Package ‘dSVA’

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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)
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R topics documented:

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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          Example data for dSVA

Description

Example data for dSVA.
Example

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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