Package: dSVA (via r-universe)

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Type Package

Title Direct Surrogate Variable Analysis

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Description Functions for direct surrogate variable analysis, which can identify hidden factors in high-dimensional biomedical data.

License GPL (>= 2)

Depends R (>= 2.13.0)

Imports sva

NeedsCompilation no

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Repository https://leeshawn.r-universe.dev

RemoteUrl https://github.com/cran/dSVA

RemoteRef HEAD

RemoteSha 9e44498ef0300488764ff6549bbdc8c91c67ffee

Contents

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dSVA   *direct surrogate variable analysis*

Description

Identify hidden factors in high dimensional biomedical data

Usage

```
dSVA(Y, X, ncomp=0)
```

Arguments

Y	n x m data matrix of n samples and m features.
X	n x p matrix of covariates without intercept.
ncomp	a number of surrogate variables to be estimated. If ncomp=0 (default), ncomp will be estimated using the be method in the num.sv function of the sva package.

Value

Bhat = Bhat.all[idx.test,], BhatSE= BhatSE[idx.test,], Pvalue=Pvalue

Bhat	n x m matrix of the estimated effect sizes of X
BhatSE	n x m matrix of the estimated standard error of Bhat
Pvalue	n x m matrix of the p-values of Bhat
Z	a matrix of the estimated surrogate variable
ncomp	a number of surrogate variables.

Author(s)

Seunggeun Lee

Examples

```
data(Example)
attach(Example)
out<-dSVA(Y,X, ncomp=0)
```

Example 3

Example	*Example data for dSVA*

Description

Example data for dSVA.

Format

Example contains the following objects:

Y a data matrix of 100 individuals and 5000 features

X a vector of the primary variable

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