

Package ‘SASOM’

September 17, 2020

Type Package
Title What the Package Does (Title Case)
Version 0.1.0
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Description Test for association between a set of somatic mutations and multinomial outcomes by using score statistics.
Depends CompQuadForm, nnet
License LGPL (>= 2.0)
Encoding UTF-8
LazyData true
RoxygenNote 7.1.1

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SASOM	<i>SASOM</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)
```

Arguments

<code>y</code>	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.
<code>X</code>	a covariant matrix, each row represents a subject.
<code>G</code>	a variant matrix, each row represents a subject.
<code>W</code>	a variant character matrix, each row represents a genome character, each column represents a variant. The column number of <code>W</code> is equal to the row number of <code>G</code> .
<code>rlevel</code>	reference level, <code>rlevel</code> must be a number if <code>y</code> is a matrix or a factor when <code>y</code> is a vector.

Value

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

Author(s)

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Examples

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

SASOM.data

SASOM.data

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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