Package ‘aGE’

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aGE interaction test

Description

aGE interaction test

Usage

aGE(Y, G, cov = NULL, model = c("gaussian", "binomial"),
   pow = c(1:6), n.perm = 1000, method = "Simulation", nonparaE = F,
   DF = 10, stepwise = T)

Arguments

Y a numeric vector of phenotype values
G a matrix for all RVs in the test gene or genomic region. The order of rows must
   match the order of Y. Missing is imputed as 0.
cov a matrix with first column as the environmental variable to be tested. The order
   of rows must match the order of Y.
model "binomial" for binary traits or "gaussian" for quantitative traits.
pow Gamma set used to build a family of tests, default=c(1:6) for rare variants
n.perm number of simulation to calculate the p-values, default=1000. Can increase to
   higher value depending on the significance level.
method only have one option: "Simulation", also called Monte Carlo Method.
nonparaE "T": use cubic splines for the environmental variable to fit the model; "F": use a
   linear function of the environmental variable to fit the model
DF degree of freedom to use in the cubic splines, default=10. This option only
   works when nonparaE is set to "T"
stepwise an option to speed up the simulation procedure for large n.perm number in real-
   data application. Up to $n.perm=10^8$

Value

p-values

Examples

{ set.seed(12345)
  phenotype <- c(rep(1,50), rep(0,50))
  genotype <- data.frame(g1=sample(c(rep(1,10), rep(0,90))),
    g2=sample(c(rep(1,5), rep(0,95))))
  covariates <- data.frame(envir=rnorm(100), age=rnorm(100,60,5))
  env <- list(Y=phenotype, G=genotype, X=covariates)
  age(y=exD$Y, G=exD$G, cov=exD$X, model='binomial', nonparaE=FALSE, stepwise=FALSE)
}


aGE.joint

Description

aGE joint test

Usage

aGE.joint(Y, G, cov = NULL, model = c("gaussian", "binomial"),
pow = c(1:6), n.perm = 1000, method = c("Simulation"),
nonparaE = F, DF = 10)

Arguments

Y a numeric vector of phenotype values
G a matrix or data frame for all RVs in the test gene or genomic region. The order of rows must match the order of Y. Missing is imputed as 0.
cov a matrix or data frame with first column as the environmental variable to be tested. The order of rows must match the order of Y.
model "binomial" for binary traits or "gaussian" for quantitative traits.
pow Gamma set used to build a family of tests, default=c(1:6) for rare variants
n.perm number of simulation to calculate the p-values, default=1000. Can increase to higher value depending on the signficiance level.
method 'Simulation': Monte Carlo Method
nonparaE "T": use cubic splines for the environmental variable to fit the model; "F": use a linear function of the environmental variable to fit the model
DF degree of freedom to use in the cubic splines, default=10. This option only works when nonparaE is set to "T".

Value

p-values

Examples

{
  set.seed(12345)
  phenotype <- c(rep(1,50),rep(0,50))
genotype <- data.frame(g1=sample(c(rep(1,10),rep(0,90))),g2=sample(c(rep(1,5), rep(0,95))))
covariates <- data.frame(Envir=rnorm(100), Age=rnorm(100,60,5))
exD <- list(Y=phenotype, G=genotype, X=covariates)
aGE.joint(Y=exD$Y, G=exD$G, cov=exD$X, model='binomial')
}
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