

# Package ‘DASC’

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**Type** Package

**Title** Detecting hidden batch factors through data adaptive adjustment for biological effects

**Version** 0.99.11

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**Description** The package is used for identifying batches in high-dimensional dataset.

**Depends** R (>= 3.4.0),

**Imports** NMF (>= 0.20.6), cvxclustr (>= 1.1.1), Biobase

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**biocViews** BatchEffect, RNASeq, GeneExpression, Normalization, Preprocessing, QualityControl, StatisticalMethod, GeneTarget, Clustering

**RoxygenNote** 6.0.1

**Suggests** BiocStyle, knitr, rmarkdown, DESeq2, pcaExplorer, testthat, ggplot2

**VignetteBuilder** knitr

**NeedsCompilation** no

## R topics documented:

adj2vector . . . . .	2
DASC . . . . .	2
get_father . . . . .	4
Ini_SemiNMF . . . . .	4
Loss_Fro . . . . .	5
merge . . . . .	5
Semi_NMF . . . . .	6
Sptree . . . . .	7
stanfordData . . . . .	7
trans_ADJ . . . . .	8
trans_Laplace . . . . .	8
update_G . . . . .	9

**Index****10**


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adj2vector	<i>Transform the adjacency matrix to a vector</i>
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**Description**

Transform the adjacency matrix to a vector

**Usage**

```
adj2vector(Adjacency, n)
```

**Arguments**

Adjacency	the adjacency matrix of factor
n	number of samples

**Value**

w the vector of the adjacency matrix

**Author(s)**

Haidong Yi, Ayush T. Raman

**Examples**

```
W <- matrix(c(0,1,0,0,1,0,0,0,0,0,0,0,0,0,0),nrow=4)
w <- adj2vector(W,4)
```

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DASC	<i>Detecting hidden batch factors through data adaptive shrinkage and clustering (DASC)</i>
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**Description**

Detecting hidden batch factors through data adaptive shrinkage and clustering (DASC)

Batch factor detection via DASC (Data-adaptive Shrinkage and Clustering-DASC)

**Usage**

```
DASC(edata, pdata, factor, method = "ama", type = 3, lambda, rank, nrun,
spanning = FALSE, annotation)
```

**Arguments**

<code>edata</code>	the normalized target matrix, a data.frame The row is gene, the column is sample
<code>pdata</code>	Phenotypic data summarizes information about the samples
<code>factor</code>	A factor vector which controls the convex clustering
<code>method</code>	Algorithm to use: 'admm' or 'ama'
<code>type</code>	An integer indicating the norm used: 1 = 1-norm 2 = 2-norm 3 = 2-norm <sup>2</sup>
<code>lambda</code>	A double number A regularization parameter in the convex optimization
<code>rank</code>	integer sequence
<code>nrun</code>	the iteration numbers of Semi-NMF
<code>spanning</code>	parameter is assigned as false
<code>annotation</code>	An annotation of the dataset

**Details**

The DASC function is the main function of our algorithm DASC (Data-adaptive Shrinkage and Clustering-DASC) package. The DASC includes two main steps

- Data-adaptive shrinkage using convex clustering shrinkage (Implemented by convex optimization.);
- Extract batch factors using matrix factorization.

**Value**

outputs the result of semi-NMF. It classifies each sample to its batch factor.

**Author(s)**

Haidong Yi, Ayush T. Raman

Haidong Yi, Ayush T. Raman

**See Also**

[cvxclust\\_path\\_ama](#) and [cvxclust\\_path\\_admm](#) for the detailed algorithm

**Examples**

```
library(NMF)
library(cvxclustr)
library(Biobase)
dat <- data.frame(matrix(rnbinom(n=200, mu=100, size=1/0.5), ncol=4))
pdat <- data.frame(sample = colnames(dat), type = c(rep('A',2), rep('B',2)))
rownames(pdat) <- colnames(dat)
res <- DASC(edata=dat, pdata=pdat, factor=pdat$type, method='ama', type=3,
lambda = 1, rank = 2, nrun = 50, spanning = FALSE,
annotation='simulated dataset')
```

---

 get\_father

*Representing node in this subtype*


---

**Description**

Representing node in this subtype

**Usage**

```
get_father(v, X)
```

**Arguments**

v                    the index of the node  
 X                    the saved vector with the information of the parent of every node

**Value**

r the parent index of the node

**Author(s)**

Haidong Yi, Ayush T. Raman

**Examples**

```
nodes <- c(2,3,4,4)
get_father(2, nodes)
```

---

 Ini\_SemiNMF

*Initialization of the semi-NMF*


---

**Description**

Initialization of the semi-NMF

**Usage**

```
Ini_SemiNMF(model, target)
```

**Arguments**

model                Object of class: NMFfit  
 target               gene expression matrix

**Value**

model The initial objective of class: NMFfit

**Author(s)**

Haidong Yi, Ayush T. Raman

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Loss\_Fro

*Get the error of Semi-NMF using frobenius norm*

---

**Description**

Get the error of Semi-NMF using frobenius norm

**Usage**

```
Loss_Fro(model, target)
```

**Arguments**

model	Object of class: NMFfit
target	gene expression matrix

**Details**

This is a customized function defined in terms of `nmf`. For more information, please go through the NMF vignette <https://cran.r-project.org/web/packages/NMF/vignettes/NMF-vignette.pdf>

**Value**

The result of semi-NMF for the current iteration

**Author(s)**

Haidong Yi, Ayush T. Raman

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merge

*Combine two trees into one*

---

**Description**

Combine two trees into one

**Usage**

```
merge(x, y, X)
```

**Arguments**

x	the index of the node
y	the index of the node
X	the saved vector with the information of the parent of every node

**Details**

During the traversal of the graph matrix, merge function joins two disjoint sets into a single subset. It is a union step of Disjoint-set algorithm by Bernard A. Galler and Michael J. Fischer. For further details, please refer to: [https://en.wikipedia.org/wiki/Disjoint-set\\_data\\_structure](https://en.wikipedia.org/wiki/Disjoint-set_data_structure)

**Value**

X A updated X vector with updates on father of every node

**Author(s)**

Haidong Yi, Ayush T. Raman

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Semi\_NMF

*Main function of semi-NMF*

---

**Description**

Main function of semi-NMF

**Usage**

```
Semi_NMF(target, model, iternum = 100)
```

**Arguments**

target	gene expression matrix
model	Object of class: NMFfit
iternum	Number of iterations

**Value**

model the result from the semi-NMF algorithm

**Author(s)**

Haidong Yi, Ayush T. Raman

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Sptree

*Get Spanning tree from adjacency matrix*

---

### Description

Get Spanning tree from adjacency matrix

### Usage

```
Sptree(ADJ)
```

### Arguments

ADJ                    the adjacency matrix of the factor

### Value

ADJ the spanning tree of the adjacency matrix

### Author(s)

Haidong Yi, Ayush T. Raman

### Examples

```
W <- matrix(c(0,1,1,1,1,0,1,1,1,1,0,1,1,1,1,0), nrow=4)
Sptree(W)
```

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stanfordData

*Stanford RNA-Seq dataset*

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### Description

Stanford RNA-Seq dataset

### Format

A list with two components.

Stanford gene expression dataset (Chen et. al. PNAS, 2015; Gilad et. al. F1000 Research, 2015). It is a filtered raw counts dataset which was published by Gilad et al. F1000 Research. 30 expression & mitochondrial genes were removed (Gilad et al.F1000 Research)

**rawCounts** is a DataFrame object where each column represents a sample and each row represents a gene.

**metadata** is a metadata information about each samples

### Source

<https://f1000research.com/articles/4-121/v1>

**References**

1. Gilad Y and Mizrahi-Man O. A reanalysis of mouse ENCODE comparative gene expression data. F1000Research (2015)
2. in S, Lin Y, Nery JR, et al.: Comparison of the transcriptional landscapes between human and mouse tissues. Proc Natl Acad Sci USA (2014)

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trans_ADJ	<i>Outputs Adjacency matrix from the factor vector</i>
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**Description**

Outputs Adjacency matrix from the factor vector

**Usage**

```
trans_ADJ(col_data)
```

**Arguments**

col\_data            A factor vector

**Value**

adjacency Adjacency matrix of col\_data

**Author(s)**

Haidong Yi, Ayush T. Raman

**Examples**

```
batch.factor <- c(rep('human',13),rep('mouse',13))
batch.factor <- as.factor(batch.factor)
adj <- trans_Laplace(batch.factor)
```

---

trans_Laplace	<i>Get Laplace matrix from factor vector</i>
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**Description**

Get Laplace matrix from factor vector

**Usage**

```
trans_Laplace(col_data)
```

**Arguments**

col\_data            A factor vector

**Value**

adjacency The Laplace matrix of col\_data

**Author(s)**

Haidong Yi, Ayush T. Raman

**Examples**

```
batch.factor <- c(rep('human',13),rep('mouse',13))
batch.factor <- as.factor(batch.factor)
adj <- trans_Laplace(batch.factor)
```

---

update\_G

*Update G in Semi-NMF*

---

**Description**

Update G in Semi-NMF

**Usage**

```
update_G(X, mf, mg)
```

**Arguments**

X	Data expression matrix need to be factorized
mf	The basis matrix
mg	The co-efficient matrix

**Details**

By definition, G is a graph adjacency matrix. The update\_G updates G after every iteration.

**Value**

G The basis matrix

**Author(s)**

Haidong Yi, Ayush T. Raman

**Examples**

```
X <- matrix(1:12,nrow=4)
mf <- matrix(1:8,nrow=4)
mg <- matrix(1:6,ncol=2)
mg <- update_G(X,mf,mg)
```

# Index

## \*Topic **datasets**

stanfordData, [7](#)

## \*Topic **package**

DASC, [2](#)

adj2vector, [2](#)

cvxclust\_path\_admm, [3](#)

cvxclust\_path\_ama, [3](#)

DASC, [2](#)

DASC-package (DASC), [2](#)

get\_father, [4](#)

Ini\_SemiNMF, [4](#)

Loss\_Fro, [5](#)

merge, [5](#)

nmf, [5](#)

Semi\_NMF, [6](#)

Sptree, [7](#)

stanfordData, [7](#)

trans\_ADJ, [8](#)

trans\_Laplace, [8](#)

update\_G, [9](#)