

# Package ‘JADE’

January 2, 2012

**Type** Package

**Title** JADE and ICA performance criteria

**Version** 1.0-4

**Date** 2011-09-05

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**Depends** clue

**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.

**License** GPL (>= 2)

**Repository** CRAN

**Date/Publication** 2011-09-05 19:37:23

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 JADE-package

*JADE and ICA performance criteria*


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### 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  
 Type: Package  
 Version: 1.0-4  
 Date: 2011-09-05  
 License: GPL (>= 2)

### Author(s)

Klaus Nordhausen, Jean-Francois Cardoso, Hannu Oja, Esa Ollila  
 Maintainer: Klaus Nordhausen <klaus.nordhausen@uta.fi>

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 amari.error

*Amari Error*


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### 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)
```

---

ComonGAP

*Comon's Gap*

---

**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)
```

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MD

*Minimum Distance index MD*


---

**Description**

Computes the Minimum Distance index MD to evaluate the performance of an ICA algorithm.

**Usage**

```
MD(W.hat, A)
```

**Arguments**

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

**Details**

$$MD(\hat{W}, A) = \frac{1}{\sqrt{p-1}} \inf_{PD} \|PD\hat{W}A - I\|,$$

where  $P$  is a permutation matrix and  $D$  a diagonal matrix with nonzero diagonal entries.

The step that minimizes the index of the set over all permutation matrix can be expressed as a linear sum assignment problem (LSAP) for which we use as solver the Hungarian method implemented as `solve_LASP` in the **coin** package.

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 MD index 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 MD index.

**Author(s)**

Klaus Nordhausen, <klaus.nordhausen@uta.fi>

**References**

*Ilmonen, P., Nordhausen, K., Oja, H. and Ollila, E. (2010): A New Performance Index for ICA: Properties, Computation and Asymptotic Analysis. In Vigneron, V., Zarzoso, V., Moreau, E., Gibonval, R. and Vincent, E. (editors) Latent Variable Analysis and Signal Separation, 229–236, Springer.*

**See Also**

[ComonGAP](#), [SIR](#), [amari.error](#), `solve_LASP`

**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
MD(W.hat, A)
```

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)
```

**Arguments**

X	A matrix of $k$ stacked $p \times p$ matrices with dimension $c(kp, p)$ or an array with dimension $c(p, p, k)$ .
eps	Convergence tolerance.
maxiter	Maximum number of iterations.
na.action	A function which indicates what should happen when the data contain 'NA's. Default is to fail.

**Details**

Denote the square matrices as  $A_i, i = 1, \dots, k$ . This algorithm searches then an orthogonal matrix  $V$  so that  $D_i = V' A_i V$  is diagonal for all  $i$ . If the  $A_i$  commute then there is an exact solution. If not, the function will perform an approximate joint diagonalization by trying to make the  $D_i$  as diagonal as possible.

Cardoso points out that notion of approximate joint diagonalization is ad hoc and very small values of eps make in that case not much sense since the diagonality criterion is ad hoc itself.

**Value**

A list with the components

V	An orthogonal matrix.
D	A stacked matrix with the diagonal matrices or an array with the diagonal matrices. The form of the output depends on the form of the input.

**Author(s)**

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

**References**

Cardoso, J.-F. and Souloumiac, A., (1996), *Jacobi angles for simultaneous diagonalization*, SIAM J. Mat. Anal. Appl., **17**, 161–164.

**Examples**

```

Z <- matrix(runif(9), ncol = 3)
U <- eigen(Z %% t(Z))$vectors
D1 <- diag(runif(3))
D2 <- diag(runif(3))
D3 <- diag(runif(3))
D4 <- diag(runif(3))

X.matrix <- rbind(t(U) %% D1 %% U, t(U) %% D2 %% U,
                 t(U) %% D3 %% U, t(U) %% D4 %% U)
res.matrix <- rjd(X.matrix)
res.matrix$V
round(U %% res.matrix$V, 4) # should be a signed permutation
                           # matrix if V is correct.

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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