

Package ‘JADE’

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Type Package

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Description The package ports JF Cardoso’s JADE algorithm as well as his function for joint diagonalization. There are also several criteria for performance evaluation of ICA algorithms.

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 JADE-package

JADE and ICA performance criteria

Description

The package ports J. F. Cardoso's ICA algorithm JADE to R as well as his function for joint diagonalization. Furthermore provides the package several criteria to evaluate ICA algorithms in simulation studies.

Details

Package: JADE
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 License: GPL (>= 2)

Author(s)

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 amari.error

Amari Error

Description

Computes the Amari Error to evaluate the performance of an ICA algorithm.

Usage

```
amari.error(W.hat, A, standardize = F)
```

Arguments

W.hat The estimated square unmixing matrix W.
 A The true square mixing matrix A.
 standardize Logical value if A and W.hat need to be standardized. Default is FALSE.

Details

The Amari Error can be used in simulation studies to evaluate the performance of an ICA algorithm. The Amari error is permutation invariant but not scale invariant. Therefore if different algorithms should be compared the matrices should be scaled in the same way. If `standardize` is `TRUE`, this will be done by the function by standardizing 'W.hat' and the inverse of 'A' in such a way, that every row has length 1, the largest absolute value of the row has a positive sign and the rows are ordered decreasingly according to their largest values.

Note that this function assumes the ICA model is $X = SA'$, as is assumed by `JADE` and `ics`. However `fastICA` and `PearsonICA` assume $X = SA$. Therefore matrices from those functions have to be transposed first.

The Amari Error is scaled in such a way, that it takes a value between 0 and 1. And 0 corresponds to an optimal separation.

Value

The value of the Amari Error.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Amari, S., Cichocki, A. and Yang, H.H. (1996), *A new learning algorithm for blind signal separation*, Advances in Neural Information Processing Systems, **8**, 757–763.

See Also

[ComonGAP](#), [SIR](#)

Examples

```
S <- cbind(rt(1000, 4), rnorm(1000), runif(1000))
A <- matrix(rnorm(9), ncol = 3)
X <- S %*% t(A)

W.hat <- JADE(X, 3)$W
amari.error(W.hat, A)
amari.error(W.hat, A, TRUE)
```

Description

Comon's GAP criterion to evaluate the performance of an ICA algorithm.

Usage

```
ComonGAP(A, A.hat)
```

Arguments

A	The true square mixing matrix.
A.hat	The estimated square mixing matrix.

Details

Comon's GAP criterion is permutation and scale invariant. It can take every positive value and 0 corresponds to an optimal separation. If A is however nearly singular the values of the criterion can be huge.

Note that this function assumes the ICA model is $X = SA'$, as is assumed by [JADE](#) and `ics`. However `fastICA` and `PearsonICA` assume $X = SA$. Therefore matrices from those functions have to be transposed first.

Value

The value of the Comon's GAP.

Author(s)

Klaus Nordhausen, klaus.nordhausen@uta.fi

References

Comon, P., (1994), *Independent Component Analysis, A new concept?*, Signal Processing, **36**, 287–314.

See Also

[amari.error](#), [SIR](#)

Examples

```
S <- cbind(rt(1000, 4), rnorm(1000), runif(1000))
A <- matrix(rnorm(9), ncol = 3)
X <- S %*% t(A)

A.hat <- JADE(X, 3)$A
ComonGAP(A, A.hat)
```

Description

This is an **R** version of Cardoso's JADE ICA algorithm for real data ported from matlab. The ported version is 1.5, some minor changes compared to the matlab function are explained in the details section. The matlab code can be found for example on the ICA central homepage.

Usage

```
JADE(X, n.comp = NULL, eps = 1e-06, maxiter = 100, na.action = na.fail)
```

Arguments

<code>X</code>	Numeric data matrix or dataframe.
<code>n.comp</code>	Number of components to extract.
<code>eps</code>	Convergence tolerance.
<code>maxiter</code>	Maximum number of iterations.
<code>na.action</code>	A function which indicates what should happen when the data contain 'NA's. Default is to fail.

Details

Some minor modifications were done when porting the function to **R**, and they are:

- 1 the model assumed here is $X = SA' + \mu$. Therefore S and X have one row per observation. Note that this still differs from the model definition in **R** of `FastICA` and `PearsonICA` but agrees with `ics`.
- 2 The whitening covariance matrix is divided by $n-1$ and not n (n = number of observations).
- 3 The initial value for the joint diagonalisation is always I .
- 4 The original `eps` would be $\frac{1}{100\sqrt{n}}$.

Worth mentioning is also that the estimated independent components S are scaled to unit variance and are ordered in such a way, that the most energetic component comes first. The signs of the unmixing matrix W are fixed such, that the first column of W has positive elements.

For further details see also the documentation of the original matlab code ("MatlabjadeR.m") on the ICA central homepage (<http://www.tsi.enst.fr/icacentral/>).

Value

A list with the components

<code>A</code>	The estimated mixing matrix.
<code>W</code>	The estimated unmixing matrix.
<code>S</code>	Dataframe with the estimated independent components.
<code>Xmu</code>	The location of the original data.

Author(s)

Jean-Francois Cardoso. Ported to **R** by Klaus Nordhausen, <klaus.nordhausen@uta.fi>

References

Cardoso, J.-F. and Souloumiac, A., (1993), *Blind beamforming for non Gaussian signals*, IEE Proceedings-F, **140**, 362–370. <ftp://sig.enst.fr/pub/jfc/Papers/iee.ps.gz>.

Examples

```
# 3 source and 3 signals

S <- cbind(rt(1000, 4), rnorm(1000), runif(1000))
A <- matrix(rnorm(9), ncol = 3)
X <- S %*% t(A)
res<-JADE(X,3)
res$A
res$W
res$S[1:10,]
(sweep(X,2,res$Xmu) %*% t(res$W))[1:10,]
round(res$W %*% A, 4)

# 2 sources and 3 signals

S2 <- cbind(rt(1000, 4), rnorm(1000))
A2 <- matrix(rnorm(6), ncol = 2)
X2 <- S2 %*% t(A2)
res2 <-JADE(X2,2)
res2$A
res2$W
res2$S[1:10,]
(sweep(X2,2,res2$Xmu) %*% t(res2$W))[1:10,]
SIR(S2,res2$S)
```

rjd

Joint Diagonalization of Real Matrices

Description

This is an **R** version of Cardoso's rjd matlab function for joint diagonalization of k real-valued square matrices.

Usage

```
rjd(X, eps = 1e-06, maxiter = 100, na.action = na.fail)
```



```
round(res.matrix$D, 4)

X.array <- aperm(array(t(X.matrix), dim = c(3,3,4)), c(2,1,3))

res.array <- rjd(X.array)
round(res.array$D, 4)
```

SIR

Signal to Interference Ratio

Description

Computes the signal to interference ratio between true and estimated signals

Usage

```
SIR(S, S.hat)
```

Arguments

S	Matrix or dataframe with the true numeric signals.
S.hat	Matrix or dataframe with the estimated numeric signals.

Details

The signal to interference ratio is measured in dB and values over 20 are thought to be good. It is scale and permutation invariant and can be seen as measuring the correlation between the matched true and estimated signals.

Value

The value of the signal to interference ratio.

Author(s)

Klaus Nordhausen, (klaus.nordhausen@uta.fi)

References

Eriksson, J., Karvanen, J. and Koivunen, V. (2000), Source distribution adaptive maximum likelihood estimation in ICA model, Proceedings of the second international workshop on independent component analysis and blind source separation (ICA 2000), 227–232.

See Also

[amari.error](#), [ComonGAP](#)

Examples

```
S <- cbind(rt(1000, 4), rnorm(1000), runif(1000))
A <- matrix(rnorm(9), ncol = 3)
X <- S %*% t(A)

S.hat <- JADE(X, 3)$S
SIR(S, S.hat)
```

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