

Package ‘CovCorTest’

July 30, 2026

Title Statistical Tests for Covariance and Correlation Matrices and their Structures

Version 1.2.0

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Description A compilation of tests for hypotheses regarding covariance and correlation matrices for one or more groups. The hypothesis can be specified through a corresponding hypothesis matrix and a vector or by choosing one of the basic hypotheses, while for the structure test, only the latter works. Thereby Monte-Carlo and Bootstrap-techniques are used, and the respective method must be chosen, and the functions provide p-values and mostly also estimators of calculated covariance matrices of test statistics. For more details on the methodology, see Sattler et al. (2022) <[doi:10.1016/j.jspi.2021.12.001](https://doi.org/10.1016/j.jspi.2021.12.001)>, Sattler and Pauly (2024) <[doi:10.1007/s11749-023-00906-6](https://doi.org/10.1007/s11749-023-00906-6)>, Sattler and Dobler (2026) <[doi:10.1016/j.jmva.2025.105517](https://doi.org/10.1016/j.jmva.2025.105517)>, and Sattler and Jedhoff (2025) <[doi:10.48550/arXiv.2507.03406](https://doi.org/10.48550/arXiv.2507.03406)>.

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Imports MANOVA.RM, matrixcalc, Rdpack

Suggests testthat (>= 3.0.0)

RdMacros Rdpack

Config/testthat/edition 3

Encoding UTF-8

URL <https://github.com/sjedhoff/CovCorTest>

BugReports <https://github.com/sjedhoff/CovCorTest/issues>

Config/roxygen2/version 8.0.0

RoxygenNote 7.3.3

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-07-30 13:20:02 UTC

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CovCorTest-package	<i>CovCorTest: Tests for covariance and correlation matrices</i>
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Description

The **CovCorTest** package provides statistical tests for hypotheses about covariance matrices, correlation matrices, and structured covariance or correlation matrices. It also provides a combined procedure for comparing the covariance and correlation matrices of two groups.

The procedures are based on ANOVA-type statistics and use bootstrap, Monte Carlo, or Taylor-based Monte Carlo approximations, depending on the selected test. The methods require comparatively weak distributional assumptions and support both one-sample and multiple-group designs.

Data format

The main testing functions accept observations in either of two forms:

- A numeric matrix or data frame with observations in rows and variables in columns.
- A list of numeric matrices or data frames, with one element per group. Within every element, observations are stored in rows and variables in columns.

If multiple groups are combined into one matrix, the argument `nv` specifies the sample size of each group. When a list is supplied, the group sizes can be inferred from the numbers of rows.

All groups must contain the same variables. Observations containing missing values are removed before the test is calculated.

Tests for covariance matrices

`test_covariance()` tests hypotheses about one or more covariance matrices. A predefined hypothesis can be selected using the `hypothesis` argument. The available hypotheses are:

"equal" Tests equality of covariance matrices across groups. For a single group, it tests equality of the diagonal elements.

"equal-trace" Tests equality of covariance-matrix traces across multiple groups.

"equal-diagonals" Tests equality of the diagonal elements across multiple groups.

"given-trace" Tests whether the trace of a single covariance matrix is equal to a specified scalar.

"given-matrix" Tests whether a single covariance matrix is equal to a specified matrix.

"uncorrelated" Tests whether all off-diagonal elements of a single covariance matrix are zero.

Custom linear hypotheses can be specified using a hypothesis matrix C and a corresponding null vector ξ . The underlying covariance-testing methodology is described by Sattler et al. (2022).

Tests for correlation matrices

`test_correlation()` tests hypotheses about one or more correlation matrices. The predefined hypotheses are:

"equal-correlated" Tests equality of correlation matrices across groups.

"uncorrelated" Tests whether all correlations in a single group are zero.

As with `test_covariance()`, custom linear hypotheses can be supplied using C and ξ . The correlation-testing methodology is described by Sattler and Pauly (2024).

Covariance-structure tests

`test_covariance_structure()` tests whether the covariance matrix of one group has a specified structure. The implemented structures include:

- autoregressive, "autoregressive" or "ar";
- first-order autoregressive, "F0-autoregressive" or "F0-ar";
- diagonal, "diagonal" or "diag";
- sphericity, "sphericity" or "spher";
- compound symmetry, "compoundsymmetry" or "cs";
- Toeplitz, "toeplitz" or "toep";
- constant off-diagonal, "constant-offdiagonal" or "const-offdiag";
- standard Toeplitz, "standard-toeplitz" or "std-toep";
- banded, "banded" or "band";
- banded Toeplitz, "banded-toeplitz" or "band-toep".

For banded structures, `bandwidth` specifies the number of off-diagonals that may be nonzero.

Correlation-structure tests

`test_correlation_structure()` tests whether the correlation matrix of one group has a specified structure. The implemented structures include:

- heterogeneous autoregressive, "Hautoregressive" or "Har";
- diagonal, "diagonal" or "diag";
- heterogeneous compound symmetry, "Hcompoundsymmetry" or "Hcs";
- heterogeneous Toeplitz, "Htoeplitz" or "Htoep";
- banded, "banded" or "band";
- banded Toeplitz, "banded-toeplitz" or "band-toep".

The covariance- and correlation-structure procedures are described by Sattler and Dobler (2026).

Combined test

`test_combined()` simultaneously compares the variances and correlations of exactly two groups. It returns separate p-values for equality of the variances and equality of the correlations, together with a p-value for the global combined hypothesis.

The combined procedure is based on the correlation-testing methodology of Sattler and Pauly (2024).

Resampling methods

Depending on the function, the following methods are available:

"BT" A parametric bootstrap approximation.

"MC" A Monte Carlo approximation based on the estimated asymptotic distribution.

"TAY" A Taylor-based Monte Carlo approximation available for correlation procedures.

The `repetitions` argument controls the number of generated resampling observations. At least 500 repetitions are recommended. Larger values generally provide more precise p-values but require more computation time.

Alternative hypothesis matrices

By default, the main procedures use $AM = 1$. This replaces the original hypothesis matrix with a lower-dimensional companion matrix that yields the same ANOVA-type test statistic. The original and transformed hypothesis matrices are retained in the returned object. This approach is described by Sattler and Rosenbaum (2025).

Setting $AM = 0$ disables this transformation.

Constructing custom hypotheses

`get_hypothesis()` constructs a hypothesis matrix and vector for a linear covariance model. It can be used together with `test_covariance()` when the required hypothesis is not among the predefined alternatives.

Returned objects

Covariance, correlation, and structure tests return an object of class `CovTest`. Important components include:

- `pvalue`: the estimated p-value;
- `Teststatistic`: the observed ANOVA-type statistic;
- `CovarianceMatrix`: the estimated covariance matrix of the statistic;
- `C` and `Xi`: the hypothesis used in the calculation;
- `C_original` and `Xi_original`: the hypothesis before the optional companion-matrix transformation;
- `resampling_method`: the selected approximation;
- `repetitions`: the number of resampling repetitions;
- `nv`: the sample sizes.

The combined test returns an object of class `CombTest` containing separate variance, correlation, and global p-values.

Citation

When using **CovCorTest**, cite the package paper (Sattler and Jedhoff 2025).

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References

Sattler P, Bathke AC, Pauly M (2022). “Testing Hypotheses about Covariance Matrices in General MANOVA Designs.” *Journal of Statistical Planning and Inference*, **219**, 134–146. doi:10.1016/j.jspi.2021.12.001.

Sattler P, Dobler D (2026). “Testing for Patterns and Structures in Covariance and Correlation Matrices.” *Journal of Multivariate Analysis*, **211**, 105517. doi:10.1016/j.jmva.2025.105517.

Sattler P, Jedhoff S (2025). “Testing Hypotheses Regarding Covariance and Correlation Matrices with the R Package CovCorTest.” *arXiv*. doi:10.48550/arXiv.2507.03406, arXiv:2507.03406, <https://arxiv.org/abs/2507.03406>.

Sattler P, Pauly M (2024). “Testing hypotheses about correlation matrices in general MANOVA designs.” *TEST*, **33**(2), 496–516. ISSN 1863-8260, doi:10.1007/s11749023009066.

Sattler P, Rosenbaum M (2025). “Choice of the hypothesis matrix for using the Anova-type-statistic.” *Statistics & Probability Letters*, **219**, 110356. doi:10.1016/j.spl.2025.110356.

See Also

```
test_covariance(), test_correlation(), test_covariance_structure(), test_correlation_structure(),  
test_combined(), and get_hypothesis().
```

CheckBandwidth	<i>Check bandwidth argument</i>
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Description

Checks whether the bandwidth argument is valid for banded covariance or correlation structures. The bandwidth specifies the number of off-diagonals that are allowed to be non-zero. It must be a positive integer and smaller than the maximal possible bandwidth, since bandwidth zero corresponds to a diagonal structure and the maximal bandwidth would impose no restriction.

Usage

```
CheckBandwidth(bandwidth, d)
```

Arguments

- bandwidth A positive integer specifying the number of allowed off-diagonals.
- d Integer. Dimension of the covariance or correlation matrix.

Value

The checked bandwidth as an integer.

CheckRepetitions	<i>Validate the number of resampling repetitions</i>
------------------	--

Description

Checks that the requested number of repetitions is a single, finite, positive integer. A warning is issued when the number is below the recommended minimum because the resulting p-value may be imprecise.

Usage

```
CheckRepetitions(repetitions, minimum_recommended = 500L)
```

Arguments

- `repetitions` A single positive integer specifying the number of resampling repetitions.
- `minimum_recommended` A single positive integer specifying the number of repetitions below which a warning is issued. The default is 500.

Value

The validated number of repetitions as an integer.

CombTest

Combined covariance and correlation test result

Description

Constructs an object of class CombTest. Objects of this class represent results from the combined test for equality of covariance and correlation matrices.

Usage

```
CombTest(
  pvalue_Variiances = NA_real_,
  pvalue_Correlations = NA_real_,
  pvalue_Total = NA_real_,
  Teststatistic = NA_real_,
  repetitions = NA_integer_,
  nv = integer()
)
```

Arguments

- `pvalue_Variiances` Numeric. The p-value for equality of the variances.
- `pvalue_Correlations` Numeric. The p-value for equality of the correlations.
- `pvalue_Total` Numeric. The p-value for the global combined hypothesis.
- `Teststatistic` Numeric. The value of the combined test statistic.
- `repetitions` Integer. The number of resampling repetitions.
- `nv` Integer vector containing the sample sizes of the two groups.

Details

A CombTest object contains the following components:

pvalue_Variances Numeric. The p-value for equality of the variances.

pvalue_Correlations Numeric. The p-value for equality of the correlations.

pvalue_Total Numeric. The p-value for the global combined hypothesis.

Teststatistic Numeric. The value of the combined test statistic.

repetitions Integer. The number of resampling repetitions.

nv Integer vector. The sample sizes of the two groups.

Value

An object of class CombTest.

Examples

```
result <- CombTest(
  pvalue_Variances = 0.12,
  pvalue_Correlations = 0.08,
  pvalue_Total = 0.08,
  Teststatistic = 2.4,
  repetitions = 1000L,
  nv = c(20L, 25L)
)
```

get_extended_matrix	<i>Extend a matrix to full rank using identity columns</i>
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Description

This function extends a matrix V (assumed to have fewer than p columns) to full rank by iteratively appending standard basis vectors from the identity matrix, ensuring that each added column increases the rank.

Usage

```
get_extended_matrix(V, tol = sqrt(.Machine$double.eps))
```

Arguments

V	A numeric matrix with p rows and fewer than p columns.
tol	A non-negative numeric scalar specifying the tolerance used by qr when determining the numerical rank of V . Columns associated with values smaller than this tolerance are treated as linearly dependent. The default is <code>sqrt(.Machine\$double.eps)</code> .

Details

The function assumes that `nrow(V)` equals the intended dimension p of the parameter space. It adds columns from the identity matrix (i.e., standard basis vectors) only when they increase the rank, and stops when full rank is achieved.

Value

A numeric matrix of dimension $p \times p$ with full column rank.

<code>get_hypothesis</code>	<i>Construct hypothesis matrix and vector from linear covariance model structure</i>
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Description

Computes a hypothesis matrix C and hypothesis vector ζ based on a given parameter vector v_0 and a matrix V representing the model structure (e.g., vectorized components of a linear covariance structure model).

Usage

`get_hypothesis(v0, V)`

Arguments

- `v0` A numeric vector of length p (number of parameters). Represents the parameter vector at which the hypothesis is to be evaluated.
- `V` A numeric matrix of size $p \times q$, representing the structured design or constraint matrix for the model. Here, the vectorised matrices from the linear covariance structure model build the columns of V .

Details

The function extends V to full rank using [get_extended_matrix](#), constructs a contrast matrix E for the complement of the model-implied space, and computes the corresponding hypothesis matrix C .

Value

- A list with two elements:
- `hypothesis_matrix` A numeric matrix C such that the hypothesis can be written as $C \%*\% \theta = \zeta$
 - `hypothesis_vector` The numeric vector ζ , computed as $C \%*\% v_0$

References

Sattler P, Dobler D (2026). “Testing for Patterns and Structures in Covariance and Correlation Matrices.” *Journal of Multivariate Analysis*, **211**, 105517. doi:10.1016/j.jmva.2025.105517.

Examples

```
# Load the data
data("EEGwide", package = "MANOVA.RM")

X <- as.matrix(EEGwide[EEGwide$sex == "W" & EEGwide$diagnosis == "AD",
  c("brainrate_temporal", "brainrate_frontal", "brainrate_central",
    "complexity_temporal", "complexity_frontal", "complexity_central")])
v0 <- rep(0,21)
v_auxiliary <- c(1, rep(0,5), 1, rep(0,4), 1, rep(0,3), 1, rep(0,2), 1, 0, 1)
V <- cbind(v_auxiliary, 1-v_auxiliary)
h <- get_hypothesis(v0,V)
set.seed(123)
test_covariance(X = X,C = h$hypothesis_matrix, Xi = h$hypothesis_vector,
  method = "MC", repetitions = 1000)
```

`print.CombTest`

Print function for CombTest object

Description

Print function for CombTest object

Usage

```
## S3 method for class 'CombTest'
print(x, ...)
```

Arguments

`x` an [CombTest](#) object

`...` additional parameters

Value

no return, just print

print.CovTest	<i>Print function for CovTest object</i>
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Description

Print function for CovTest object

Usage

```
## S3 method for class 'CovTest'
print(x, ...)
```

Arguments

x	an CovTest object
...	additional parameters

Value

no return, just print

test_combined	<i>Combined test for equality of covariance matrices and correlation matrices</i>
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Description

For two groups a combined test for equality of covariance matrices and equality of correlation matrices between these groups is conducted. Both hypotheses can be rejected or only the larger one, the equality of the covariance matrices

Usage

```
test_combined(X, nv = NULL, repetitions = 1000)
```

Arguments

X	a list or matrix containing the observation vectors. In case of a list, each matrix in this list is another group, where the observation vectors are the rows. For a matrix, all groups are together in one matrix and nv is used to indicate the group sizes.
nv	vector of group sizes
repetitions	a scalar, indicate the number of runs for the chosen method. The predefined value is 1.000, and the number should not be below 500.

Value

an object of the class `CovTest`.

Examples

```
# Load the data
data("EEGwide", package = "MANOVA.RM")

vars <- colnames(EEGwide)[1:6]

# Part the data into two diagnosis groups
X_list <- list(EEGwide[EEGwide$sex=="M" & EEGwide$diagnosis=="AD",vars],
              EEGwide[EEGwide$sex=="M" & EEGwide$diagnosis=="MCI",vars])

nv <- unlist(lapply(X_list, nrow))
set.seed(31415)
test_combined(X_list, nv)
```

test_correlation	<i>Test for Correlation Matrices</i>
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Description

This function conducts statistical tests for hypotheses regarding correlation matrices. Users can either select from predefined hypotheses or provide their own contrast matrix C and vector χ_i for custom hypotheses. It supports both bootstrap and Monte Carlo resampling methods to obtain the p-value of the ANOVA-type statistic (ATS).

Usage

```
test_correlation(
  X,
  nv = NULL,
  C = NULL,
  Xi = NULL,
  AM = 1,
  hypothesis = NULL,
  method = "BT",
  repetitions = 1000
)
```

Arguments

X	A list or a matrix containing the observation vectors. If a list, each entry is a group, with observations as rows. If a matrix, all groups are combined, and nv must be used to indicate group sizes.
-----	--

nv	(Optional) A vector indicating group sizes, needed when X is a combined matrix or for multiple groups.
C	A hypothesis matrix specifying the null hypothesis. Optional if hypothesis is provided.
Xi	A numeric vector specifying the expected values of the contrasts under the null hypothesis. Optional if hypothesis is provided.
AM	Binary variable indicating whether the computations should use an alternative hypothesis matrix as proposed by Sattler and Rosenbaum (2025). This matrix has fewer rows than the original hypothesis matrix while leaving the resulting test statistics unchanged. By default, this alternative matrix is used.
hypothesis	A character specifying one of the predefined hypotheses: • "equal-correlated" — equal correlation matrices • "uncorrelated" — test if variables are uncorrelated (single group only) If C and Xi are provided, this can be set to NULL.
method	Character string indicating the resampling method to use. One of "BT" (bootstrap), "MC" (Monte Carlo), or "TAY" (Taylor approximation).
repetitions	Integer. Number of resampling repetitions (default is 1000).

Value

An object of class "CovTest".

References

Sattler, P. and Pauly, M. (2024). Testing hypotheses about correlation matrices in general MANOVA designs. *TEST*, 33(2), 496–516. doi:10.1007/s11749023009066

Examples

```
# Example with one group:
set.seed(31415)
X <- matrix(rnorm(5 * 100), ncol = 5)
test_correlation(X, hypothesis = "uncorrelated",
  method = "BT", repetitions = 100)
```

test_correlation_structure	<i>Test for structure of data's correlation matrix</i>
----------------------------	--

Description

With this function the correlation matrix of data can be checked for one of the predefined structures. Depending on the chosen method a bootstrap, the Taylor-based Monte-Carlo approach or Monte-Carlo-technique is used to calculate the p-value of the Anova-type-statistic(ATS) based on a specified number of runs.

Usage

```
test_correlation_structure(
  X,
  structure,
  AM = 1,
  method = "BT",
  repetitions = 1000,
  bandwidth = NA
)
```

Arguments

X	a matrix containing the observation vectors as rows (one group)
structure	a character specifying the structure regarding the correlation matrix should be checked. Options are "Hautoregressive" ("Har"), "diagonal" ("diag"), "Hcompoundsymmetry" ("Hcs") and "Htoeplitz" ("Htoep"), "banded" ("band"), and "banded-toeplitz" ("band-toep"). For banded structures, all correlations outside the specified bandwidth, i.e. from the bandwidth + 1-th off-diagonal onward, are assumed to be zero.
AM	Binary variable indicating whether the computations should use an alternative hypothesis matrix as proposed by Sattler and Rosenbaum (2025). This matrix has fewer rows than the original hypothesis matrix while leaving the resulting test statistics unchanged. By default, this alternative matrix is used.
method	a character, to choose whether bootstrap("BT") or Taylor-based Monte-Carlo-approach("TAY") or Monte-Carlo-technique("MC") is used, while bootstrap is the predefined method.
repetitions	a scalar, indicate the number of runs for the chosen method. The predefined value is 1,000, and the number should not be below 500.
bandwidth	Optional positive integer specifying the number of off-diagonals allowed to be non-zero for banded correlation structures. Only used for "banded" and "banded-toeplitz" structures, with default NA.

Value

an object of the class `CovTest`

References

Sattler P, Dobler D (2026). "Testing for Patterns and Structures in Covariance and Correlation Matrices." *Journal of Multivariate Analysis*, **211**, 105517. doi:10.1016/j.jmva.2025.105517.

Examples

```
# Load the data
data("EEGwide", package = "MANOVA.RM")

# Select only the females with the diagnosis AD
X <- as.matrix(EEGwide[EEGwide$sex == "W" & EEGwide$diagnosis == "AD",
```

```
      c("brainrate_temporal", "brainrate_frontal", "brainrate_central",
        "complexity_temporal", "complexity_frontal",
        "complexity_central")])

test_correlation_structure(X = X, structure = "diagonal", method = "MC")
```

test_covariance	<i>Test for Covariance Matrices</i>
-----------------	-------------------------------------

Description

This function conducts statistical tests for hypotheses regarding covariance matrices. Users can either select from predefined hypotheses (e.g., equal covariance, equal trace, etc.) or provide their own contrast matrix C and vector Xi for custom hypotheses. It supports both bootstrap and Monte Carlo resampling methods to obtain the p-value of the ANOVA-type statistic (ATS).

Usage

```
test_covariance(
  X,
  nv = NULL,
  C = NULL,
  Xi = NULL,
  AM = 1,
  hypothesis = NULL,
  A = NULL,
  method = "MC",
  repetitions = 1000
)
```

Arguments

X	A list or a matrix containing the observation vectors. If a list, each entry is a group, with observations as rows. If a matrix, all groups are combined, and nv must be used to indicate group sizes.
nv	(Optional) A vector indicating group sizes, needed when X is a combined matrix or for multiple groups.
C	(Optional) A user-defined contrast matrix for testing custom hypotheses. Must match dimensions with Xi.
Xi	(Optional) A numeric vector used in combination with C to specify a custom hypothesis.
AM	Binary variable indicating whether the computations should use an alternative hypothesis matrix as proposed by Sattler and Rosenbaum (2025). This matrix has fewer rows than the original hypothesis matrix while leaving the resulting test statistics unchanged. By default, this alternative matrix is used.

hypothesis	A character specifying one of the predefined hypotheses: • "equal" — equal covariance matrices • "equal-trace" — equal traces across groups • "equal-diagonals" — equal variances across groups • "given-trace" — test against a given trace (single group only) • "given-matrix" — test against a given covariance matrix (single group only) • "uncorrelated" — test if variables are uncorrelated (single group only) If C and Xi are provided, this can be set to NULL.
A	Optional scalar or matrix to define the hypothesis value when hypothesis is "given-trace" (scalar) or "given-matrix" (matrix). Ignored for other hypotheses.
method	A character indicating the resampling method: "BT" (Bootstrap) or "MC" (Monte Carlo).
repetitions	Number of repetitions to use for the resampling method (default: 1000, should be ≥ 500).

Value

An object of class `CovTest`.

References

Sattler P, Bathke AC, Pauly M (2022). "Testing Hypotheses about Covariance Matrices in General MANOVA Designs." *Journal of Statistical Planning and Inference*, **219**, 134–146. doi:[10.1016/j.jspi.2021.12.001](https://doi.org/10.1016/j.jspi.2021.12.001).

Examples

```
# Load the data
data("EEGwide", package = "MANOVA.RM")

vars <- colnames(EEGwide)[1:6]

X <- EEGwide[EEGwide$sex == "M" & EEGwide$diagnosis == "AD",vars]

# Testing the trace
C <- matrix(c(1,0,0,0,0,0,1,0,0,0,0,1,0,0,0,1,0,0,1,0,1),
            nrow = 1, ncol = 21)
Xi <- 2
set.seed(31415)
test_covariance(X = X, nv = NULL, C = C, Xi = Xi, AM = 1,
               method = "BT", repetitions = 1000)
```

test_covariance_structure

Test for structure of data's covariance matrix

Description

This function conducts the test for the covariance matrix of data regarding structures. Depending on the chosen method a bootstrap or Monte-Carlo-technique is used to calculate p-value of the Anova-type-statistic(ATS) based on a specified number of runs.

Usage

```
test_covariance_structure(
  X,
  structure,
  AM = 1,
  method = "BT",
  repetitions = 1000,
  bandwidth = NA
)
```

Arguments

X	a matrix or data frame containing the observation vectors as rows (one group only)
structure	a character specifying the structure regarding the covariance matrix should be checked. Options are "autoregressive" ("ar"), "FO-autoregressive" ("FO-ar"), "diagonal" ("diag"), "sphericity" ("spher"), "compound symmetry" ("cs") and "toeplitz" ("toep"), "constant-offdiagonal" ("const-offdiag"), "standard-toeplitz" ("std-toep"), "banded" ("band"), and "banded-toeplitz" ("band-toep"). For banded structures, all entries outside the specified bandwidth, i.e. from the bandwidth + 1-th off-diagonal onward, are assumed to be zero.
AM	Binary variable indicating whether the computations should use an alternative hypothesis matrix as proposed by Sattler and Rosenbaum (2025). This matrix has fewer rows than the original hypothesis matrix while leaving the resulting test statistics unchanged. By default, this alternative matrix is used.
method	a character, to chose whether bootstrap("BT") or Monte-Carlo-technique("MC") is used, while bootstrap is the predefined method.
repetitions	a scalar, indicate the number of runs for the chosen method. The predefined value is 1,000, and the number should not be below 500.
bandwidth	Optional positive integer specifying the number of off-diagonals allowed to be non-zero for banded covariance structures. Only used for "banded" and "banded-toeplitz" structures, with default NA.

Value

an object of the class `CovTest`

References

Sattler P, Dobler D (2026). “Testing for Patterns and Structures in Covariance and Correlation Matrices.” *Journal of Multivariate Analysis*, **211**, 105517. doi:10.1016/j.jmva.2025.105517.

Examples

```
# Load the data
data("EEGwide", package = "MANOVA.RM")

# Select only the females with the diagnosis AD
X <- as.matrix(EEGwide[EEGwide$sex == "W" & EEGwide$diagnosis == "AD",
  c("brainrate_temporal", "brainrate_frontal",
    "brainrate_central", "complexity_temporal",
    "complexity_frontal", "complexity_central")])

test_covariance_structure(X = X, structure = "diagonal", method = "MC")
```

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