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AWRcca

Adaptive Wrapped Robust Canonical Correlation Analysis

Description

Fits the Adaptive Wrapped Robust Canonical Correlation Analysis (AWRcca) estimator. The procedure combines columnwise robust wrapping, analytical shrinkage of the joint correlation matrix, and MCD reweighting in a low-dimensional canonical score space. The score-space weights enter a second shrinkage-regularized CCA fit, which remains well defined when $p + q > n$.

Usage

```
AWRcca(
  X,
  Y,
  b = 1.5,
  c = 4,
  alpha = 0.975,
  q1 = 1.540793,
  q2 = 0.8622731,
  max_score_components = 5L,
  lambda_cap = 1,
  n_xi = NULL
)
```

Arguments

<code>X</code>	Numeric $n \times p$ matrix.
<code>Y</code>	Numeric $n \times q$ matrix with the same number of rows as <code>X</code> .
<code>b</code>	Lower wrapping threshold. The reference value is 1.5.
<code>c</code>	Upper wrapping threshold, with $0 < b < c$. The reference value is 4.
<code>alpha</code>	Probability used for the chi-squared robust-distance cutoff. The reference value is 0.975.
<code>q1, q2</code>	Smooth wrapping constants. Their reference values are 1.540793 and 0.8622731, respectively.
<code>max_score_components</code>	Maximum number of canonical score pairs used for MCD reweighting. The reference value is 5.
<code>lambda_cap</code>	Optional upper bound for each analytical shrinkage intensity. The default, 1, leaves the analytical estimate uncapped.
<code>n_xi</code>	Deprecated compatibility argument. The consistency factor is now evaluated deterministically by numerical integration, so this argument is ignored.

Details

Each column is centered by its median, scaled by its Gaussian-consistent MAD, and transformed with a smooth redescending wrapping function. The Gaussian consistency factor is evaluated deterministically rather than by Monte Carlo.

An analytical Ledoit–Wolf-type shrinkage estimate regularizes the initial joint correlation matrix. Robust distances are then computed from at most `max_score_components` pairs of initial canonical scores. Binary weights obtained from these distances are used to construct a second joint correlation matrix, which is again shrinkage regularized before the final canonical decomposition. If score-space MCD estimation is unavailable or too few observations are retained, the initial regularized solution is returned.

Value

A list containing:

- `cor`: final canonical correlations.
- `a, b`: final canonical direction matrices.
- `weights`: binary score-space observation weights.
- `retained`: number of observations with weight one.
- `reweighted_final`: whether the second weighted fit was used.
- `shrink_initial, shrink_final`: shrinkage intensities.
- `shrink_used`: backward-compatible alias of `shrink_final`.
- `xi`: deterministic Gaussian consistency factor.
- `wrapping`: wrapping constants used by the fit.
- `u1, v1`: first initial canonical score pair.

Examples

```

set.seed(123)
n <- 60
p <- 40
q <- 50
latent <- rnorm(n)
X <- outer(latent, seq(0.80, 0.30, length.out = p)) +
  matrix(rnorm(n * p), n, p)
Y <- outer(latent, seq(0.75, 0.25, length.out = q)) +
  matrix(rnorm(n * q), n, q)
fit <- AWRcca(X, Y)
fit$cor[1]
fit$retained
fit$shrink_final

```

Bcov

*Bartlett's Test for One Sample Covariance Matrix***Description**

Bcov function tests whether the covariance matrix is equal to a given matrix or not.

Usage

```
Bcov(data, Sigma)
```

Arguments

data	a data frame.
Sigma	The covariance matrix in NULL hypothesis.

Details

This function computes Bartlett's test statistic for the covariance matrix of one sample.

Value

a list with 3 elements:

ChiSquare	The value of Test Statistic
df	The Chi-Square statistic's degree of freedom
p.value	p value

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Rencher, A. C. (2003). Methods of multivariate analysis (Vol. 492). John Wiley & Sons.

Examples

```
data(iris)
S<-matrix(c(5.71,-0.8,-0.6,-0.5,-0.8,4.09,-0.74,-0.54,-0.6,
           -0.74,7.38,-0.18,-0.5,-0.54,-0.18,8.33),ncol=4,nrow=4)
result <- Bcov(data=iris[,1:4],Sigma=S)
summary(result)
```

BoxM	<i>Box's M Test</i>
------	---------------------

Description

BoxM function tests whether the covariance matrices of independent samples are equal or not.

Usage

```
BoxM(data, group)
```

Arguments

data	a data frame.
group	grouping vector.

Details

This function computes Box-M test statistic for the covariance matrices of independent samples. The hypotheses are defined as H0:The Covariance matrices are homogeneous and H1:The Covariance matrices are not homogeneous

Value

a list with 3 elements:

ChiSquare	The value of Test Statistic
df	The Chi-Square statistic's degree of freedom
p.value	p value

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Rencher, A. C. (2003). Methods of multivariate analysis (Vol. 492). John Wiley & Sons.

Examples

```
data(iris)
results <- BoxM(data=iris[,1:4],group=iris[,5])
summary(results)
```

Bsper

*Bartlett's Sphericity Test***Description**

Bsper function tests whether a correlation matrix is equal to the identity matrix or not.

Usage

```
Bsper(data)
```

Arguments

data a data frame.

Details

This function computes Bartlett's test statistic for Sphericity Test. The hypotheses are $H_0: R$ is equal to I and $H_1: R$ is not equal to I .

Value

a list with 4 elements:

ChiSquare	The value of Test Statistic
df	The Chi-Square statistic's degree of freedom
p.value	p value
R	Correlation matrix

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Tatlidil, H. (1996). Uygulamali Cok Degiskenli Istatistiksel Yontemler. Cem Web.

Examples

```
data(iris)
results <- Bsper(data=iris[,1:4])
summary(results)
```

`ccc`*Concordance Correlation Coefficient*

Description

Classical Concordance Correlation Coefficient

Usage

```
ccc(x, y)
```

Arguments

<code>x</code>	the vector which contains the first variable values
<code>y</code>	the vector which contains the second variable values

Details

ccc function calculates directly classical concordance correlation coefficient.

Value

a list with 1 elements:

<code>coef</code>	The value of concordance correlation coefficient
-------------------	--

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H (2025). A Robust Concordance Correlation Coefficient. (Unpublished)

Lin, L. I. "A Concordance Correlation-Coefficient to Evaluate Reproducibility." Biometrics 45, no. 1 (1989): 255-68.

Examples

```
x<-rnorm(50)
y<-2+3*x+rnorm(50,mean = 3)
ccc(x,y)
```

CellMCDT2

Cellwise Robust Permutation Hotelling T^2 Test for Two Independent Samples

Description

Performs a cellMCD-based robust two-sample Hotelling T^2 test for comparing the mean vectors of two independent multivariate samples. The p-value is obtained by a permutation procedure.

Usage

```
CellMCDT2(
  X1,
  X2,
  B = 999,
  alpha = 0.75,
  quant = 0.99,
  crit = 1e-04,
  seed = NULL,
  na.rm = TRUE,
  ...
)
```

Arguments

X1	A numeric matrix or data frame for the first group.
X2	A numeric matrix or data frame for the second group.
B	Number of permutations. Default is 999.
alpha	The cellMCD alpha parameter. Default is 0.75.
quant	Quantile used in the cellMCD procedure. Default is 0.99.
crit	Convergence criterion used in the cellMCD procedure. Default is 1e-04.
seed	Optional random seed.
na.rm	Logical. If TRUE, rows with missing values are removed. Default is TRUE.
...	Additional arguments passed to <code>cellwise::cellMCD()</code> .

Value

An object of class `MVTests` containing the test statistic, permutation p-value, number of successful permutations, and related information.

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Raymaekers, J. and Rousseeuw, P. J. (2024). The cellwise minimum covariance determinant estimator. *Journal of the American Statistical Association*, 119(548), 2610–2621.

Bulut, H. and Esmeray, M. A cellwise robust Hotelling test for two-sample comparisons (Unpublished).

Examples

```
if (requireNamespace("mvtnorm", quietly = TRUE) &&
    requireNamespace("cellWise", quietly = TRUE)) {
  set.seed(123)
  x1 <- mvtnorm::rmvnorm(n = 30, mean = rep(0, 5), sigma = diag(5))
  x2 <- mvtnorm::rmvnorm(n = 30, mean = rep(0, 5), sigma = diag(5))

  fit <- CellMCDT2(X1 = x1, X2 = x2, B = 9, seed = 123)
  fit$p.value
}
```

Coated	<i>Coated</i>
--------	---------------

Description

The data set is given in Table 5.3 in Rencher (2003). The data set consists of 2 variables (Depth and Number), 2 treatments and 15 observations. The first column of the data is Location numbers.

Usage

Coated

Format

- A data frame with 15 rows and 5 columns. The columns are as follows:
- Location** The location numbers of observations.
 - Coating1.Depth1** The Depth values in the first treatment
 - Coating1.Number1** The Number values in the first treatment
 - Coating2.Depth2** The Depth values in the second treatment
 - Coating2.Number2** The Number values in the second treatment

Source

The data set is used in the book entitled *Methods of Multivariate Analysis* (Rencher,2003).

References

Rencher, A. C. (2003). *Methods of multivariate analysis* (Vol. 492). John Wiley & Sons.

iris

*Iris Data***Description**

The Iris dataset is consists of 4 variables, 3 groups and 150 observations. The last column of the data is Iris species.

Usage

iris

Format

A data frame with 150 rows and 5 columns. The columns are as follows:

Sepal.Length The Sepal length values of iris flowers

Sepal.Width The Sepal width values of iris flowers

Petal.Length The Petal length values of iris flowers

Petal.Width The Petal width values of iris flowers

Species The species of iris flowers

Source

<https://archive.ics.uci.edu/ml/datasets/Iris>

Mhg

*Pair-Wise comparison between hth and gth sample***Description**

Pair-Wise comparison of covariance matrices between hth and gth sample

Usage

Mhg(Sh, Sg, S, nh, ng, n)

Arguments

Sh	the robust covariance matrix of the hth sample
Sg	the robust covariance matrix of the gth sample
S	the robust pooled covariance matrix.
nh	the sample size of the hth sample
ng	the sample size of the gth sample
n	the sample size of the full data

Details

Mhg function computes proposed Mgh values as defined in the paper.

Value

a list with 1 elements:

Mhg	Mgh value
-----	-----------

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H (2024). A robust permutational test to compare covariance matrices in high dimensional data. (Unpublished)

Examples

```
if (requireNamespace("rrcov", quietly=TRUE)) {
  x1<-rmvnorm::rmvnorm(n = 10,mean = rep(0,20),sigma = diag(20))
  x2<-rmvnorm::rmvnorm(n = 10,mean = rep(0,20),sigma = 2*diag(20))
  x3<-rmvnorm::rmvnorm(n = 10,mean = rep(0,20),sigma = 3*diag(20))
  data<-rbind(x1,x2,x3)
  group_label<-c(rep(1,10),rep(2,10),rep(3,10))
  n <- nrow(data)
  p <- ncol(data)
  nk <- table(group_label)
  g <- length(nk)
  Levels <- unique(group_label)
  Si.matrices<-lapply(1:g, function(i) rrcov::CovMrcd(data[(group_label==Levels[i]),],
  alpha=0.9)cov)
  Spool <- Reduce("+", Map("*", nk, Si.matrices)) / n
  #for the first and second groups
  Mhg(Sh = Si.matrices[[1]], Sg = Si.matrices[[2]],S = Spool, nh = nk[1], ng = nk[2], n = n)}
```

Mpaired

Multivariate Paired Test

Description

Mpaired function computes the value of test statistic based on Hotelling T Square approach in multivariate paired data sets.

Usage

Mpaired(T1, T2)

Arguments

T1	The first treatment data.
T2	The second treatment data.

Details

This function computes one sample Hotelling T^2 statistics for paired data sets.

Value

a list with 7 elements:

HT2	The value of Hotelling T^2 Test Statistic
F	The value of F Statistic
df	The F statistic's degree of freedom
p.value	p value
Descriptive1	The descriptive statistics of the first treatment
Descriptive2	The descriptive statistics of the second treatment
Descriptive.Difference	The descriptive statistics of the differences

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Rencher, A. C. (2003). Methods of multivariate analysis (Vol. 492). John Wiley & Sons.

Examples

```
data(Coated)
X<-Coated[,2:3]; Y<-Coated[,4:5]
result <- Mpaired(T1=X,T2=Y)
summary(result)
```

OneSampleHT2

One Sample Hotelling T^2 Test

Description

OneSampleHT2 computes one sample Hotelling T^2 statistics and gives confidence intervals

Usage

```
OneSampleHT2(data, mu0, alpha = 0.05)
```

Arguments

data	a data frame.
mu0	mean vector that is used to test whether population mean parameter is equal to it.
alpha	Significance Level that will be used for confidence intervals. default alpha=0.05.

Details

This function computes one sample Hotelling T^2 statistics that is used to test whether population mean vector is equal to a vector given by a user. When H_0 is rejected, this function computes confidence intervals for all variables.

Value

a list with 7 elements:

HT2	The value of Hotelling T^2 Test Statistic
F	The value of F Statistic
df	The F statistic's degree of freedom
p.value	p value
CI	The lower and upper limits of confidence intervals obtained for all variables
alpha	The alpha value using in confidence intervals
Descriptive	Descriptive Statistics

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

- Rencher, A. C. (2003). Methods of multivariate analysis (Vol. 492). John Wiley & Sons.
- Tatlidil, H. (1996). Uygulamali Cok Degiskenli Istatistiksel Yontemler. Cem Web.

Examples

```
data(iris)

mean0<-c(6,3,1,0.25)
result <- OneSampleHT2(data=iris[1:50,-5],mu0=mean0,alpha=0.05)
summary(result)
```

rccc

*Robust Concordance Correlation Coefficient (rCCC)***Description**

Computes a robust concordance correlation coefficient using Minimum Covariance Determinant (MCD) estimates.

Usage

```
rccc(x, y, alpha = 0.75)
```

Arguments

x	Numeric vector; first variable.
y	Numeric vector; second variable.
alpha	Numeric in (0.5, 1]; MCD subset size proportion. Default 0.75.

Details

The rCCC replaces means and (co)variances in Lin's CCC with their MCD counterparts: $\rho_c = \frac{2\sigma_{xy}}{\sigma_x^2 + \sigma_y^2 + (\mu_x - \mu_y)^2}$.

Value

A list with one element:

coef	Robust concordance correlation coefficient
------	--

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H. (2025). A Robust Concordance Correlation Coefficient. (Unpublished)

Examples

```
if (requireNamespace("robustbase", quietly = TRUE)) {
  set.seed(1)
  x <- rnorm(50)
  y <- 2 + 3*x + rnorm(50, mean = 3)
  rccc(x, y)
}
```

RHT2

*Robust Hotelling T^2 Test for One Sample in High Dimensional Data***Description**

Robust Hotelling T^2 Test for One Sample in high Dimensional Data

Usage

```
RHT2(data, mu0, alpha = 0.75, d, q)
```

Arguments

data	the data. It must be matrix or data.frame.
mu0	the mean vector which will be used to test the null hypothesis.
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized. Allowed values are between 0.5 and 1 and the default is 0.75.
d	the constant in Equation (11) in the study by Bulut (2021).
q	the second degree of freedom value of the approximate F distribution in Equation (11) in the study by Bulut (2021).

Details

RHT2 function performs a robust Hotelling T^2 test in high dimensional test based on the minimum regularized covariance determinant estimators. This function needs the q and d values. These values can be obtained simRHT2 function. For more detailed information, you can see the study by Bulut (2021).

Value

a list with 3 elements:

T2	The Robust Hotelling T^2 value in high dimensional data
Fval	The F value based on T2
pval	The p value based on the approximate F distribution

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H (2021). A robust Hotelling test statistic for one sample case in high dimensional data, Communication in Statistics: Theory and Methods.

Examples

```
if (requireNamespace("rrcov", quietly = TRUE)) {
  utils::data("octane", package = "rrcov")
  mu.clean <- colMeans(octane[-c(25,26,36,37,38,39), ])
  RHT2(data = octane, mu0 = mu.clean, alpha = 0.84, d = 1396.59, q = 1132.99)}
```

Rob_CovTest

*Robust Test for Covariance Matrices***Description**

Robust Test for Covariance Matrices in High Dimensional Data

Usage

```
Rob_CovTest(x, group, alpha = 0.75)
```

Arguments

x	the data matrix
group	the grouping vector. It must be factor.
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized. Allowed values are between 0.5 and 1 and the default is 0.75.

Details

Rob_CovTest function computes the calculated value of the test statistic for covariance matrices of two or more independent samples in high dimensional data based on the minimum regularized covariance determinant estimators.

Value

a list with 1 elements:

TM	The calculated value of test statistics based on raw data
----	---

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H (2024). A robust permutational test to compare covariance matrices in high dimensional data. (Unpublished)

Examples

```

if (requireNamespace("rrcov", quietly=TRUE)) {
  x1<-mvtnorm::rmvnorm(n = 8,mean = rep(0,10),sigma = diag(10))
  x2<-mvtnorm::rmvnorm(n = 8,mean = rep(0,10),sigma = 2*diag(10))
  x3<-mvtnorm::rmvnorm(n = 8,mean = rep(0,10),sigma = 3*diag(10))
  data<-rbind(x1,x2,x3)
  group_label<-c(rep(1,8),rep(2,8),rep(3,8))
  Rob_CovTest(x=data, group=group_label)}

```

RobCat

*Robust CAT Algorithm***Description**

RobCat computes p value based on robust CAT algorithm to compare two means vectors under multivariate Behrens-Fisher problem.

Usage

```
RobCat(X, Y, M = 1000, alpha = 0.75)
```

Arguments

X	a matrix or data frame for first group.
Y	a matrix or data frame for second group.
M	iteration number and the default is 1000.
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized; roughly $\alpha \cdot n$, observations are used for computing the determinant. Allowed values are between 0.5 and 1 and the default is 0.75.

Details

This function computes p value based on robust CAT algorithm to compare two means vectors under multivariate Behrens-Fisher problem. When p value < 0.05, it means the difference of two mean vectors is significant statistically.

Value

a list with 2 elements:

Cstat	Calculated value of test statistic
pval	The p value

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

Examples

```
data(iris)
if (requireNamespace("robustbase", quietly=TRUE)) {
  RobCat(X=iris[1:20,-5],Y=iris[81:100,-5])}
```

RobCellT2_onesample	<i>Cellwise Robust One-Sample Hotelling T^2 Test</i>
---------------------	---

Description

Performs a cellwise robust one-sample Hotelling T^2 test based on the cellwise minimum covariance determinant (cellMCD) estimator.

Usage

```
RobCellT2_onesample(
  data,
  mu0,
  d,
  q,
  alpha = 0.75,
  quant = 0.99,
  crit = 1e-04,
  na.rm = TRUE,
  ...
)
```

Arguments

data	A numeric matrix or data frame.
mu0	The hypothesized mean vector under the null hypothesis.
d	The scaling constant of the approximate F distribution.
q	The second degree of freedom of the approximate F distribution.
alpha	The cellMCD alpha parameter. Default is 0.75.
quant	Quantile used in the cellMCD procedure. Default is 0.99.
crit	Convergence criterion used in the cellMCD procedure. Default is 1e-04.
na.rm	Logical. If TRUE, rows with missing values are removed. Default is TRUE.
...	Additional arguments passed to <code>cellwise::cellMCD()</code> .

Details

The function computes a robust Hotelling T^2 statistic by replacing the classical sample mean vector and covariance matrix with the cellMCD location and scatter estimates. The statistic is converted to an approximate F statistic using the constants d and q . These constants can be obtained by the `simRobCellT2_onesample()` function. The scaled-F distribution is an empirical, moment-matched approximation, not a theoretically derived exact distribution. The constants must come from a calibration compatible with the number of complete observations n , dimension p , null covariance Σ , and all cellMCD settings used in this test (including arguments passed through `...`). Supply X and the required μ_0 to the calibration function for a robust covariance estimate from raw X , or supply an explicit Σ . Perform complete-case handling before calibration and use those same observations in this test. Calibration uses default cellMCD settings. This parametric bootstrap uses the specified null mean, not the observed fitted location. Its approximation depends on the estimated covariance.

Since cellMCD is not affine equivariant, calibration can depend on the covariance structure. Diagonal rescaling or standardization does not remove dependence on the correlation structure. General whitening changes the coordinate-wise cell structure and is not recommended as routine preprocessing.

Value

An object of class `MVTests` containing:

<code>T2</code>	The cellMCD-based robust Hotelling T^2 statistic.
<code>Fval</code>	The approximate F statistic.
<code>p.value</code>	The p-value based on the approximate F distribution.
<code>mu</code>	The cellMCD location estimate.
<code>S</code>	The cellMCD scatter estimate.

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

- Raymaekers, J. and Rousseeuw, P. J. (2024). The cellwise minimum covariance determinant estimator. *Journal of the American Statistical Association*, 119(548), 2610–2621.
- Willems, G., Pison, G., Rousseeuw, P. J., and Van Aelst, S. (2002). A robust Hotelling test. *Metrika*, 55, 125–138.

Examples

```
if (requireNamespace("MASS", quietly = TRUE) &&
    requireNamespace("cellWise", quietly = TRUE)) {
  set.seed(123)
  mu0 <- c(1, -1)
  Sigma <- matrix(c(2, 0.4, 0.4, 1), 2)
  X <- MASS::mvrnorm(n = 30, mu = mu0, Sigma = Sigma)
```

```

set.seed(1)
const <- simRobCellT2_onesample(X = X, mu0 = mu0, nper = 50)

fit <- RobCellT2_onesample(
  data = X,
  mu0 = mu0,
  d = const$d,
  q = const$q
)

fit$p.value
}

```

RobHDMANOVA

Weighted MRCD-Based Robust MANOVA Test for High-Dimensional Data

Description

Performs a weighted minimum regularized covariance determinant (MRCD)-based robust one-way MANOVA test for high-dimensional data.

Usage

```

RobHDMANOVA(
  x,
  group,
  N = 100,
  alpha = 0.75,
  tau = 0.975,
  cutoff = c("normal", "chisq"),
  seed = NULL,
  verbose = FALSE
)

```

Arguments

x	A numeric data matrix or data frame. Rows represent observations and columns represent variables.
group	A grouping vector indicating the group membership of each observation. It will be internally converted to a factor.
N	The number of permutations used to approximate the null distribution. The default is $N = 100$.
alpha	Numeric parameter controlling the size of the subsets over which the MRCD determinant is minimized. Allowed values are between 0.5 and 1. The default is $\alpha = 0.75$.

tau	Cutoff probability used in the robust distance-based reweighting step. The default is tau = 0.975.
cutoff	The cutoff rule for robust distances. Options are "normal" and "chisq". If cutoff = "normal", the cutoff is computed from the median and MAD of the robust distances. If cutoff = "chisq", the cutoff is computed as $\sqrt{\chi_{p,\tau}^2}$. The default is "normal", which is the recommended option for the proposed method.
seed	An optional integer used to set the random seed for the permutation procedure. The default is NULL.
verbose	Logical. If TRUE, progress information is printed during the permutation procedure. The default is FALSE.

Details

The RobHDMANOVA function tests the equality of multivariate group location vectors in one-way MANOVA settings, particularly when the number of variables is large relative to the sample size and the data may contain outlying observations.

The procedure first computes groupwise MRCD location estimates. Then, a pooled MRCD covariance matrix is obtained from group-centered observations. Robust distances are calculated using this pooled covariance matrix, and binary weights are assigned according to a robust distance cutoff. Reweighted group means are then used to construct a robust between-group scatter matrix. A robust Wilks-type statistic is computed as

$$\Lambda_R = \frac{|W_R|}{|W_R + B_R|},$$

where W_R is the pooled MRCD covariance matrix and B_R is the robust between-group scatter matrix. The test statistic is

$$T_R = -\log(\Lambda_R).$$

Since the finite-sample null distribution is unknown, the p-value is obtained using a permutation procedure.

Value

A list of class MVTests with the following elements:

Lambda	The robust Wilks' Lambda value.
TR	The observed robust MANOVA test statistic.
p.value	The permutation-based p-value.
Permutations_TR	The test statistic values obtained from permutations.
alpha	The trimming parameter used in MRCD estimation.
tau	The cutoff probability used for robust distance-based reweighting.
cutoff	The cutoff rule used for robust distances.
group.centers	The reweighted robust group centers.
weights	The binary robust weights for observations in each group.
Test	The name of the test.

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

- Boudt, K., Rousseeuw, P. J., Vanduffel, S., and Verdonck, T. (2020). The minimum regularized covariance determinant estimator. *Statistics and Computing*, 30, 113–128.
- Todorov, V. and Filzmoser, P. (2010). Robust statistic for the one-way MANOVA. *Computational Statistics and Data Analysis*, 54, 37–48.
- Bulut, H. (2020). Mahalanobis distance based on minimum regularized covariance determinant estimators for high dimensional data. *Communications in Statistics - Theory and Methods*, 49, 5897–5907.

Examples

```
if (requireNamespace("rrcov", quietly = TRUE) &&
    requireNamespace("mvtnorm", quietly = TRUE)) {

  set.seed(123)
  x1 <- mvtnorm::rmvnorm(n = 10, mean = rep(0, 20), sigma = diag(20))
  x2 <- mvtnorm::rmvnorm(n = 10, mean = rep(0, 20), sigma = diag(20))
  x3 <- mvtnorm::rmvnorm(n = 10, mean = rep(0, 20), sigma = diag(20))

  x <- rbind(x1, x2, x3)
  group <- c(rep(1, 10), rep(2, 10), rep(3, 10))

  RobHDMANOVA(x = x, group = group, N = 19, alpha = 0.75,
              tau = 0.975, seed = 123)
}
```

RobPer_CovTest

Robust Permutation Test for Covariance Matrices

Description

Robust Permutation Test for Covariance Matrices in High Dimensional Data

Usage

```
RobPer_CovTest(x, group, N = 100, alpha = 0.75)
```

Arguments

- | | |
|-------|--|
| x | the data matrix |
| group | the grouping vector. It must be factor. |
| N | the permutation number and the default value is 100. |
| alpha | numeric parameter controlling the size of the subsets over which the determinant is minimized. Allowed values are between 0.5 and 1 and the default is 0.75. |

Details

RobPer_CovTest function calculates directly p-value based on the calculated value of test statistics and the permutational distribution of test statistics for covariance matrices of two or more independent samples in high dimensional data based on the minimum regularized covariance determinant estimators.

Value

a list with 3 elements:

pval	p-value of the robust permutation test process
TM	The calculated value of test statistics based on raw data
Permutations_TM	The calculated values of test statistics based on each permutational data

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H (2024). A robust permutational test to compare covariance matrices in high dimensional data. (Unpublished)

Examples

```
if (requireNamespace("rrcov", quietly=TRUE)) {
  x1<-mvtnorm::rmvnorm(n = 10,mean = rep(0,20),sigma = diag(20))
  x2<-mvtnorm::rmvnorm(n = 10,mean = rep(0,20),sigma = 2*diag(20))
  x3<-mvtnorm::rmvnorm(n = 10,mean = rep(0,20),sigma = 3*diag(20))
  data<-rbind(x1,x2,x3)
  group_label<-c(rep(1,10),rep(2,10),rep(3,10))
  RobPer_CovTest(x=data, group=group_label)}
```

RobPer_GVTest	<i>Robust permutation test for equality of generalized variances</i>
---------------	--

Description

Computes an MCD-based permutation test for $H_0 : |\Sigma_1| = \dots = |\Sigma_k|$ in a low-dimensional multivariate setting. Group-specific robust shape transformations are applied before the generalized-variance statistic is recalculated. The scale component is retained; it is not divided out after transformation.

Usage

```
RobPer_GVTest(x, group, B = 999, alpha = 0.75, seed = NULL, na.rm = TRUE)
```

Arguments

x	A numeric matrix or data frame. Rows are observations and columns are variables.
group	A vector identifying the population or group of each row.
B	Integer number of permutations. The default is 999.
alpha	Numeric MCD coverage fraction in $(0.5, 1]$. The default is 0.75.
seed	Optional integer random seed.
na.rm	Logical; if 'TRUE', rows containing missing values are removed. If 'FALSE', missing values produce an error.

Details

The permutation p-value is calculated as

$$(1 + \sum_b I(T_b^* \geq T_{obs})) / (1 + B_{ok}),$$

where the sum is over successful permutations and 'B_ok' is the number of successful permutation fits. The observed and permuted statistics use the same MCD-based transformation and refitting pipeline.

If S_i is the group-specific MCD scatter matrix, the robust scale component is $a_i = |S_i|^{1/p}$ and the shape matrix is $Q_i = S_i/a_i$. The transformed observations are multiplied by $Q_i^{-1/2}$. No additional division by $\sqrt{a_i}$ is applied, because that would remove the generalized-variance information being tested.

Value

An object of class 'RobPer_GVTest', 'MVTests', and 'list' with the following components: 'statistic', 'p.value', 'successful', 'failed', 'permutation.statistics', 'B', 'alpha', 'group.sizes', 'p', 'k', and 'method'.

Examples

```
## Not run:
if (requireNamespace("rrcov", quietly = TRUE)) {
  set.seed(1)
  x <- rbind(matrix(rnorm(60), 20, 3),
              matrix(rnorm(60), 20, 3))
  g <- rep(c("A", "B"), each = 20)
  fit <- RobPer_GVTest(x, g, B = 99, seed = 123)
  fit
  summary(fit)
}

## End(Not run)
```

RperT2

*Robust Permutation Hotelling T^2 Test in High Dimensional Data***Description**

Robust Permutation Hotelling T^2 Test for Two Independent Samples in high Dimensional Data

Usage

```
RperT2(X1, X2, alpha = 0.75, N = 100)
```

Arguments

X1	the data matrix for the first group. It must be matrix or data.frame.
X2	the data matrix for the first group. It must be matrix or data.frame.
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized. Allowed values are between 0.5 and 1 and the default is 0.75.
N	the permutation number

Details

RperT2 function performs a robust permutation Hotelling T^2 test for two independent samples in high dimensional test based on the minimum regularized covariance determinant estimators.

Value

a list with 2 elements:

T2	The calculated value of Robust Hotelling T^2 statistic based on MRCD estimations
p.value	p value obtained from test process

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut et al. (2024). A Robust High-Dimensional Test for Two-Sample Comparisons, Axioms.

Examples

```
if (requireNamespace("rrcov", quietly=TRUE)) {
  x<-rmvnorm::rmvnorm(n=10,sigma=diag(20),mean=rep(0,20))
  y<-rmvnorm::rmvnorm(n=10,sigma=diag(20),mean=rep(1,20))
  RperT2(X1=x,X2=y)$p.value}
```

simRHT2

*Monte Carlo Simulation to obtain d and q constants for RHT2 function***Description**

Monte Carlo Simulation to obtain d and q constants for RHT2 function

Usage

```
simRHT2(n, p, nrep = 500, alpha = 0.75)
```

Arguments

n	the sample size
p	the number of variables
nrep	the number of iteration. The default value is 500.
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized. Allowed values are between 0.5 and 1 and the default is 0.75.

Details

simRHT2 function computes d and q constants to construct an approximate F distribution of robust Hotelling T^2 statistic in high dimensional data. These constants are used in RHT2 function. For more detailed information, you can see the study by Bulut (2021).

Value

a list with 2 elements:

q	The q value
d	The d value

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut, H (2021). A robust Hotelling test statistic for one sample case in highdimensional data, Communication in Statistics: Theory and Methods.

simRobCellT2_onesample

Monte Carlo Calibration for the One-Sample cellMCD Hotelling Test

Description

Estimates d and q for an empirical scaled-F approximation to the one-sample cellMCD Hotelling T^2 statistic under a Gaussian null model with fixed mean μ_0 .

Usage

```
simRobCellT2_onesample(
  X = NULL,
  mu0,
  Sigma = NULL,
  n = NULL,
  p = NULL,
  nper = 3000
)
```

Arguments

X	Optional finite numeric matrix or data frame of observed data. If supplied, its row and column counts determine n and p . Missing values are rejected; perform complete-case handling before calling this function and use the same retained observations in the test.
mu0	Required finite numeric null mean vector of length p .
Sigma	Optional finite symmetric positive-definite p -by- p covariance matrix. If supplied it takes precedence over covariance estimation from X . Otherwise X is required and the bias-corrected scatter S from <code>cellWise::cellMCD(X)</code> is used.
n	Optional integer sample size greater than 1. Required without X ; when supplied with X it must equal <code>nrow(X)</code> .
p	Optional integer dimension greater than 1. Required without X ; when supplied with X it must equal <code>ncol(X)</code> .
nper	Positive integer number of Monte Carlo replications; default 3000.

Details

When `Sigma` is omitted, `cellMCD` is applied to the raw X with its default settings and a free location. This differs from the fixed-center plug-in design of the earlier data-based interface. The observed fitted location is never used as the simulation mean: every Monte Carlo sample is generated from $N_p(\mu_0, \text{Sigma})$, and its `cellMCD` location estimate is compared with the fixed μ_0 in the statistic $n(\text{location} - \mu_0)^T S^{-1}(\text{location} - \mu_0)$.

All `cellMCD` fits use the installed API's default settings, including $\alpha = 0.75$, $\text{quant} = 0.99$ and $\text{crit} = 1e-04$. Match those settings and the effective n and p when applying `RobCellT2_onesample()`. Actual settings are recorded in the result. Use `set.seed()` before calling for reproducibility.

The d and q values match the Monte Carlo mean and variance to $d * F(p, q)$. They define an empirical approximation, not a theoretically exact or universally covariance-invariant distribution. A plug-in covariance is an estimate, not guaranteed to recover the population covariance exactly. At least 10 positive finite statistics are required. Failed fits or invalid statistics are recorded, and returned moments use successful replications. Unstable moments, including matches that cannot yield finite $q > 4$, produce an error. Inspect failure counts and consider increasing n_{per} .

The pre-2.3.6 $n/p/nrep/seed/data$ interface is available as `simRobCellT2_onesample_legacy()`, with a deprecation warning and its original semantics. This function's six-argument signature does not accept `nrep`, `seed`, `data` or additional `cellMCD` arguments. Migration requires explicit `mu0`; use `nper` instead of `nrep`, `X` instead of `data`, and `set.seed()` instead of `seed`.

Value

A list containing `d`, `q`, `mean.T2`, `var.T2`, `Sigma`, `mu0`, `n`, `p`, `nper`, `n.success` and `n.failed`. It also contains `failure.messages`, `covariance.source`, `mode`, `cellMCD.settings`, `covariance.settings` and `cellWise.version`. The `nrep` element is retained as an alias for `nper` for consumers of earlier results.

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

See Also

[RobCellT2_onesample](#), [simRobCellT2_onesample_legacy](#)

Examples

```
if (requireNamespace("MASS", quietly = TRUE) &&
    requireNamespace("cellWise", quietly = TRUE)) {
  mu0 <- c(1, -1)
  Sigma <- matrix(c(2, 0.4, 0.4, 1), 2)
  set.seed(123)
  X <- MASS::mvrnorm(30, mu0, Sigma)
  set.seed(1)
  constants <- simRobCellT2_onesample(X = X, mu0 = mu0, nper = 50)
  set.seed(1)
  simRobCellT2_onesample(mu0 = mu0, Sigma = Sigma, n = 30, p = 2, nper = 50)
}
```

`simRobCellT2_onesample_legacy`

Legacy Interface for One-Sample cellMCD Calibration

Description

Compatibility interface for calls written before version 2.3.6. Prefer `simRobCellT2_onesample(X, mu0, Sigma, n, p, nper)` for new code. This interface retains the old `n/p/nrep/seed/data` arguments and the old fixed-center plug-in design, and signals deprecation. Computes the constants d and q required for the approximate F distribution of the cellMCD-based robust one-sample Hotelling T^2 statistic.

Usage

```
simRobCellT2_onesample_legacy(
  n,
  p,
  nrep = 3000,
  alpha = 0.75,
  quant = 0.99,
  crit = 1e-04,
  seed = NULL,
  Sigma = diag(p),
  ...,
  data = NULL,
  mu0 = NULL,
  na.rm = TRUE
)
```

Arguments

<code>n</code>	The sample size in explicit-covariance mode; omit when supplying data.
<code>p</code>	The number of variables in explicit-covariance mode; omit with data.
<code>nrep</code>	The number of Monte Carlo replications. Default is 3000.
<code>alpha</code>	The cellMCD alpha parameter. Default is 0.75.
<code>quant</code>	Quantile used in the cellMCD procedure. Default is 0.99.
<code>crit</code>	Convergence criterion used in the cellMCD procedure. Default is 1e-04.
<code>seed</code>	Optional random seed.
<code>Sigma</code>	Finite numeric positive-definite p-by-p covariance matrix under the null model. Defaults to <code>diag(p)</code> . Omitting it warns that the calibration assumes independence and may be inappropriate for correlated data. Supply either explicit <code>n</code> , <code>p</code> and <code>Sigma</code> or <code>data</code> , not both.
<code>...</code>	Additional arguments passed to <code>cellwise::cellMCD()</code> .
<code>data</code>	Optional observed numeric matrix or data frame. Supplying data selects data-based plug-in calibration and derives <code>n</code> and <code>p</code> after row removal.
<code>mu0</code>	Finite numeric null mean vector of length <code>p</code> . Required with <code>data</code> ; defaults to the zero vector in explicit-covariance mode.
<code>na.rm</code>	Logical; remove incomplete rows when TRUE (default), matching <code>RobCellT2_onesample()</code> . With FALSE, missing cells are retained for cellMCD; infinite values are always rejected.

Details

The scaled-F reference is an empirical, moment-matched approximation, not a theoretically exact distribution. Calibration must match the test's sample size, dimension, null covariance and cellMCD settings (including `...`).

In data-based mode, cellMCD is fit to data centered at `mu0` with `fixedCenter = TRUE`, when supported by the installed API. Its bias-corrected scatter `S` is the robust plug-in null covariance. If

fixedCenter is unavailable, a free-center fit of the centered data is used with a warning and recorded in the settings. Failed fits never fall back to classical covariance. The observed location estimate is not the simulation mean: every sample is generated from $N_p(\mu_0, \Sigma)$ and refit to calculate T^2 from the fitted location minus the fixed μ_0 . This is parametric bootstrap/Monte Carlo calibration, not permutation calibration.

All cellMCD settings agree between the plug-in and replicate fits except that the replicate location is free. In data-based mode, do not set fixedCenter = TRUE through ...; that would fix the location whose deviation the test measures. The plug-in covariance is an estimate, not an exactly unbiased or guaranteed recovery of population covariance. The approximation depends on that estimate and is not universally covariance invariant. A supplied seed is set before the plug-in fit and simulations.

Moment matching requires positive finite moments and a finite second degree of freedom greater than 4. Incompatible or numerically unstable moments produce an error; increasing nrep may help.

Value

A list with the following elements:

d	The scaling constant of the approximate F distribution.
q	The second degree of freedom of the approximate F distribution.
mean.T2	The Monte Carlo mean of the simulated T^2 statistics.
var.T2	The Monte Carlo variance of the simulated T^2 statistics.
Sigma	The covariance matrix used to generate calibration samples.
mode	Either explicit or data.
n, p, mu0	Effective sample size, dimension and simulation null mean.
n.omitted, na.rm	Number of omitted rows and missing-data setting.
cellMCD.settings, covariance.settings	Actual arguments, including API defaults, for replicate and plug-in fits (the latter is NULL in explicit mode).
covariance.source, cellWise.version, seed	Covariance source, installed API version and supplied seed.
n.failed	Number of failed or invalid replications.
n.success	The number of successful Monte Carlo replications.

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

Examples

```
if (requireNamespace("MASS", quietly = TRUE) &&
    requireNamespace("cellWise", quietly = TRUE)) {
  mu0 <- c(1, -1)
  Sigma <- matrix(c(2, 0.4, 0.4, 1), 2)
  set.seed(123)
  X <- MASS::mvrnorm(30, mu0, Sigma)
```

```

suppressWarnings(simRobCellT2_onesample_legacy(
  data = X, mu0 = mu0, nrep = 50, seed = 1))
suppressWarnings(simRobCellT2_onesample_legacy(
  30, 2, nrep = 50, seed = 1, Sigma = Sigma))
}

```

summary.MVTests

*Summarizing Results in MVTests Package***Description**

summary.MVTests function summarizes of results of functions in this package.

Usage

```

## S3 method for class 'MVTests'
summary(object, ...)

```

Arguments

object	an object of class MVTests.
...	additional parameters.

Details

This function prints a summary of the results of multivariate hypothesis tests in the MVTests package.

Value

the input object is returned silently.

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

Examples

```

# One Sample Hotelling T Square Test
data(iris)
X <- iris[1:50, 1:4]
mean0 <- c(6, 3, 1, 0.25)
result.onesample <- OneSampleHT2(data = X, mu0 = mean0, alpha = 0.05)
summary(result.onesample)

# Two Independent Sample Hotelling T Square Test
data(iris)
G <- c(rep(1, 50), rep(2, 50))

```

```

result.twosamples <- TwoSamplesHT2(data = iris[1:100, 1:4],
                                   group = G, alpha = 0.05)
summary(result.twosamples)

# Box's M Test
data(iris)
result.BoxM <- BoxM(data = iris[, 1:4], group = iris[, 5])
summary(result.BoxM)

# Bartlett's Test of Sphericity
data(iris)
result.Bsper <- Bsper(data = iris[, 1:4])
summary(result.Bsper)

# Bartlett's Test for One Sample Covariance Matrix
data(iris)
S <- matrix(c(5.71, -0.8, -0.6, -0.5,
              -0.8, 4.09, -0.74, -0.54,
              -0.6, -0.74, 7.38, -0.18,
              -0.5, -0.54, -0.18, 8.33),
            ncol = 4, nrow = 4)
result.bcov <- Bcov(data = iris[, 1:4], Sigma = S)
summary(result.bcov)

```

TR2

Robust Hotelling T^2 Test Statistic

Description

Robust Hotelling T^2 Test Statistic for Two Independent Samples in high Dimensional Data

Usage

```
TR2(x1, x2, alpha = 0.75)
```

Arguments

x1	the data matrix for the first group. It must be matrix or data.frame.
x2	the data matrix for the first group. It must be matrix or data.frame.
alpha	numeric parameter controlling the size of the subsets over which the determinant is minimized. Allowed values are between 0.5 and 1 and the default is 0.75.

Details

TR2 function calculates the robust Hotelling T^2 test statistic for two independent samples in high dimensional data based on the minimum regularized covariance determinant estimators.

Value

a list with 2 elements:

TR2	The calculated value of Robust Hotelling T^2 statistic based on MRCD estimations
-----	--

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

Bulut et al. (2024). A Robust High-Dimensional Test for Two-Sample Comparisons, Axioms

Examples

```
if (requireNamespace("rrcov", quietly=TRUE)) {
  x<-rmvnorm::rmvnorm(n=10,sigma=diag(20),mean=rep(0,20))
  y<-rmvnorm::rmvnorm(n=10,sigma=diag(20),mean=rep(1,20))
  TR2(x1=x,x2=y)}
```

TwoSamplesHT2	<i>Two Independent Samples Hotelling T^2 Test</i>
---------------	--

Description

TwoSamplesHT2 function computes Hotelling T^2 statistic for two independent samples and gives confidence intervals.

Usage

```
TwoSamplesHT2(data, group, alpha = 0.05, Homogeneity = TRUE)
```

Arguments

data	a data frame.
group	a group vector consisting of 1 and 2 values.
alpha	Significance Level that will be used for confidence intervals. default=0.05
Homogeneity	a logical argument. If sample covariance matrices are homogeneity,then Homogeneity=TRUE. Otherwise Homogeneity=FALSE The homogeneity of covariance matrices can be investigated with BoxM function.

Details

This function computes two independent samples Hotelling T^2 statistics that is used to test whether two population mean vectors are equal to each other. When H_0 is rejected, this function computes confidence intervals for all variables to determine variable(s) affecting on rejection decision. Moreover, when covariance matrices are not homogeneity, the approach proposed by D. G. Nel and V. D. Merwe (1986) is used.

Value

a list with 8 elements:

HT2	The value of Hotelling T^2 Test Statistic
F	The value of F Statistic
df	The F statistic's degree of freedom
p.value	p value
CI	The lower and upper limits of confidence intervals obtained for all variables
alpha	The alpha value using in confidence intervals
Descriptive1	Descriptive Statistics for the first group
Descriptive2	Descriptive Statistics for the second group

Author(s)

Hasan BULUT <hasan.bulut@omu.edu.tr>

References

- Rencher, A. C. (2003). Methods of multivariate analysis (Vol. 492). John Wiley & Sons.
- Tatlidil, H. (1996). Uygulamali Cok Degiskenli Istatistiksel Yontemler. Cem Web.
- D.G. Nel & C.A. Van Der Merwe (1986) A solution to the multivariate behrens fisher problem, Communications in Statistics:Theory and Methods, 15:12, 3719-3735

Examples

```
data(iris)
G<-c(rep(1,50),rep(2,50))
# When covariances matrices are homogeneity
results1 <- TwoSamplesHT2(data=iris[1:100,1:4],group=G,alpha=0.05)
summary(results1)
# When covariances matrices are not homogeneity
results2 <- TwoSamplesHT2(data=iris[1:100,1:4],group=G,Homogeneity=FALSE)
summary(results2)
```

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