

Package ‘cwot’

July 22, 2025

Type Package

Title Cauchy Weighted Joint Test for Pharmacogenetics Analysis

Version 0.1.0

Description A flexible and robust joint test of the single nucleotide polymorphism (SNP) main effect and genotype-by-treatment interaction effect for continuous and binary endpoints. Two analytic procedures, Cauchy weighted joint test (CWOT) and adaptively weighted joint test (AWOT), are proposed to accurately calculate the joint test p-value. The proposed methods are evaluated through extensive simulations under various scenarios. The results show that the proposed AWOT and CWOT control type I error well and outperform existing methods in detecting the most interesting signal patterns in pharmacogenetics (PGx) association studies. For reference, see Hong Zhang, Devan Mehrotra and Judong Shen (2022) <[doi:10.13140/RG.2.2.28323.53280](https://doi.org/10.13140/RG.2.2.28323.53280)>.

License GPL-2

Imports stats, SPAtest, mvtnorm

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

Author Hong Zhang [aut, cre] (ORCID: <<https://orcid.org/0000-0002-8869-8671>>)

Maintainer Hong Zhang <hzhang@wpi.edu>

Repository CRAN

Date/Publication 2022-09-23 14:40:02 UTC

Contents

| | |
|---------------------|----------|
| awot | 2 |
| awot_null | 3 |
| cwot | 3 |
| cwot_null | 4 |
| Index | 6 |

| | |
|------|--|
| awot | <i>Adaptively weighted joint test for main effect and genotype-by-treatment interaction effect for continuous endpoints.</i> |
|------|--|

Description

Adaptively weighted joint test for main effect and genotype-by-treatment interaction effect for continuous endpoints.

Usage

```
awot(nullmod, g, weights = seq(-1, 1, 0.1))
```

Arguments

| | |
|---------|--|
| nullmod | - The null model object from the output of <code>awot_null</code> . |
| g | - The variable of interest, e.g., the genotype. |
| weights | - The pre-specified weights. The default choice is a vector of -1, -0.9,..., 0.9, 1. |

Value

The p-value of AWOT and the individual p-values of the composite genotypes.

References

Hong Zhang, Qing Li, Devan Mehrotra and Judong Shen. "CauchyCP: a powerful test under non-proportional hazards using Cauchy combination of change-point Cox regressions", arXiv:2101.00059.

Examples

```
n = 100
y = rbinom(n, 1, 0.3)
x = data.frame(x1=rnorm(n))
tr = rbinom(n, 1, 0.5)
g = rbinom(n, 2, 0.1)
nullmod = awot_null(y, tr, x)
awot(nullmod, g, weights=seq(-1,1,0.1))
```

| | |
|-----------|-------------------------------------|
| awot_null | <i>Prepare null model for awot.</i> |
|-----------|-------------------------------------|

Description

Prepare null model for awot.

Usage

```
awot_null(y, tr, x = NULL)
```

Arguments

y - Continuous response variable.
tr - Binary treatment variable, 1 for treated, 0 for placebo.
x - Covariates in addition to treatment variable.

Value

A list of objects needed for awot.

References

Hong Zhang, Devan Mehrotra and Judong Shen, "AWOT and CWOT for Genotype and Genotype by Treatment Interaction Joint Analysis in Pharmacogenetics GWAS".

Examples

```
n = 100  
y = rnorm(n)  
x = data.frame(x1=rnorm(n))  
tr = rbinom(n, 1, 0.5)  
nullmod = awot_null(y, tr, x)
```

| | |
|------|--|
| cwot | <i>Cauchy weighted joint test for main effect and genotype-by-treatment interaction effect for binary endpoints.</i> |
|------|--|

Description

Cauchy weighted joint test for main effect and genotype-by-treatment interaction effect for binary endpoints.

Usage

```
cwot(nullmod, g, weights = seq(-1, 1, 0.1))
```

Arguments

- nullmod - The null model object from the output of cwot_null.
- g - The variable of interest, e.g., the genotype.
- weights - The pre-specified weights. The default choice is a vector of -1, -0.9,..., 0.9, 1.

Value

The p-values of CWOT, CWOT_Score, CWOT_LRT and the individual p-values of the composite genotypes.

References

Hong Zhang, Qing Li, Devan Mehrotra and Judong Shen. "CauchyCP: a powerful test under non-proportional hazards using Cauchy combination of change-point Cox regressions", arXiv:2101.00059.

Examples

```
n = 100
y = rbinom(n, 1, 0.3)
x = data.frame(x1=rnorm(n))
tr = rbinom(n, 1, 0.5)
g = rbinom(n, 2, 0.1)
nullmod = cwot_null(y, tr, x)
cwot(nullmod, g, weights=seq(-1,1,0.1))
```

cwot_null

Prepare null model for cwot.

Description

Prepare null model for cwot.

Usage

```
cwot_null(y, tr, x = NULL)
```

Arguments

- y - Binary response variable.
- tr - Binary treatment variable, 1 for treated, 0 for placebo.
- x - Covariates in addition to treatment variable.

Value

A list of objects needed for cwot.

References

Hong Zhang, Devan Mehrotra and Judong Shen, "AWOT and CWOT for Genotype and Genotype by Treatment Interaction Joint Analysis in Pharmacogenetics GWAS".

Examples

```
n = 100
y = rbinom(n, 1, 0.3)
x = data.frame(x1=rnorm(n))
tr = rbinom(n, 1, 0.5)
nullmod = cwot_null(y, tr, x)
```

Index

awot, 2
awot_null, 3

cwot, 3
cwot_null, 4