

# 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
```

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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 ( $\lambda$ ): 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

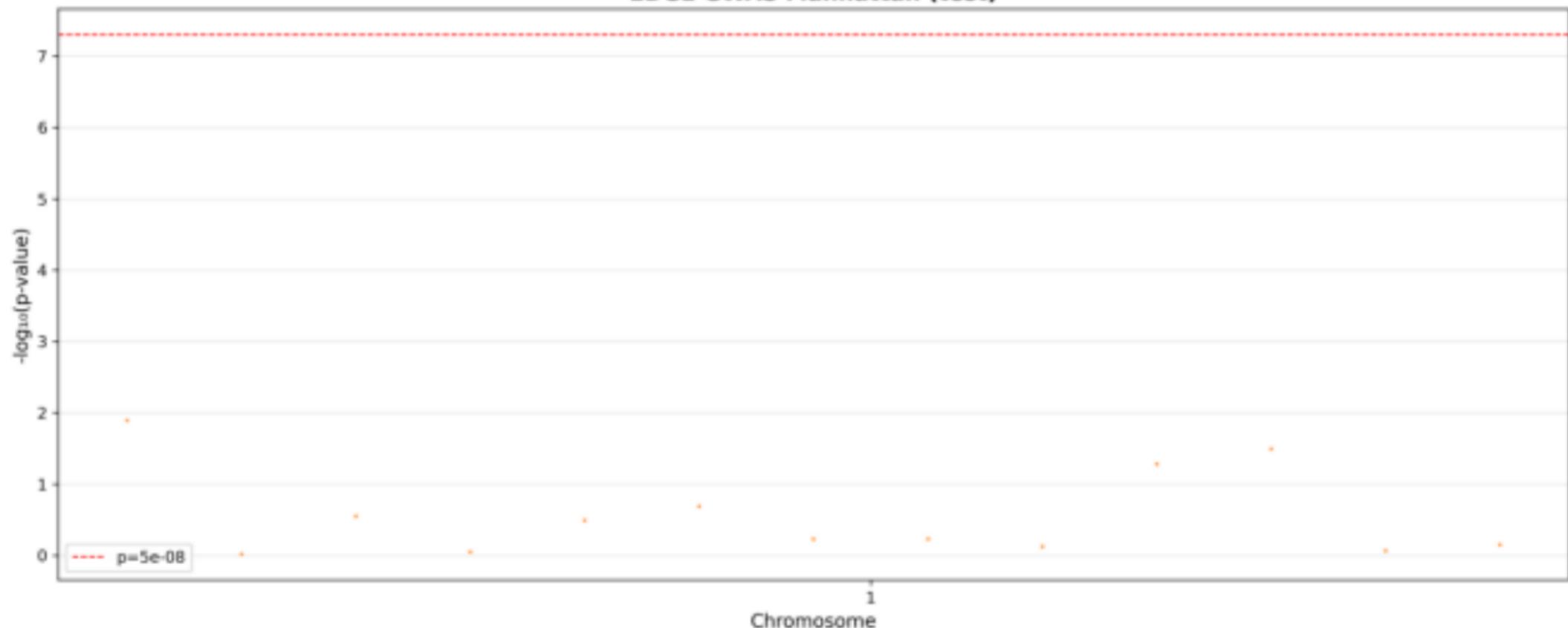
[15] Optional (skip if no data/tools)
[SKIP] load_pgen_data: pgenlib is required to load PGEN files. Install with: pip install pgenlib
[SKIP] load_bgen_data: bgen_reader is required to load BGEN files. Install with: pip install bgen-reader
[OK] calculate_pca_plink
[OK] calculate_pca_pcpair
[OK] calculate_grm_gcta
[SKIP] load_grm_gcta: no files
[OK] identify_related_samples
[OK] filter_related_samples
```

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```

All function tests passed.

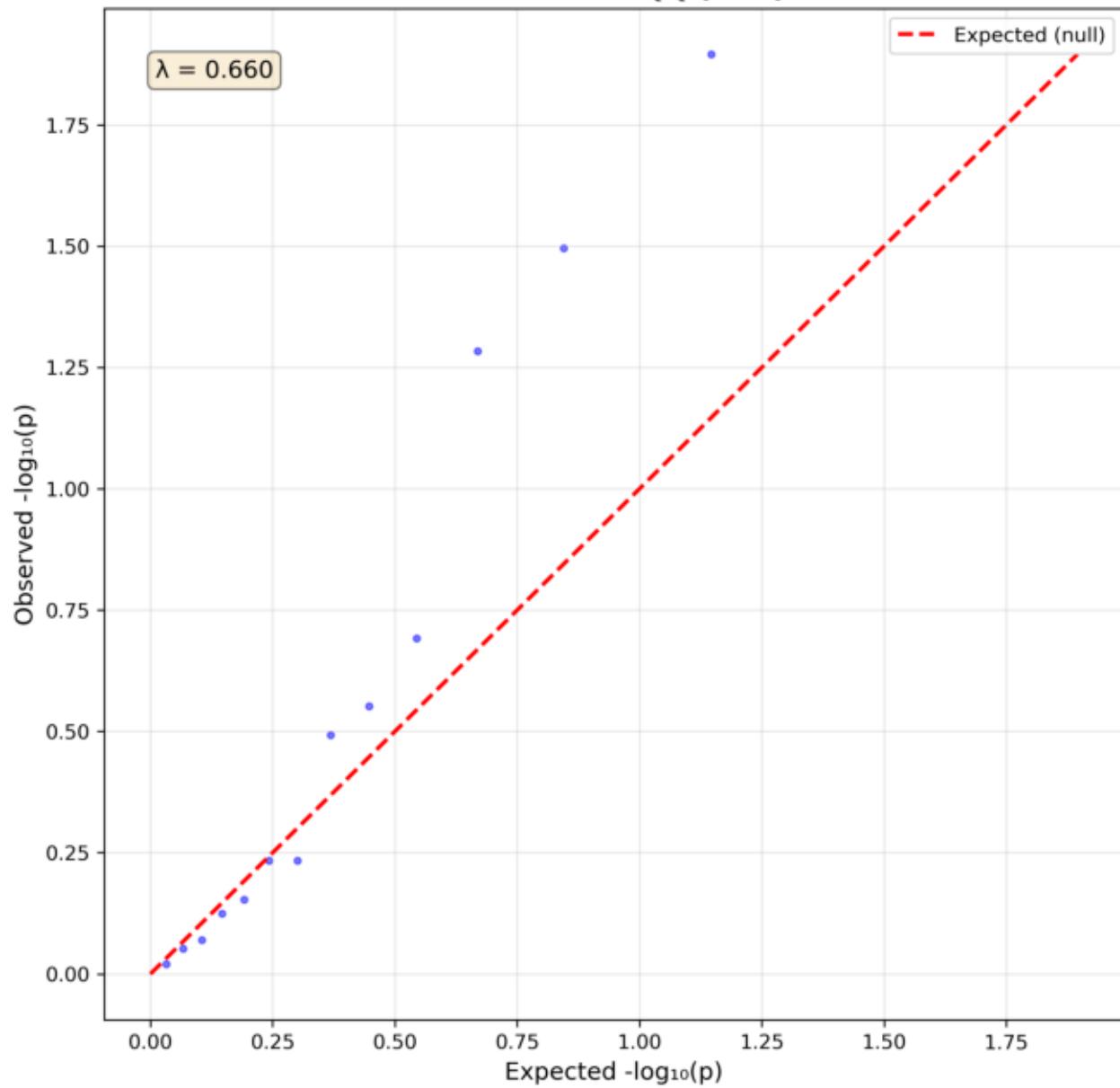
manhattan.png

EDGE GWAS Manhattan (test)



qq\_plot.png

## EDGE GWAS QQ (test)



alpha\_distribution.png

### Distribution of EDGE Alpha Values

