

# Package ‘epilogi’

October 1, 2023

**Type** Package

**Title** The ‘epilogi’ Variable Selection Algorithm for Continuous Data

**Version** 1.0

**Date** 2023-09-29

**Author** Michail Tsagris [aut, cre]

**Maintainer** Michail Tsagris <mtsagris@uoc.gr>

**Depends** R (>= 4.0)

**Imports** Rfast, stats

**Description** The ‘epilogi’ variable selection algorithm is implemented for the case of continuous response and predictor variables. The relevant paper is: Lakiotaki K., Papadovasilakis Z., Lagani V., Fafalios S., Charonyktakis P., Tsagris M. and Tsamardinos I. (2023). “Automated machine learning for Genome Wide Association Studies”. *Bioinformatics*. <[doi:10.1002/sim.4780120902](https://doi.org/10.1002/sim.4780120902)>.

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2023-10-01 15:30:02 UTC

## R topics documented:

epilogi-package . . . . .	2
epilogi . . . . .	2
pcor.equiv . . . . .	4
<b>Index</b>	<b>6</b>

---

epilogi-package

*The 'epilogi' Variable Selection Algorithm for Continuous Data.*

---

### Description

The 'epilogi' Variable Selection Algorithm for Continuous Data.

### Details

Package: epilogi  
Type: Package  
Version: 1.0  
Date: 2023-09-29  
License: GPL-2

### Maintainers

Michail Tsagris <mtsagris@uoc.gr>.

### Author(s)

Michail Tsagris <mtsagris@uoc.gr>.

### References

Lakiotaki K., Papadovasilakis Z., Lagani V., Fafalios S., Charonyktakis P., Tsagris M. and Tsamardinos I. (2023). Automated machine learning for Genome Wide Association Studies. *Bioinformatics*.

Tsagris M., Papadovasilakis Z., Lakiotaki K. and Tsamardinos I. (2022). The  $\gamma$ -OMP algorithm for feature selection with application to gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2): 1214–1224.

---

epilogi

*The epilogi Variable Selection Algorithm for Continuous Data.*

---

### Description

The epilogi Variable Selection Algorithm for Continuous Data.

### Usage

```
epilogi(y, x, tol = 0.01, alpha = 0.05)
```

**Arguments**

<code>y</code>	A vector with the continuous response variable.
<code>x</code>	A matrix with the continuous predictor variables.
<code>tol</code>	The tolerance value for the algorithm to terminate. This takes values greater than 0 and it refers to the change between two successive $R^2$ -adjusted values.
<code>alpha</code>	The significance level to deem a predictor variable is statistically equivalent to a selected variable.

**Details**

The `epilogi` variable selection algorithm (Lakiotaki et al., 2023) is a generalisation of the  $\gamma$ -OMP algorithm (Tsagris et al. 2022). It applies the aforementioned algorithm with the addition that it returns possible statistically equivalent predictor(s) for each selected predictor. Once a variable is selected the algorithm searches for possible equivalent predictors using the partial correlation between the residuals.

The heuristic method to consider two predictors  $R$  and  $C$  informationally equivalent given the current selected predictor  $S$  is determined as follows: first, the residuals  $r$  of the model using  $S$  are computed. Then, if the following two conditions hold  $R$  and  $C$  are considered equivalent:  $\text{Ind}(R; r \mid C)$  and  $\text{Ind}(r; C \mid R)$ , where  $\text{Ind}(R; r \mid C)$  denotes the conditional independence of  $R$  with  $r$  given  $C$ . When linearity is assumed, the test can be implemented by testing for significance the corresponding partial correlation. The tests  $\text{Ind}$  return a p-value and independence is accepted when it is larger than a threshold (significance value, argument `alpha`). Intuitively,  $R$  and  $C$  are heuristically considered equivalent, if  $C$  is known, then  $R$  provides no additional information for the residuals  $r$ , and if  $R$  is known, then  $C$  provides no additional information for  $r$ .

**Value**

A list including:

<code>runtime</code>	The runtime of the algorithm.
<code>result</code>	A matrix with two columns. The selected predictor(s) and the adjusted $R^2$ -values.
<code>equiv</code>	A list with the equivalent predictors (if any) corresponding to each selected predictor.

**Author(s)**

Michail Tsagris.

R implementation and documentation: Michail Tsagris <mtsagris@uoc.gr>.

**References**

- Lakiotaki K., Papadovasilakis Z., Lagani V., Fafalios S., Charonyktakis P., Tsagris M. and Tsamardinis I. (2023). Automated machine learning for Genome Wide Association Studies. *Bioinformatics*.
- Tsagris M., Papadovasilakis Z., Lakiotaki K. and Tsamardinis I. (2022). The  $\gamma$ -OMP algorithm for feature selection with application to gene expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19(2): 1214–1224.

**See Also**[pcor.equiv](#)**Examples**

```
#simulate a dataset with continuous data
set.seed(1234)
n <- 500
x <- matrix( rnorm(n * 50, 0, 30), ncol = 50 )

#define a simulated class variable
y <- 2 * x[, 1] - 1.5 * x[, 2] + x[, 3] + rnorm(n, 0, 15)

# define some simulated equivalences
x[, 4] <- x[, 1] + rnorm(n, 0, 1)
x[, 5] <- x[, 2] + rnorm(n, 0, 1)

epilogi(y, x, tol = 0.05)
```

---

pcor.equiv

*Equivalence test using partial correlation*

---

**Description**

Equivalence test using partial correlation.

**Usage**

```
pcor.equiv(res, y, x, alpha = 0.05)
```

**Arguments**

res	A vector with the residuals of the linear model.
y	A vector with a selected predictor.
x	A matrix with other predictors.
alpha	The significance level to check for predictors from x that are equivalent to y.

**Value**

A vector with 0s and 1s. 0s indicate that the predictors are not equivalent, while 1s indicate the equivalent predictors.

**Author(s)**

Michail Tsagris.

R implementation and documentation: Michail Tsagris <mtsagris@uoc.gr>.

**See Also**[epilogi](#)**Examples**

```
#simulate a dataset with continuous data
set.seed(1234)
n <- 500
x <- matrix( rnorm(n * 50, 0, 30), ncol = 50 )

#define a simulated class variable
y <- 2 * x[, 1] - 1.5 * x[, 2] + x[, 3] + rnorm(n, 0, 15)

# define some simulated equivalences
x[, 4] <- x[, 1] + rnorm(n, 0, 1)
x[, 5] <- x[, 2] + rnorm(n, 0, 1)

b <- epilogi(y, x, tol = 0.05)
sel <- b$result[2, 1]
## standardise the y and x first
y <- (y - mean(y)) / Rfast::Var(y, std = TRUE)
x <- Rfast::standardise(x)

res <- resid( lm(y ~ x[, sel] ) )
sela <- b$result[2:3, 1]
pcor.equiv(res, x[, sela[2]], x[, -sela] )
## bear in mind that this gives the third variable after removing the first two,
## so this is essentially the 5th variable in the "x" matrix.
```

# Index

epilogi, [2](#), [5](#)

epilogi-package, [2](#)

pcor.equiv, [4](#), [4](#)