Package 'steadyICA'

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Type Package

Title ICA and Tests of Independence via Multivariate Distance Covariance

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Description Functions related to multivariate measures of independence and ICA:
-estimate independent components by minimizing distance covariance;
-conduct a test of mutual independence based on distance covariance;
-estimate independent components via infomax (a popular method but generally performs poorer than mdcovica, ProDenICA, and/or fastICA, but is useful for comparisons);
-order indepedent components by skewness;
-match independent components from multiple estimates;
-other functions useful in ICA.

License GPL (>= 2)

Depends Rcpp (>= 0.9.13), MASS, clue, combinat

Suggests irlba, JADE, ProDenICA, fastICA, energy

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`steadyICA-package` *ICA via distance covariance, tests of mutual independence, and other ICA functions*

Description

Functions related to multivariate measures of independence and ICA:
-estimate independent components by minimizing distance covariance;
-conduct a test of mutual independence based on distance covariance;
-estimate independent components via infomax (a popular method but generally performs poorer than steadyICA or ProDenICA but is useful for comparisons);
-order independent components by skewness;
-match independent components from multiple estimates;
-other functions useful in ICA.

Details

Package:	steadyICA
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Version:	1.0
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License:	GPL (>= 2)
Depends:	Rcpp (>= 0.9.13), MASS
Suggests:	irlba, JADE, ProDenICA, fastICA

Author(s)

Benjamin B. Risk and Nicholas A. James and David S. Matteson.
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References

Bernaards, C. & Jennrich, R. (2005) Gradient projection algorithms and software for arbitrary rotation criteria in factor analysis. *Educational and Psychological Measurement* 65, 676-696

Matteson, D. S. & Tsay, R. Independent component analysis via U-Statistics. <http://www.stat.cornell.edu/~matteson/#ICA>

Szekely, G., Rizzo, M. & Bakirov, N. Measuring and testing dependence by correlation of distances. (2007) *The Annals of Statistics*, 35, 2769-2794.

Tichavsky, P. & Koldovsky, Z. Optimal pairing of signal components separated by blind techniques. (2004) *Signal Processing Letters* 11, 119-122.

See Also

`fastICA` `ProDenICA::ProDenICA`

Examples

```
#see steadyICA
```

`compInd` *Complete Measure of Mutual Multivariate Independence*

Description

Calculates a complete empirical measure of mutual multivariate independence. Makes use of the utils::combn function.

Usage

```
compInd(S,group=1:ncol(S),alpha=1)
```

Arguments

`S`	The n x d matrix for which you wish to calculate the dependence between d columns from n samples.
`group`	A length d vector which indicates group membership for each component.
`alpha`	The index used in calculating the distance between sample observations.

Value

Returns a scalar equal to the empirical multivariate distance between the observed samples, and their grouped counterpart.

Note

Suppose that the each component belongs to exactly one of C groups. This method makes use of the utils::combn and combinat::permn functions. As a result it will be both computationally and memory intensive, even for small to moderate n and small C.

Author(s)

Nicholas James

References

Chasalow, Scott (2012) combinat: Combinatorics Utilities <http://CRAN.R-project.org/package=combinat

See Also

dcovustat, energy::dcov

Examples

```
library(steadyICA)
library(combinat)
set.seed(100)
S = matrix(rnorm(40),ncol=4)
group = c(1,2,3,3)
compInd(S,group,1)
```

---

dcovICA *ICA via distance covariance for 2 components*

Description

This algorithm finds the rotation which minimizes the distance covariance between two orthogonal components via the angular parameterization of a 2x2 orthogonal matrix with the function stats::optimize. The results will be (approximately) equivalent to steadyICA but this function is much faster (but does not extend to higher dimensions).

Usage

```
dcovICA(Z, theta.0 = 0)
```

Arguments

Z	The whitened n x d data matrix, where n is the number of observations and d the number of components.
theta.0	Determines the interval to be searched by the optimizer: lower bound = theta.0, upper bound = pi/2. Changing theta.0 affects the initial value, where the initial value = theta.0+(1/2+sqrt(5)/2)*pi/2, see optimize.

Value

theta.hat	Estimated minimum.
W	W = t(theta2W(theta.hat))
S	Estimated independent components.
obj	The distance covariance of S.

Author(s)

David Matteson and Benjamin Risk

References

Matteson, D. S. & Tsay, R. Independent component analysis via U-Statistics. <http://www.stat.cornell.edu/~matteson/#ICA>

See Also

steadyICA, optimize

Examples

```
library(JADE)
library(ProDenICA)
set.seed(123)
simS = cbind(rjordan(letter='j',n=1024),rjordan(letter='m',n=1024))
simM = mixmat(p=2)
xData = simS%*%simM
xWhitened = whitener(xData)

#Define true unmixing matrix as true M multiplied by the estimated whitener:
#Call this the target matrix:
W.true <- solve(simM%*%xWhitened$whitener)


a=Sys.time()
est.dCovICA = dcovICA(Z = xWhitened$Z,theta.0=0)
Sys.time()-a

#See the example with steadyICA for an explanation
#of the parameterization used in amari.error:
amari.error(t(est.dCovICA$W),W.true)

##NOTE: also try theta.0 = pi/4 since there may be local minima
  ## Not run: est.dcovICA = dcovICA(Z = xWhitened$Z,theta.0=pi/4)
  amari.error(t(est.dcovICA$W),W.true)
## End(Not run)

a=Sys.time()
est.steadyICA = steadyICA(X=xWhitened$Z,verbose=TRUE)
Sys.time()-a
amari.error(t(est.steadyICA$W),W.true)
##theta parameterization with optimize is much faster
```

---

dcovustat *Calculate distance covariance via U-statistics*

Description

Calculates the square of the U-statistic formulation of distance covariance. This is faster than the function 'dcov' in the R package 'energy' and requires less memory. Note that negative values are possible in this version.

Usage

```
dcovustat(x,y,alpha=1)
```

Arguments

x	A vector or matrix.
y	A vector or matrix with the same number of observations as x, though the number of columns of x and y may differ
alpha	A scaling parameter in the interval (0,2] used for calculating distances.

Value

Returns the distance covariance U-statistic.

Note

The value returned by dcovustat is equal to the square of the value returned by energy::dcov in the limit.

In dcovustat, a vector of length n is stored; in energy::dcov, an n x n matrix is stored. Thus, dcovustat requires far less memory and works for very large datasets.

Even though dcovustat converges to the square of the distance covariance of the random variables x and y, it can be negative.

Author(s)

David Matteson

References

Matteson, D. S. & Tsay, R. Independent component analysis via U-Statistics. <http://www.stat.cornell.edu/~matteson/#ICA>

Szekely, G., Rizzo, M. & Bakirov, N. Measuring and testing dependence by correlation of distances. (2007) *The Annals of Statistics*, 35, 2769-2794.

See Also

multidcov, energy::dcov

Examples

```
x = rnorm(5000)
y = rbinom(5000,1,0.5)
y = y - 1*(y==0)
z = y*exp(-x) #some non-linear dependence

dcovustat(x[1:1000],y[1:1000]) #close to zero

a = Sys.time()
dcovustat(x[1:1000],z[1:1000]) #greater than zero
a = Sys.time() - a

#measures of linear dependence close to zero:
cov(x,z)
cor(rank(x),rank(z))


## Not run:
#dcovustat differs from energy::dcov but are equal in the limit
library(energy)
b = Sys.time()
(dcov(x[1:1000],z[1:1000]))^2
b = Sys.time() - b
as.double(b)/as.double(a) #dcovustat is much faster

## energy::dcov and dcovustat become approximately equal as n increases:
c = Sys.time()
dcovustat(x,z)
c = difftime(Sys.time(), c, sec)
d = Sys.time()
(dcov(x,z)^2)
d = difftime(Sys.time(), d, sec)
as.double(d)/as.double(c)

## End(Not run)
```

`frobICA` *match mixing matrices or ICs and calculate their Frobenius distance*

Description

The ICA model is only identifiable up to signed permutations of the ICs. This function provides a similarity measure between two mixing matrices for the model X = S M + E, where X is n x p, S is n x d, and M is d x p. The input is either two mixing matrices M1 and M2 or two matrices of independent components S1 and S2. For M1 and M2, frobICA() finds the signed row permutation of M2 that minimizes the Frobenius norm between M1 and M2 using the Hungarian method. For S1 and S2, frobICA() finds the signed column permutation of S2 that minimizes the Frobenius norm between S1 and S2. This function allows the mixing matrices (or independent components) to have differing numbers of rows (respectively, columns) such that the similarity measure is defined by the matching rows (resp., columns), and the non-matching rows (resp., columns) are discarded.

Usage

```
frobICA(M1 = NULL, M2 = NULL, S1 = NULL, S2 = NULL, standardize = FALSE)
```

Arguments

M1	A d x p mixing matrix
M2	A d x q mixing matrix
S1	An n x d matrix of independent components
S2	An n x q matrix of independent components
standardize	Logical. See Note.

Details

frobICA(M1,M2) = 0 if there exists a signed permutation of the rows of M2 such that M1 = P%*%M2, where P is a d x q signed permutation matrix, i.e., composed of 0, 1, and -1, with d <= q; the function also allows d > q, in which case frobICA(M1,M2) = 0 if there exists a P such that P%*% M1 = M2. Unlike other ICA performance measures, this function can accomodate non-square mixing matrices.

Value

returns the Frobenius norm divided by p*min(d,q) (or n*min(d,q)) of the matched mixing matrices (resp., matched independent components).

Note

If standardize=TRUE, then scales the rows of M1 and M2 to have unit norm or the columns of S1 and S2 to have zero mean and sample variance equal to one. The user can supply either M1 and M2 or S1 and S2 but not both.

Author(s)

Benjamin Risk

References

Kuhn, H. The Hungarian Method for the assignment problem Naval Research Logistics Quarterly, 1955, 2, 83 - 97

Risk, B.B., D.S. Matteson, D. Ruppert, A. Eloyan, B.S. Caffo. In review, 2013. Evaluating ICA methods with an application to resting state fMRI.

See Also

JADE::MD clue::solve_LSAP matchICA

Examples

```
mat1 <- matrix(rnorm(4*6),nrow=4)
perm <- matrix(c(-1,0,0,0,0,0,1,0,0,1,0,0,0,0,0,1),4,4)
mat2 <- perm%*%mat1
sqrt(sum((mat1-mat2)^2))
frobICA(M1=mat1,M2=mat2)

#Another example showing invariance to permutations:
covMat <- t(mat1)%*%mat1
mvsample <- matrix(rnorm(400),100,4)%*%mat1
frobICA(M1=cov(mvsample),M2=covMat)
frobICA(M1=cov(mvsample),M2=covMat[sample(1:6),])

#Example using independent components:
nObs=300
simS<-cbind(rgamma(nObs, shape = 1, scale = 2),
            rgamma(nObs, shape = 3, scale = 2),
            rgamma(nObs, shape = 3, scale = 2),
            rgamma(nObs, shape = 9, scale = 0.5))

#not necessary in this example, but this should be done when used with ICA:
simS <- apply(simS,2,scale)
frobICA(S1=simS,S2=simS%*%perm)
## Not run:
#returns an error if S1 and S2 are not explicitly defined:
frobICA(simS,simS%*%perm)

## End(Not run)
```

`gmultidcov` *Symmetric multivariate distance covariance for grouped components*

Description

Calculate either the symmetric or asymmetric multivariate distance covariance statistic for a given grouping of the components.

Usage

```
gmultidcov(S,group=1:ncol(S),alpha=1,symmetric=TRUE)
```

Arguments

`S`	The n x d matrix for which you wish to calculate the dependence between d columns from n samples
`group`	A length d vector which indicates group membership for each component

alpha	A scaling parameter in the interval (0,2] used for calculating distances.
symmetric	logical; if TRUE (the default), calculates the symmetric version of the multivariate distance covariance. See details.

Details

Suppose that the groups are numbered 1,2,...,C and that group is a vector indicating group membership for each component. If symmetric==TRUE, calculates: sum_i=1^C dcovustat(S[,group==i],S[,group!=i]) If symmetric==FALSE, calculates: sum_i=1^C-1 dcovustat(S[,group==i],S[,group>i])

Value

Returns a scalar equal to the multivariate distance covariance statistic for grouped components of S.

Author(s)

Nicholas James

See Also

dcovustat, energy::dcov

Examples

```
library(steadyICA)
S = matrix(rnorm(300),ncol=3)
group = c(1,2,2)
gmultidcov(S,group,TRUE) # close to zero
gmultidcov(S,group,FALSE) # sill close to zero

Sigma = matrix(c(1,0.7,0,0.7,1,-0.2,0,-0.2,1),ncol=3)
X = MASS::mvrnorm(100,rep(0,3),Sigma)
gmultidcov(X,group,TRUE) # further from zero
gmultidcov(X,group,FALSE) # further from zero
```

---

infomaxICA *Estimates independent components via infomax*

Description

Estimate independent components using the infomax criteria, which is equivalent to maximum likelihood using the logistic density, exp(-S)/(1+exp(-S))^2.

Usage

```
infomaxICA(X, n.comp, W.list = NULL, whiten = FALSE, maxit = 500, eps = 1e-08,
alpha.eps = 1e-08, verbose = FALSE, restarts=0)
```

Arguments

X	the n x p data matrix
n.comp	number of components to be estimated
W.list	list of orthogonal matrices for initialization
whiten	Whitens the data before applying ICA, i.e., X%*%whitener = Z, where Z has mean zero and empirical covariance equal to the identity matrix, and Z is then used as the input.
maxit	maximum number of iterations
eps	algorithm terminates when the norm of the gradient is less than eps
alpha.eps	tolerance controlling the level of annealing: algorithm terminates with a warning if the learning parameter is less than alpha.eps
verbose	if TRUE, prints (1) the value of the infomax objective function at each iteration, (2) the norm of the gradient, and (3) current value of the learning parameter alpha.
restarts	An integer determining the number of initial matrices to use in estimating the ICA model. The objective function has local optima, so multiple starting values are recommended. If whiten=TRUE, then generates random orthogonal matrices. If whiten=FALSE, generate random matrices from rnorm(). See code for details.

Details

This is an R version of ICA using the infomax criteria that provides an alternative to Matlab code (ftp://ftp.cnl.salk.edu/pub/tony/sep96.public), but with a few modifications. First, we use the full data (the so-called offline algorithm) in each iteration rather than an online algorithm with batches. Secondly, we use an adaptive method to choose the step size (based upon Bernaards and Jennrich 2005), which speeds up convergence. We also omitted the bias term (intercept) included in the original formulation because we centered our data.

Value

S	the estimated independent components
W	if whiten=TRUE, returns the orthogonal unmixing matrix; no value is returned when whiten=FALSE
M	Returns the estimated mixing matrix for the model X = S M, where X is not pre-whitened (although X is centered)
f	the value of the objective function at the estimated S
Table	summarizes algorithm status at each iteration
convergence	1 if norm of the gradient is less than eps, 2 if the learning parameter was smaller than alpha.eps, which usually means the gradient is sufficiently small, 0 otherwise

Note

In contrast to most other ICA methods, W is not contrained to be orthogonal.

Author(s)

Benjamin Risk

References

Bell, A. & Sejnowski, T. An information-maximization approach to blind separation and blind deconvolution Neural computation, *Neural computation*, 1995, 7, 1129-1159.

Bernaards, C. A. and Jennrich, R. I. (2005) Gradient Projection Algorithms and Software for Arbitrary Rotation Criteria in Factor Analysis, *Educational and Psychological Measurement* 65, 676-696. <http://www.stat.ucla.edu/research/gpa>

Examples

```
## Example when p > d. The MD function and amari measures
# are not defined for M. We can compare the
# "true W inverse", which is the mixing matrix multiplied
# by the whitening matrix; alternatively, we can use
# multidcov::frobICA. These two approaches are
# demonstrated below:

set.seed(999)
nObs <- 1024
nComp <- 3

# simulate from gamma distributions with
# varying amounts of skewness:
simS<-cbind(rgamma(nObs, shape = 1, scale = 2),
            rgamma(nObs, shape = 3, scale = 2),
            rgamma(nObs, shape = 9, scale = 0.5))

#standardize by expected value and variance:
simS[,1] = (simS[,1] - 1*2)/sqrt(1*2^2)
simS[,2] = (simS[,2] - 3*2)/sqrt(3*2^2)
simS[,3] = (simS[,3] - 9*0.5)/sqrt(9*0.5^2)

# slightly revised 'mixmat' function (from ProDenICA)
# for p>=d: uses fastICA and ProDenICA parameterization:
myMixmat <- function (p = 2, d = NULL) {
  if(is.null(d)) d = p
  a <- matrix(rnorm(d * p), d, p)
  sa <- La.svd(a)
  dL <- sort(runif(d) + 1)
  mat <- sa$u%*%(sa$vt*dL)
  attr(mat, "condition") <- dL[d]/dL[1]
  mat
}

simM <- myMixmat(p = 6, d = nComp)
xData <- simS%*%simM
xWhitened <- whitener(xData, n.comp = nComp)
#Define a 'true' W (uses the estimated whitening matrix):
```

```
W.true <- solve(simM%*%xWhitened$whitener)

estInfomax <- infomaxICA(X = xData, n.comp = nComp, whiten = TRUE, verbose = TRUE)

frobICA(estInfomax$M,simM)
library(JADE)
MD(t(estInfomax$W),t(solve(W.true)))
amari.error(t(estInfomax$W),t(solve(W.true)))
```

`matchICA` *match independent components using the Hungarian method*

Description

The ICA model is only identifiable up to signed permutations of the ICs. This function finds the signed permutation of a matrix S such that ||S%*%P - template|| is minimized. Optionally also matches the mixing matrix M.

Usage

```
matchICA(S, template, M = NULL)
```

Arguments

`S`	the n x d matrix of ICs to be matched
`template`	the n x d matrix that S is matched to.
`M`	an optional d x p mixing matrix corresponding to S that will also be matched to the template

Value

Returns the signed permutation of S that is matched to the template. If the optional argument M is provided, returns a list with the permuted S and M matrices.

Author(s)

Benjamin Risk

References

Kuhn, H. The Hungarian Method for the assignment problem Naval Research Logistics Quarterly, 1955, 2, 83 - 97

Risk, B.B., D.S. Matteson, D. Ruppert, A. Eloyan, B.S. Caffo. In review, 2013. Evaluating ICA methods with an application to resting state fMRI.

See Also

`frobICA` `clue::solve_LSAP`

Examples

```
set.seed(999)
nObs <- 1024
nComp <- 3
# simulate from some gamma distributions:
simS<-cbind(rgamma(nObs, shape = 1, scale = 2),
            rgamma(nObs, shape = 3, scale = 2),
            rgamma(nObs, shape = 9, scale = 0.5))

simM <- matrix(rnorm(9),3)
pMat <- matrix(c(0,-1,0,1,0,0,0,0,-1),3)
permS <- simS%*%pMat
permM <- t(pMat)%*%simM

matchedS <- matchICA(S = permS, template = simS, M = permM)
sum(abs(matchedS$S - simS))
sum(abs(simM - matchedS$M))
```

---

multidcov *Symmetric multivariate distance covariance*

Description

Calculate either the symmetric or asymmetric multivariate distance covariance statistic.

Usage

```
multidcov(S,symmetric=TRUE,alpha=1)
```

Arguments

S	the n x d matrix for which you wish to calculate the dependence between d columns from n samples
alpha	A scaling parameter in the interval (0,2] used for calculating distances.
symmetric	logical; if TRUE (the default), calculates the symmetric version of the multivariate distance covariance. See details.

Details

If symmetric==TRUE, calculates: sum_i=1^d dcovustat(S[,i],S[,-i]) If symmetric==FALSE, calculates: sum_i=1^d-1 dcovustat(S[,i],S[,(i+1):d])

Value

returns a scalar equal to the multivariate distance covariance statistic for the columns of S

Author(s)

David Matteson

See Also

dcovustat, energy::dcov

Examples

```
nObs <- 1024
nComp <- 3

simM <- matrix(rnorm(nComp*nComp),nComp)

# simulate some data:
simS<-cbind(rgamma(nObs, shape = 1, scale = 2),
            rgamma(nObs, shape = 3, scale = 2),
            rgamma(nObs, shape = 9, scale = 0.5))


simS <- scale(simS) #Standardize variance for identifiability

#mix the sources:
xData <- simS %*% simM

multidcov(simS) #close to zero
multidcov(whitener(xData)$Z) #should be larger than simS
multidcov(xData) #greater than zero
```

---

permTest *Permutation test for mutual independence.*

Description

Calculates an approximate p-values based upon a permutation test for mutual independence.

Usage

```
permTest(S, group=1:ncol(S), R=199, FUN=c('gmultidcov','compInd'), ...)
```

Arguments

S	The n x d matrix for which you wish to test the dependence between d columns from n samples
group	A length d vector which indicates group membership for each component
R	The number of permutations to perform in order to obtain the approximate p-value.
FUN	The function used to determine mutual independence. This is one of either gmultidcov or compInd.
...	Additionl arguments passed to FUN. See details.

Details

Suppose that the groups are numbered 1,2,...,C and that group is a vector indicating group membership for each component. If symmetric==TRUE, calculates: sum_i=1^C dcovustat(S[,group==i],S[,group!=i]) If symmetric==FALSE, calculates: sum_i=1^C-1 dcovustat(S[,group==i],S[,group>i])

If no additional arguments are supplied for FUN then the default values are used. In the case of gmultidcov, values for alpha and symmetric can be supplied. While for compInd only the value of alpha is needed.

Value

Returns an approximate p-values based upon a permutation test.

Author(s)

Nicholas James

See Also

`dcovustat`, `energy::dcov`

`rightskew` *force ICs to have positive skewness and order by skewness*

Description

The ICA model is only identifiable up to signed permutations. This function provides a canonical ordering for ICA that is useful for fMRI or studies where signals are skewed. Multiplies columns of S that are left-skewed by -1 to force right skewness. Optionally orders the columns by descending skewness.

Usage

```
rightskew(S, M = NULL, order.skew = TRUE)
```

Arguments

`S`	n x d matrix
`M`	d x p mixing matrix
`order.skew`	Option to return the permutation of columns of S from largest to smallest skewness. Also returns a permuted version of M that corresponds with the permuted S.

Value

Returns the matrix S such that all columns have positive skewness. If optional argument M is supplied, returns a list with the new S and corresponding M.

Author(s)

Benjamin Risk

References

Eloyan, A. & Ghosh, S. A Semiparametric Approach to Source Separation using Independent Component Analysis Computational Statistics and Data Analysis, 2013, 58, 383 - 396.

Examples

```
nObs = 1024
simS<-cbind(rgamma(nObs, shape = 1, scale = 2),
            rgamma(nObs, shape = 9, scale = 0.5),
            -1*rgamma(nObs, shape = 3, scale = 2))

apply(simS,2,function(x){
  (sum((x - mean(x))^3)/length(x))/(sum((x - mean(x))^2)/length(x))^(3/2)})

canonicalS <- rightskew(simS)

apply(canonicalS,2,function(x){
 (sum((x - mean(x))^3)/length(x))/(sum((x - mean(x))^2)/length(x))^(3/2)})
```

---

steadyICA *Estimate independent components by minimizing distance covariance*

Description

The model is: X = S M + E, where X is n x p and has mean zero, S is n x d, M is d x p, and E is measurement error. For whitened data, we have Z = S t(W), where W is orthogonal. We find the matrix M such that S minimizes the distance covariance dependency measure.

Usage

```
steadyICA(X, n.comp = ncol(X), w.init = NULL, PIT = FALSE, bw = 'SJ', adjust = 1,
whiten = FALSE, irlba = FALSE, symmetric = FALSE, eps = 1e-08, alpha.eps = 1e-08,
maxit = 100, method = c('Cpp','R'), verbose = FALSE)
```

Arguments

X	The n x p data matrix, where n is the number of observations.
n.comp	number of components to be estimated
w.init	a p x d initial unmixing matrix
PIT	logical; if TRUE, the distribution and density of the independent components are estimated using gaussian kernel density estimates.
bw	Argument for bandwidth selection method; defaults to 'SJ'; see stats::density

adjust	adjust bandwidth selection; e.g., if observations are correlated, consider using adjust > 1; see stats::density
whiten	logical; if TRUE, whitens the data before applying ICA, i.e., X%*%whitener = Z, where Z has mean zero and empirical covariance equal to the identity matrix, and Z is then used as the input.
irlba	logical; when whiten=TRUE, irlbA=TRUE uses the R-package 'irlba' in the whitening, which is generally faster than base::svd though sometimes less accurate
symmetric	logical; if TRUE, implements the symmetric version of the ICA algorithm, which is invariant to the ordering of the columns of X but is slower
eps	algorithm terminates when the norm of the gradient of multidcov is less than eps
maxit	maximum number of iterations
alpha.eps	tolerance controlling the level of annealing: algorithm terminates with a warning if the learning parameter is less than alpha.eps
method	options 'Cpp' (default), which requires the package 'Rcpp', or 'R', which is solely written in R but is much slower
verbose	logical; if TRUE, prints the value of multidcov, norm of the gradient, and current value of the learning parameter.

Value

S	the estimated independent components
W	the estimated unmixing matrix: if whiten=TRUE, W is orthogonal and corresponds to Z W = S; if whiten=FALSE, corresponds to X ginv(M) = S
M	Returns the estimated mixing matrix for the model X = S M, where X is not pre-whitened (although X is centered)
f	the value of the objective function at the estimated S
Table	summarizes algorithm status at each iteration
convergence	1 if norm of the gradient is less than eps, 2 if the learning parameter was smaller than alpha.eps, which usually means the gradient is sufficiently small, 0 otherwise

Author(s)

Benjamin Risk

References

Matteson, D. S. & Tsay, R. Independent component analysis via U-Statistics. <http://www.stat.cornell.edu/~matteson/#ICA>

See Also

multidcov

Examples

```
set.seed(999)
nObs <- 1024
nComp <- 3
# simulate from some gamma distributions:
simS<-cbind(rgamma(nObs, shape = 1, scale = 2),
            rgamma(nObs, shape = 3, scale = 2),
            rgamma(nObs, shape = 9, scale = 0.5))

#standardize by expected value and variance:
simS[,1] = (simS[,1] - 1*2)/sqrt(1*2^2)
simS[,2] = (simS[,2] - 3*2)/sqrt(3*2^2)
simS[,3] = (simS[,3] - 9*0.5)/sqrt(9*0.5^2)

# slightly revised 'mixmat' function (from ProDenICA)
# for p>=d: uses fastICA and ProDenICA parameterization:
myMixmat <- function (p = 2, d = NULL) {
  if(is.null(d)) d = p
  a <- matrix(rnorm(d * p), d, p)
  sa <- La.svd(a)
  dL <- sort(runif(d) + 1)
  mat <- sa$u%*%(sa$vt*dL)
  attr(mat, "condition") <- dL[d]/dL[1]
  mat
}

simM <- myMixmat(p = 6, d = nComp)
xData <- simS%*%simM
xWhitened <- whitener(xData, n.comp = nComp)

#estimate mixing matrix:
est.steadyICA.v1 = steadyICA(X = xData,whiten=TRUE,n.comp=nComp,verbose = TRUE)

#Define the 'true' W:
W.true <- solve(simM%*%xWhitened$whitener)

frobICA(M1=est.steadyICA.v1$M,M2=simM)
frobICA(S1=est.steadyICA.v1$S,S2=simS)

## Not run:
#now initiate from target:
est.steadyICA.v2 = steadyICA(X = xData, w.init= W.true, n.comp = nComp, whiten=TRUE, verbose=TRUE)

#estimate using PIT steadyICA such that dimension reduction is via ICA:
est.steadyICA.v3 = steadyICA(X = xData, w.init=ginv(est.steadyICA.v2$M),
PIT=TRUE, n.comp = nComp, whiten=FALSE, verbose=TRUE)

frobICA(M1=est.steadyICA.v2$M,M2=simM)
frobICA(M1=est.steadyICA.v3$M,M2=simM)
frobICA(S1=est.steadyICA.v2$S,S2=simS)

#tends to be lower than PCA-based (i.e., whitening) methods:
```

```
frobICA(S1=est.steadyICA.v3$S,S2=simS)

# JADE uses a different parameterization and different notation.
# Using our parameterization and notation, the arguments for
# JADE::amari.error correspond to:
amari.error(t(W.hat), W.true)

library(JADE)

amari.error(t(est.steadyICA.v1$W), W.true)
amari.error(t(est.steadyICA.v2$W), W.true)
##note that a square W is not estimated if PIT=TRUE and whiten=FALSE

#Compare performance to fastICA:
library(fastICA)
est.fastICA = fastICA(X = xData, n.comp = 3, tol=1e-07)
amari.error(t(est.fastICA$W), W.true)
##steadyICA usually outperforms fastICA

##Compare performance to ProDenICA:
library(ProDenICA)
est.ProDenICA = ProDenICA(x = xWhitened$Z, k = 3, maxit=40,trace=TRUE)
amari.error(t(est.ProDenICA$W), W.true)
##ProDenICA and steadyICA tend to be similar when sources
##are continuously differentiable

## End(Not run)
```

`theta2W` *Convert angles to an orthogonal matrix.*

Description

Convert d*(d-1)/2 angles from a sequence of Givens rotations to a d x d orthogonal matrix.

Usage

```
theta2W(theta)
```

Arguments

`theta`	A scalar or vector of length d*(d-1)/2 of values from which the d x d orthogonal matrix is calculated.

Value

A d x d orthogonal matrix resulting from the sequence of d*(d-1)/2 Givens rotation matrices.

Author(s)

David S. Matteson

References

Golub, G. & Van Loan, C. 1996. Matrix computations. Johns Hopkins University Press.

See Also

W2theta

Examples

```
#Generate orthogonal matrix:
mat <- matrix(rnorm(9),3,3)
W = svd(mat)$u

theta <- W2theta(W)

#Recovers W:
theta2W(theta)
```

W2theta *Convert an orthogonal matrix to its angular parameterization.*

Description

Convert a d x d orthogonal matrix to a sequence of d*(d-1)/2 Givens rotations.

Usage

```
W2theta(W)
```

Arguments

W	A d x d orthogonal matrix.

Details

A d x d orthogonal matrix can be decomposed into a series of d*(d-1)/2 Givens rotation matrices, where each matrix is parameterized by a single angle.

Value

A vector of length d*(d-1)/2 comprised of the angles.

Author(s)

David S. Matteson

References

Golub, G. & Van Loan, C. 1996. Matrix computations. Johns Hopkins University Press.

See Also

theta2W

Examples

```
theta = c(pi/6,pi/4,pi/2)

(W = theta2W(theta))

#Recover theta:
W2theta(W)
```

---

whitener *Whitening function*

Description

Subtract column means and transform columns such that the empirical covariance is equal to the identity matrix. Uses the SVD.

Usage

```
whitener(X, n.comp = ncol(X), center.row = FALSE, irlba = FALSE)
```

Arguments

X	n x p matrix
n.comp	number of components to retain, i.e., first n.comp left eigenvectors from svd are retained
center.row	center both rows and columns prior to applying SVD (the resulting whitened data does not have zero-mean rows)
irlba	if TRUE, uses irlba to approximate the first n.comp left eigenvectors. See Note.

Value

whitener	the matrix such that X%*%whitener has zero mean and covariance equal to the identity matrix
Z	the whitened data, i.e., X%*%whitener = Z

Note

The use of the option 'irlba = TRUE' requires the package irlba and is very useful for large p. The function irlba only calculates the first n.comp eigenvectors and is much faster than svd for p » n.comp, for e.g., in groupICA of fMRI data.

Author(s)

Benjamin Risk

See Also

svd, irlba::irlba

Examples

```
simData <- cbind(rnorm(1000,1,2),rnorm(1000,-1,3),rnorm(1000,4,1))
simMVN <- simData%*%matrix(rnorm(12),3,4)
simWhiten <- whitener(simMVN,n.comp = 3)
colMeans(simWhiten$Z)
cov(simWhiten$Z)
```

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