Package 'CKAT'

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Type Package

Title Composite Kernel Association Test for Pharmacogenetics Studies

Version 0.1.0

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Description Composite Kernel Association Test (CKAT) is a flexible and robust kernel machine based approach to jointly test the genetic main effect and gene-treatment interaction effect for a set of single-nucleotide polymorphisms (SNPs) in pharmacogenetics (PGx) assessments embedded within randomized clinical trials.

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CKAT	*Composite kernel association test for SNP-set analysis in pharmaco-genetics (PGx) studies.*

Description

Composite kernel association test for SNP-set analysis in pharmacogenetics (PGx) studies.

Usage

```
CKAT(G, Tr, X, y, trait = "continuous", ker = "linear", grids = c(0,
  0.5, 1), n_a = 1000, method = "liu", subdiv = 10^6)
```

Arguments

G	- genotype matrix.
Tr	- treatment vector, 0 indicates placebo, 1 indicates treatment.
X	- non-genetic covariates data matrix.
y	- response vector. Currently continuous and binary responses are supported. Survival response will be added soon.
trait	- response indicator. trait = "continuous" or "binary".
ker	- kernel. ker = "linear", "IBS", "Inter" (interaction kernel) and "RBF" (radial basis function kernel).
grids	- grids of the candidate weights.
n_a	- the number of intervals for manual integration (when integrate function fails). Default n_a = 1000.
method	- method for getting density of A (see details in the reference). Default method is Liu's method.
subdiv	- parameter of Davies' method. Default value is 1E6.

Value

pvals - p-values of each individual association test.

finalp - final p-value of the CKAT test.

Examples

```
nsamples = 500; nsnps = 10
X = rnorm(nsamples,0,1)
Tr = sample(0:1,nsamples,replace=TRUE)
G = matrix(rbinom(nsamples*nsnps, 1, 0.05), nrow = nsamples, ncol = nsnps)
GxT = G*Tr
Y0 = 0.5*X + Tr + rnorm(nsamples)
CKAT(G, Tr, X, Y0, grids=c(0,0.5,1))
```

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