

Package ‘mdw’

December 4, 2017

Title Maximum Diversity Weighting

Version 2017.12-03

Description

Dimension-reduction methods aim at defining a score that maximizes signal diversity. Two approaches, namely maximum entropy weights and maximum variance weights, are provided.

Depends R (>= 3.3.0)

Suggests MASS, RUnit

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1.9000

NeedsCompilation no

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Repository CRAN

Date/Publication 2017-12-04 10:27:06 UTC

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 asym.v.e

Asymptotic variance for maximum entropy weights

Description

asym.v.e produces estimated asymptotic covariance matrix of the first p-1 maximum entropy weights (because the p weights sum to 1).

Usage

```
asym.v.e(X, w, h)
```

Arguments

X	n by p maxtrix containing observations of p biomarkers of n subjects.
w	maximum entropy weights for dateset X with bandwidth h used
h	bandwidth for kernel density estimation.

Examples

```
library(MASS)
# a three biomarkers dataset generated from independent normal(0,1)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=diag(3), tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
h = 1
w <- entropy.weight(X,h)
asym.v.e(X,w,h)
```

 asym.v.v

Asymptotic variance for maximum variance weights

Description

asym.v.v produces estimated asymptotic covariance matrix of the first p-1 maximum variance weights (because the p weights sum to 1).

Usage

```
asym.v.v(X, w)
```

Arguments

X	n by p maxtrix containing observations of p biomarkers of n subjects.
w	maximum variance weights for dateset X

Examples

```
library(MASS)
# a three biomarkers dataset generated from independent normal(0,1)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=diag(3), tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
w <- var.weight(X)
asym.v.v(X,w)
```

entropy.weight	<i>Maximum entropy weights</i>
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Description

entropy.weight produces a set of weights that maximizes the total weighted entropy of the distribution of different biomarkers within each subject.

Usage

```
entropy.weight(X, h)
```

Arguments

X	n by p matrix containing observations of p biomarkers of n subjects.
h	bandwidth for kernel density estimation.

Examples

```
library(MASS)
# a three biomarkers dataset generated from independent normal(0,1)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=diag(3), tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
entropy.weight(X, h=1)
```

pca.weight	<i>Weights based on PCA</i>
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Description

pca.weight produce the coefficients of the first principal component

Usage

```
pca.weight(emp.cor)
```

Arguments

emp.cor	empirical correlation matrix of the dataset
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Examples

```
library(MASS)
# a three biomarkers dataset generated from independent normal(0,1)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=diag(3), tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
emp.cor <- cor(X)
pca.weight(emp.cor)
```

var.weight	<i>Maximum variance weights</i>
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Description

var.weight produces a set of weights that maximizes the total weighted variance of the distribution of different biomarkers within each subject.

Usage

```
var.weight(X)
```

Arguments

X n by p matrix containing observations of p biomarkers of n subjects.

Examples

```
library(MASS)
# a three biomarkers dataset generated from independent normal(0,1)
X = mvrnorm(n = 100, mu=rep(0,3), Sigma=diag(3), tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
var.weight(X)
```

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