edge_gwas functions with sample data

[1] Imports

[OK] All exports importable

[2] Data loading

[OK] load_plink_data: 3925 samples x 1000 variants

[OK] prepare_phenotype_data: 3925 samples

[3] Train/test split

[OK] stratified_train_test_split: train 420, test 180

[4] Filtering & QC

[OK] filter_variants_by_maf: 100 -> 100 variants

[OK] filter_variants_by_missing: 100 -> 100 variants

[OK] filter_samples_by_call_rate: 600 -> 600 samples

[OK] calculate_hwe_pvalues: 50 variants, 42 valid

[OK] filter_variants_by_hwe: -> 80 variants

[5] Utilities

[OK] calculate_genomic_inflation: lambda=1.013

[OK] get_pc_covariate_list

[6] PCA (sklearn)

[OK] calculate_pca_sklearn + attach_pcs_to_phenotype: 5 PCs, 600 samples

[7] EDGE analysis (continuous)

[OK] EDGE continuous: alpha 15, GWAS 13

[8] EDGE analysis (binary)

[OK] EDGE binary: alpha 15, GWAS 13

[9] run_full_analysis

[OK] run_full_analysis + output files

[10] IO: save_results, load_alpha, format_gwas, summary report

[OK] save_results

[OK] load_alpha_values

[OK] format_gwas_output

[OK] create_summary_report

[11] Visualization

Manhattan plot saved to /Users/nicen/edge/edge-gwas/tests/output/manhattan.png

QQ plot saved to /Users/nicen/edge/edge-gwas/tests/output/qq_plot.png

Genomic inflation factor (λ): 0.660

Alpha distribution plot saved to /Users/nicen/edge/edge-gwas/tests/output/alpha_distribution.png

Total alpha values: 13

Alpha statistics:

Mean: -1.032

Median: -0.074

Std: 5.082

Min: -17.685

Max: 2.973

[OK] manhattan_plot, qq_plot, plot_alpha_distribution

[12] load_vcf_data

[OK] load_vcf_data: 1 x 902

[13] download_test_files

[OK] download_test_files (no overwrite)

[14] check external tools

✓ PLINK2: PLINK v2.0.0-a.7 64-bit (5 Dec 2025)

✓ GCTA: *****

✓ R: R version 4.3.3 (2024-02-29) -- "Angel Food Cake"

✓ R package GENESIS: Installed

✓ R package SNPRelate: Installed

✓ R package gdsfmt: Installed

[OK] check_external_tools

[15] Optional (skip if no data/tools)

[SKIP] load_pgen_data: pgenlib is required to load PGEN files. Install with: pip install pgenlib

[SKIP] load_bgen_data: bgen_reader is required to load BGEN files. Install with: pip install bgen-reader

[OK] calculate_pca_plink

[OK] calculate_pca_pcair

[OK] calculate_grm_gcta

[SKIP] load_grm_gcta: no files

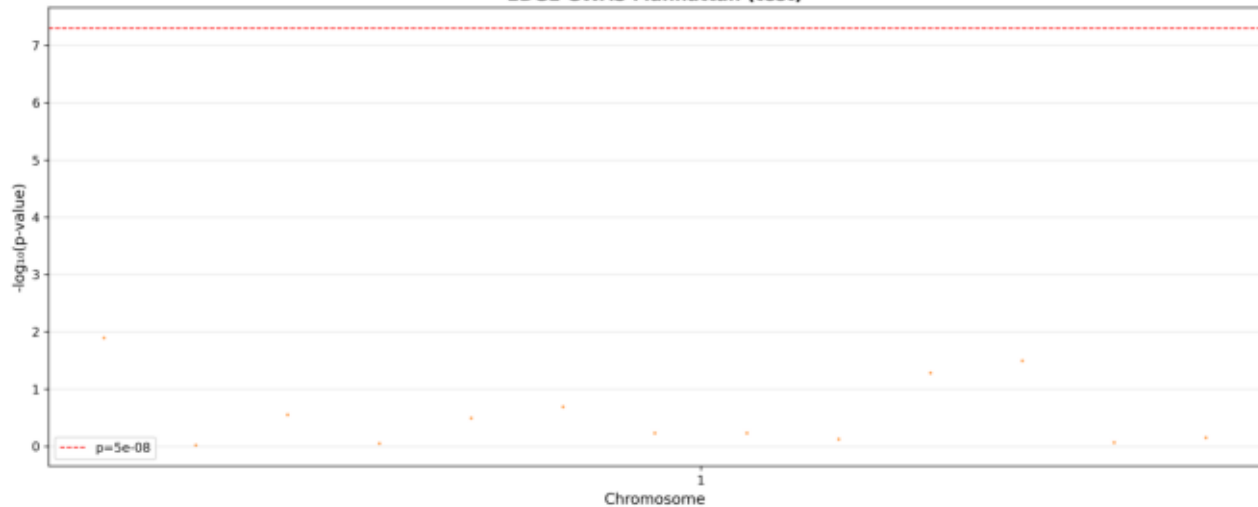
[OK] identify_related_samples

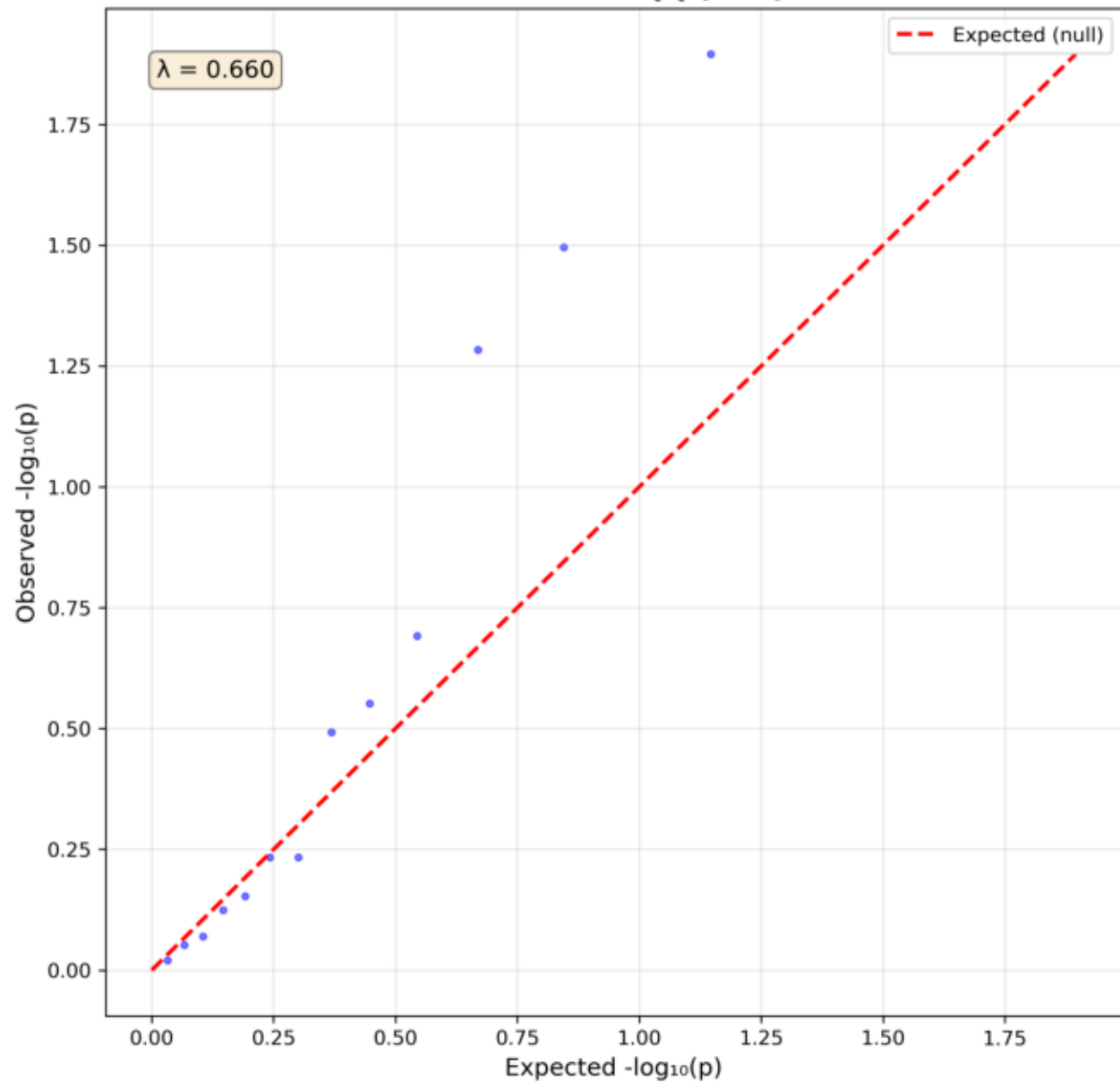
[OK] filter_related_samples

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All function tests passed.

manhattan.png

EDGE GWAS Manhattan (test)



EDGE GWAS QQ (test)

Distribution of EDGE Alpha Values