Package ‘SPAr’

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Type Package

Title Perform rare variants association analysis based on summation of partition approaches

Version 0.1

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Description This package performs robust nonparametric tests for rare variants association analysis using summation of partition approaches that incorporate gene-gene and gene-environmental interactions

License GPL (>= 2)

NeedsCompilation no

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`SPAr-package` *Rare variants association tests based on summation of partition approaches*

Description

Perform nonparametric association tests between a set of rare variants and continous or dichotomous outcomes incorporation gene-gene and gene-environmental interactions

Details

Package:	SPAr
Type:	Package
Version:	0.1
Date:	2014-02-20
License:	GPL(>=2)

Author(s)

Ruixue Fan

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References

Fan, R., Lo, S-H (2013). A robust model-free approach for rare variantss association studies incorporating gene-gene and gene-environmental interactions. *PLOS ONE* 8(12):e83057.

`print.SPA` *Print out the values and significance of SPA test scores.*

Description

This function prints out the numerical values of SPA test statistics and their p-values.

Usage

```
## S3 method for class 'SPA'
print(x,...)
```

Arguments

`x`	an SPA object, result form `SPA.I` or `SPA.I.GE`.
`...`	See `print`.

Author(s)

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References

Fan, R., Lo, S-H (2013). A robust model-free approach for rare variantss association studies incorporating gene-gene and gene-environmental interactions. *PLOS ONE* 8(12):e83057.

See Also

`SPA.I`,`SPA.I.GE`

Examples

```
data(SPA_example)
attach(SPA_example)
I1_dich <- SPA.I(x,y.d,interaction=1,nperm=100) # only compute I1 and its pvalue
print(I1_dich)
```

`SPA.I` *Compute rare variants association test scores with and(or) without gene-gene interactions*

Description

Compute the nonparametric association test scores between a set of rare variants and continous or dichotomous outcomes with and(or) without gene-gene interactions

Usage

```
SPA.I(x, y, nperm = 100, type = "dichotomous", interaction = 0)
```

Arguments

`x`	a matrix of numeric genotypes with each row as an individual and each column as a separate rare SNP. Each genotype should be coded as `0`,1 and 2.
`y`	a vector of phenotypes. The length of `y` should be the same as the number of rows of `x`.
`nperm`	the number of permutations used to obtain the significance level.
`type`	a string to indicate if the phenoype is continuous or dichotomous. It could take values "dichotomous" or "continuous".
`interaction`	an integer indicating if the interaction is considered when computing the information score. See Details.

Details

There are three types of interactions: 1 - compute the score without interaction (score I1); 2 - compute the score with interaction (score I2); 0 - compute both scores with and without interaction as well as the adaptive p* score.

Value

`I`	The numeric value of I score. Could be a vector of 3 values if interaction=0.
`pvalue`	The p-value of corresponding I score.Could be a vector of 3 values if interaction=0.
`nperm`	Number of permutations.
`call`	The matched call.
`type`	Type of methods used. Could be "I1","I2" or "p*".

Author(s)

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References

Fan, R., Lo, S-H (2013). A robust model-free approach for rare variantss association studies incorporating gene-gene and gene-environmental interactions. *PLOS ONE* 8(12):e83057.

Examples

```
data(SPA_example)
attach(SPA_example)

## compute p-values of dichotomous traits

pstar_dich <- SPA.I(x,y.d,nperm=10) #compute I1,I2 and p* and their p-values
print(pstar_dich)

I1_dich <- SPA.I(x,y.d,interaction=1,nperm=10) # only compute I1 and its pvalue
print(I1_dich)


## compute p-values of continuous traits

pstar_cont <- SPA.I(x,y.c,nperm=10,type="cont")  #compute I1,I2 and p* and their p-values
print(pstar_cont)

I1_cont <- SPA.I(x,y.c,type="cont",interaction=1,nperm=10) # only compute I1 and its pvalue
print(I1_cont)
```

`SPA.I.GE` *Rare variants association test score to evaulate the effect of gene-environmental interactions*

Description

Compute the nonparametric association information score between a set of rare variants and dichotomous outcomes, incorporating interactions with environmental factors.

Usage

```
SPA.I.GE(x, y, E, nperm = 100)
```

Arguments

`x`	a matrix of numeric genotypes with each row as an individual and each column as a separate rare SNP. Each genotype should be coded as `0`,`1` and `2`.
`y`	a vector of phenotypes. The length of `y` should be the same as the number of rows of `x`.
`E`	a vector of environmental factors. It must be a categorical variable.
`nperm`	the number of permutations used to obtain the significance level. See details.

Details

This function evaluates the gene-environmental intearction effects associated with the dichotomous trait. The phenotype `y` must be dichotomous. The significance is computed using both global permutation and local permutation.

Value

`I2star`	The numerical value of the information score.
`pvalue.global`	The p-value from global permutation.
`pvalue.local`	The p-value from local permutation.
`call`	The matched call.
`type`	Type of the method used. It is "env".

Author(s)

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References

Fan, R., Lo, S-H (2013). A robust model-free approach for rare variantss association studies incorporating gene-gene and gene-environmental interactions. *PLOS ONE* 8(12):e83057.

Examples

```
data(SPA_example)
attach(SPA_example)
SPA.I.GE <- SPA.I.GE(x,y.d,E,nperm=10)
print(SPA.I.GE)
```

`SPA_example` *Example data for SPA with continuous and dichotomous traits and an environmental factor.*

Description

Example data for SPA with continuous and dichotomous traits and an environmental factor.

Format

SPA_example contains the following objects:

- **x** a numeric genotype matrix of 1000 individuals and 20 SNPs. Each row represents a different individual and each column represents a different SNP marker.
- **y.c** a numeric vector of continuous phenotypes.
- **y.d** a numeric vector of dichotomous phenotypes.
- **E** a numeric vector of an environmental factor.

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