Tittle: A Fast and Efficient Approach for Gene-based Association Studies of Ordinal Phenotypes

Description

A fast and efficient association method to test the association between genetic variants and an ordinal phenotype.

Usage

OR\_ACAT\_CR(G, obj, xc, Cweights.beta=c(1,25), Rweights.beta=c(1,25), common.weights=NULL, rare.weights=NULL, rvt)

Description: an association test between multiple variants and an ordinal phenotype.

Arguments:

G a numeric genotype matrix with each row as a different individual and each column as a separate variant

obj an ordinal phenotype vector

xc a numeric covariate matrix with each row as a different individual and each column as a separate covariate

Cweights.beta a numeric vector of parameters for the beta weights for the weighted kernels based on common variants. If you want to use your own weights, please use the “common.weights” parameter. It will be ignored if “common.weights” parameter is not null.

Rweights.beta a numeric vector of parameters for the beta weights for the weighted kernels based on rare variants. If you want to use your own weights, please use the “rare.weights” parameter. It will be ignored if “rare.weights” parameter is not null.

common.weights a numeric vector of non-negative weights for the combined p-values of common-variant tests

rare.weights a numeric vector of non-negative weights for the combined p-values of rare-variant tests

rvt rare variant threshold

Value:

pval p-value of OR-ACAT

Usage

ord\_data\_pv(ord\_y, x1, xc)

Description: calculating variant-level p value of a likelihood ratio test between a common variant and an ordinal phenotype based on the ordinal logistic regression model .

Arguments:

x1 a numeric genotype matrix with each row as a different individual and each column as a separate variant

ord\_y an ordinal phenotype vector

xc a numeric covariate matrix with each row as a different individual and each column as a separate covariate

Value:

pval p-values of variant-level tests

order\_Burden(G, obj, xc, kernel, weights.beta, weights=NULL)

Description: Burden method to aggregate rare variants

Arguments:

G a numeric genotype matrix with each row as a different individual and each column as a separate variant

obj an ordinal phenotype vector

xc a numeric covariate matrix with each row as a different individual and each column as a separate covariate

kernel a type of kernel

weights.beta a numeric vector of parameters for the beta weights for the weighted kernels. If you want to use your own weights, please use the “weights” parameter. It will be ignored if “weights” parameter is not null.

weights a numeric vector of non-negative weights for the combined p-values

Value:

pval p-value of testing rare variants based on Burden method

ACAT (pvals, weights=NULL)

Description: Aggregated Cauchy Association Test, a general, powerful, and computationally efficient P-value combination method

(https://github.com/yaowuliu/ACAT)

Arguments:

pvals a numeric vector of p-values to be combined by ACAT

weights a numeric vector of non-negative weights for the combined p-values

Value:

pval p-value of ACAT