

Package ‘SASOM’

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Type Package
Title What the Package Does (Title Case)
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Description Test for association between a set of somatic mutations and multinomial outcomes by using score statistics.
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License LGPL (>= 2.0)
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DAPC	<i>P-value combination method</i>
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Usage

DAPC(x)

Arguments

x a vector of length 2, containing two independent p-values.

Value

p combined p-value by using DAPC method.

Author(s)

Meiling Liu, Yang Liu, and Qianchuan He

Examples

```
x = c(0.1, 0.3)
DAPC(x)
```

SASOM	<i>Score test for multinomial outcomes</i>
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Description

Test for association between a set of somatic mutations and multinomial outcomes.

Usage

```
SASOM(y, X, G, W, rlevel, p.comb)
```

Arguments

y	a matrix or a factor vector. When a matrix is given, each row represents a subject, each column corresponds to a subtype. A subject must belong to one of the subtypes, i.e. each row sums up to 1. When a vector is given, each element corresponds to the assignment of subtype for each subject.
X	a covariant matrix, each row represents a subject.
G	a variant matrix, each row represents a subject.
W	a variant character matrix, each row represents a genome character, each column represents a variant. The column number of W is equal to the row number of G.
rlevel	reference level, rlevel must be a number if y is a matrix or a factor when y is a vector.
p.comb	a character to assign p-value combination method, must be one of ("all", "DAPC", "fisher", "tippet"). When p.comb = "all", p-values were combined by using DAPC, Fisher's and Tippet's procedures.

Value

pval.theta	p-value for testing the fixed variant effect.
pval.tau	p-value for testing the random variant effect.
p.fisher	overall p-value for testing the association between a set of somatic mutations and outcomes. It combines pval.theta and pval.tau by using Fisher's procedure.
pval.tippet	overall p-value for testing the association between a set of somatic mutations and outcomes. It combines pval.theta and pval.tau by using Tippet's procedure.
pval.dapc	overall p-value for testing the association between a set of somatic mutations and outcomes. It combines pval.theta and pval.tau by using DAPC procedure.

Author(s)

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Examples

```
data("SASOM.data")
attach(SASOM.data)
out = SASOM(y, X, G, W, rlevel,"all")
out
detach(SASOM.data)
```

SASOM.data*Data example for SASOM*

Description

A numerical data example for SASOM.

Usage

```
data(SASOM.data)
```

Format

A list contains the following objects:

- y a numeric matrix of multinomial outcomes. Each row represent a subject and each subject belongs to one of the three subtypes.
- X a numeric matrix of covariates (including intercept).
- G a numeric matrix of variant.
- W a numeric matrix of variant character.
- rlevel a numeric number indicating the reference level.

Examples

```
data("SASOM.data")
```

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