

# Package ‘pcev’

July 23, 2025

**Title** Principal Component of Explained Variance

**Version** 2.2.2

**Description** Principal component of explained variance (PCEV) is a statistical tool for the analysis of a multivariate response vector. It is a dimension-reduction technique, similar to Principal component analysis (PCA), that seeks to maximize the proportion of variance (in the response vector) being explained by a set of covariates.

**Depends** R (>= 3.0.0)

**Imports** RMTstat, stats, corpcor

**License** GPL (>= 2)

**LazyData** true

**URL** <http://github.com/GreenwoodLab/pcev>

**BugReports** <http://github.com/GreenwoodLab/pcev/issues>

**Suggests** knitr

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2018-02-03 23:14:47 UTC

## Contents

|              |   |
|--------------|---|
| pcev-package | 2 |
| computePCEV  | 2 |
| estimatePcev | 4 |

|                       |           |
|-----------------------|-----------|
| methylation . . . . . | 5         |
| PcevObj . . . . .     | 6         |
| permutePval . . . . . | 6         |
| roysPval . . . . .    | 7         |
| wilksPval . . . . .   | 8         |
| <b>Index</b>          | <b>10</b> |

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|              |                                                                                  |
|--------------|----------------------------------------------------------------------------------|
| pcev-package | <i>pcev: A package for computing principal components of explained variance.</i> |
|--------------|----------------------------------------------------------------------------------|

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**Description**

PCEV is a statistical tool for the analysis of a multivariate response vector. It is a dimension-reduction technique, similar to Principal Components Analysis (PCA), which seeks the maximize the proportion of variance (in the response vector) being explained by a set of covariates.

**pcev functions**

[estimatePcev](#) [computePCEV](#) [PcevObj](#) [permutePval](#) [wilksPval](#) [roysPval](#)

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|             |                                                  |
|-------------|--------------------------------------------------|
| computePCEV | <i>Principal Component of Explained Variance</i> |
|-------------|--------------------------------------------------|

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**Description**

computePCEV computes the first PCEV and tests its significance.

**Usage**

```
computePCEV(response, covariate, confounder, estimation = c("all", "block",  
  "singular"), inference = c("exact", "permutation"), index = "adaptive",  
  shrink = FALSE, nperm = 1000, Wilks = FALSE)
```

**Arguments**

- |            |                                                                                                                   |
|------------|-------------------------------------------------------------------------------------------------------------------|
| response   | A matrix of response variables.                                                                                   |
| covariate  | An array or a data frame of covariates.                                                                           |
| confounder | An array or data frame of confounders.                                                                            |
| estimation | Character string specifying which estimation method to use: "all", "block" or "singular". Default value is "all". |
| inference  | Character string specifying which inference method to use: "exact" or "permutation". Default value is "exact".    |

|        |                                                                                                                                            |
|--------|--------------------------------------------------------------------------------------------------------------------------------------------|
| index  | Only used if estimation = "block". Default value is "adapative". See details.                                                              |
| shrink | Should we use a shrinkage estimate of the residual variance? Default value is FALSE.                                                       |
| nperm  | The number of permutations to perform if inference = "permutation" or for the Tracy-Widom empirical estimate (if estimation = "singular"). |
| Wilks  | Should we use a Wilks test instead of Roy's largest test? This is only implemented for a single covariate and with estimation = "all".     |

## Details

This is the main function. It computes the PCEV using either the classical method, block approach or singular. A p-value is also computed, testing the significance of the PCEV.

The p-value is computed using either a permutation approach or an exact test. The implemented exact tests use Wilks' Lambda (only for a single covariate) or Roy's Largest Root. The latter uses Johnstone's approximation to the null distribution. Note that for the block approach, only p-values obtained from a permutation procedure are available.

When estimation = "singular", the p-value is computed using a heuristic: using the method of moments and a small number of permutations (i.e. 25), a location-scale family of the Tracy-Widom distribution of order 1 is fitted to the null distribution. This fitted distribution is then used to compute p-values.

When estimation = "block", there are three different ways of specifying the blocks: 1) if index is a vector of the same length as the number of columns in response, then it is used to match each response to a block. 2) If index is a single positive integer, it is understood as the number of blocks, and each response is matched to a block randomly. 3) If index = "adaptive" (the default), the number of blocks is chosen so that there are about  $n/2$  responses per block, and each response is match to a block randomly. All other values of index should result in an error.

## Value

An object of class Pcev containing the first PCEV, the p-value, the estimate of the shrinkage factor, etc.

## See Also

[estimatePcev](#)

## Examples

```
set.seed(12345)
Y <- matrix(rnorm(100*20), nrow=100)
X <- rnorm(100)
pcev_out <- computePCEV(Y, X)
pcev_out2 <- computePCEV(Y, X, shrink = TRUE)
```

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estimatePcev

*Estimation of PCEV*


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## Description

estimatePcev estimates the PCEV.

## Usage

```
estimatePcev(pcevObj, ...)

## Default S3 method:
estimatePcev(pcevObj, ...)

## S3 method for class 'PcevClassical'
estimatePcev(pcevObj, shrink, index, ...)

## S3 method for class 'PcevBlock'
estimatePcev(pcevObj, shrink, index, ...)

## S3 method for class 'PcevSingular'
estimatePcev(pcevObj, shrink, index, ...)
```

## Arguments

|         |                                                                                                                             |
|---------|-----------------------------------------------------------------------------------------------------------------------------|
| pcevObj | A pcev object of class PcevClassical, PcevBlock or PcevSingular                                                             |
| ...     | Extra parameters.                                                                                                           |
| shrink  | Should we use a shrinkage estimate of the residual variance?                                                                |
| index   | If pcevObj is of class PcevBlock, index is a vector describing the block to which individual response variables correspond. |

## Value

A list containing the variance components, the first PCEV, the eigenvalues of  $V_R^{-1}V_M$  and the estimate of the shrinkage parameter  $\rho$

## See Also

[computePCEV](#)

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methylation*Methylation values around BLK gene*

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**Description**

A dataset containing methylation values for cell-separated samples. The methylation was measured using bisulfite sequencing. The data also contains the genomic position of these CpG sites, as well as a binary phenotype (i.e. whether the sample comes from a B cell).

**Usage**`methylation``pheno``position``index``pheno2``position2``methylation2`**Format**

The data comes in four objects:

**methylation** Matrix of methylation values at 5,986 sites measured on 40 samples

**pheno** Vector of phenotype, indicating whether the sample comes from a B cell

**position** Data frame recording the position of each CpG site along the chromosome

**index** Index vector used in the computation of PCEV-block

**methylation2** Matrix of methylation values at 1000 sites measured on 40 samples

**pheno2** Vector of phenotype, indicating the cell type of the sample (B cell, T cell, or Monocyte)

**position2** Data frame recording the position of each CpG site along the chromosome

**Details**

Methylation was first measured at 24,068 sites, on 40 samples. Filtering was performed to keep the 25% most variable sites. See the vignette for more detail.

A second sample of the methylation dataset was extracted. This second dataset contains methylation values at 1000 CpG dinucleotides.

**Source**

Tomi Pastinen, McGill University, Genome Quebec.

PcevObj

*Constructor functions for the different pcev objects***Description**

PcevClassical, PcevBlock and PcevSingular create the pcev objects from the provided data that are necessary to compute the PCEV according to the user's parameters.

**Usage**

```
PcevClassical(response, covariate, confounder)
```

```
PcevBlock(response, covariate, confounder)
```

```
PcevSingular(response, covariate, confounder)
```

**Arguments**

|            |                                         |
|------------|-----------------------------------------|
| response   | A matrix of response variables.         |
| covariate  | A matrix or a data frame of covariates. |
| confounder | A matrix or data frame of confounders   |

**Value**

A pcev object, of the class that corresponds to the estimation method. These objects are lists that contain the data necessary for computation.

**See Also**

[estimatePcev](#), [computePCEV](#)

permutePval

*Permutation p-value***Description**

Computes a p-value using a permutation procedure.

**Usage**

```
permutePval(pcevObj, ...)

## Default S3 method:
permutePval(pcevObj, ...)

## S3 method for class 'PcevClassical'
permutePval(pcevObj, shrink, index, nperm, ...)

## S3 method for class 'PcevBlock'
permutePval(pcevObj, shrink, index, nperm, ...)

## S3 method for class 'PcevSingular'
permutePval(pcevObj, shrink, index, nperm, ...)
```

**Arguments**

|         |                                                                                                                             |
|---------|-----------------------------------------------------------------------------------------------------------------------------|
| pcevObj | A pcev object of class PcevClassical or PcevSingular PcevBlock                                                              |
| ...     | Extra parameters.                                                                                                           |
| shrink  | Should we use a shrinkage estimate of the residual variance?                                                                |
| index   | If pcevObj is of class PcevBlock, index is a vector describing the block to which individual response variables correspond. |
| nperm   | The number of permutations to perform.                                                                                      |

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|          |                                      |
|----------|--------------------------------------|
| roysPval | <i>Roy's largest root exact test</i> |
|----------|--------------------------------------|

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**Description**

In the classical domain of PCEV applicability this function uses Johnstone's approximation to the null distribution of ' Roy's Largest Root statistic. It uses a location-scale variant of the Tracy-Widom distribution of order 1.

**Usage**

```
roysPval(pcevObj, ...)

## Default S3 method:
roysPval(pcevObj, ...)

## S3 method for class 'PcevClassical'
roysPval(pcevObj, shrink, index, ...)

## S3 method for class 'PcevSingular'
roysPval(pcevObj, shrink, index, nperm, ...)
```

```
## S3 method for class 'PcevBlock'
roysPval(pcevObj, shrink, index, ...)
```

### Arguments

|         |                                                                                                                            |
|---------|----------------------------------------------------------------------------------------------------------------------------|
| pcevObj | A pcev object of class PcevClassical or PcevBlock                                                                          |
| ...     | Extra parameters.                                                                                                          |
| shrink  | Should we use a shrinkage estimate of the residual variance?                                                               |
| index   | If pcevObj is of class PcevBlock, index is a vector describing the block to which individual response variables correspond |
| nperm   | Number of permutations for Tracy-Widom empirical estimate.                                                                 |

### Details

Note that if shrink is set to TRUE, the location-scale parameters are estimated using a small number of permutations.

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|           |                                 |
|-----------|---------------------------------|
| wilksPval | <i>Wilks' lambda exact test</i> |
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### Description

Computes a p-value using Wilks' Lambda.

### Usage

```
wilksPval(pcevObj, ...)

## Default S3 method:
wilksPval(pcevObj, ...)

## S3 method for class 'PcevClassical'
wilksPval(pcevObj, shrink, index, ...)

## S3 method for class 'PcevSingular'
wilksPval(pcevObj, shrink, index, ...)

## S3 method for class 'PcevBlock'
wilksPval(pcevObj, shrink, index, ...)
```

### Arguments

|         |                                                                                                                             |
|---------|-----------------------------------------------------------------------------------------------------------------------------|
| pcevObj | A pcev object of class PcevClassical or PcevBlock                                                                           |
| ...     | Extra parameters.                                                                                                           |
| shrink  | Should we use a shrinkage estimate of the residual variance?                                                                |
| index   | If pcevObj is of class PcevBlock, index is a vector describing the block to which individual response variables correspond. |

**Details**

The null distribution of this test statistic is only known in the case of a single covariate, and therefore this is the only case implemented.

# Index

- \* **datasets**
  - methylation, [5](#)
- computePCEV, [2](#), [2](#), [4](#), [6](#)
- estimatePcev, [2](#), [3](#), [4](#), [6](#)
- index (methylation), [5](#)
- methylation, [5](#)
- methylation2 (methylation), [5](#)
- pcev-package, [2](#)
- PcevBlock (PcevObj), [6](#)
- PcevClassical (PcevObj), [6](#)
- PcevObj, [2](#), [6](#)
- PcevSingular (PcevObj), [6](#)
- permutePval, [2](#), [6](#)
- pheno (methylation), [5](#)
- pheno2 (methylation), [5](#)
- position (methylation), [5](#)
- position2 (methylation), [5](#)
- roysPval, [2](#), [7](#)
- wilksPval, [2](#), [8](#)