

# Package ‘dSVA’

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**Type** Package

**Title** Direct Surrogate Variable Analysis

**Version** 1.0

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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

**Repository** CRAN

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dSVA *direct surrogate variable analysis*

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## 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)
```

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Example

*Example data for dSVA*

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**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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