Package 'STAMO'

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Type Package

Title Structured testing of genetic association with mixed clinical outcomes

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

Depends R (>= 3.5.0), CompQuadForm,survival

License LGPL(>=2.0)

Encoding UTF-8

LazyData true

R topics documented:

`STAMO` *Score Test for Association Between Somatic Mutations and Multivariate Outcomes*

Description

The `STAMO` function performs a score-based test to evaluate the association between somatic mutations and multivariate outcomes, such as survival time and ancillary outcomes (continuous or binary). The test accounts for both fixed and random effects of genetic variants.

Usage

```
STAMO(U, delta, Y, X, G, W)
```

Arguments

U	A numeric vector representing the right-censored survival time for each subject.
delta	A numeric vector indicating the censoring status (1 = event occurred, 0 = censored).
Y	A numeric vector representing the ancillary outcome, which can be either a continuous or binary variable.
X	A numeric matrix of covariates, where each row corresponds to a subject and each column to a covariate (e.g., age, gender, etc.).
G	A numeric matrix of genetic variants, where each row represents a subject and each column represents a variant. This matrix captures the variant information for each subject under study.
W	A numeric matrix of variant annotations, where each row represents a genomic feature (e.g., gene or pathway) and each column corresponds to a variant. The number of rows in W must match the number of columns in G.

Value

The function returns a list with the following components:

`pval.fix` P-value for testing the fixed variant effect, which assumes a consistent effect of the variant across subjects.

`pval.rand` P-value for testing the random variant effect, which allows the effect of the variant to vary between subjects.

`pval` The overall p-value for testing the association between a set of somatic mutations and multivariate outcomes. This p-value combines `pval.fix` and `pval.rand` using Fisher's procedure.

Author(s)

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References

Liu, M., Su, Y.R., Liu, Y., Hsu, L. and He, Q., 2024. Structured testing of genetic association with mixed clinical outcomes. Genetic Epidemiology.

Examples

```
# Load the example dataset
data("STAMO.data")

# Perform the STAMO test on the first dataset
out1 <- STAMO(dat1$U, dat1$delta, dat1$Y, dat1$X, dat1$G, dat1$W)
print(out1)

# Perform the STAMO test on the second dataset
out2 <- STAMO(dat2$U, dat2$delta, dat2$Y, dat2$X, dat2$G, dat2$W)
print(out2)
```

STAMO.data *Example Datasets for STAMO*

Description

This dataset provides two examples, dat1 and dat2, for use with the STAMO package: one with a binary ancillary variable and the other with a continuous ancillary variable. These examples are designed to demonstrate the application of survival analysis techniques in the presence of ancillary variables.

Usage

```
data("STAMO.data")
```

Format

Two example datasets, each provided as a list containing the following components:

U A numeric vector representing censored failure times for each subject.

delta A numeric vector indicating the censoring status (1 = event occurred, 0 = censored) for each subject.

Y A numeric vector representing the ancillary variable. This can be either binary or continuous, depending on the example.

X A numeric matrix of covariates for each subject (excluding intercept).

G A numeric matrix of genetic variants for each subject.

W A numeric matrix of variant annotations, providing additional features related to the genetic variants.

Examples

```
# Load the example dataset
data("STAMO.data")
```

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