

# Package ‘POST’

October 16, 2019

**Type** Package

**Title** Projection onto Orthogonal Space Testing for High Dimensional Data

**Version** 1.8.0

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**Description** Perform orthogonal projection of high dimensional data of a set, and statistical modeling of phenotye with projected vectors as predictor.

**Depends** R (>= 3.4.0)

**Imports** stats, CompQuadForm, Matrix, survival, Biobase, GSEABase

**License** GPL (>= 2)

**biocViews** Microarray, GeneExpression

**LazyLoad** yes

**git\_url** <https://git.bioconductor.org/packages/POST>

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**git\_last\_commit\_date** 2019-05-02

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## R topics documented:

|              |   |
|--------------|---|
| POST-package | 2 |
| POSTcoxph    | 3 |
| POSTglm      | 4 |
| sampExprSet  | 5 |
| sampGeneSet  | 6 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>7</b> |
|--------------|----------|

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POST-package

*Projection onto Orthogonal Space Testing for High Dimensional Data*

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## Description

a tool to identify gene sets that are associated with a endpoint of interest by projecting the original data of a set to an orthogonal subspace.

## Details

Package: POST  
Type: Package  
Version: 0.99.3  
Date: 2016-11-2  
License: GPL (>=2)  
LazyLoad: yes

The POST (Projection onto Orthogonal Space Testing) is performed by calling function *POSTglm* for linear model or *POSTcoxph* for Cox proportional hazard model. The genomic data such as gene expression is passed through ExpressionSet; The gene set definition is defined by a gene set collection.

## Author(s)

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## References

Hotelling H. (1936). Relations between two sets of variables. *Biometrika*, 28, 321-327

## Examples

```
## load data
data(sampExprSet)
data(sampGeneSet)
test<-POSTglm(exprSet=sampExprSet,
              geneSet=sampGeneSet,
              lamda=0.95,
              seed=13,
              nboots=100,
              model='Group ~ ',
              family=binomial(link = "logit"))
```

POSTcoxph

*POST Analysis of Cox Proportional Hazard Model***Description**

Perform POST analysis with Cox proportional hazard model

**Usage**

```
POSTcoxph (exprSet, geneSet, lamda = 0.95, nboots = 100,
           model = "Surv(EFSTIME, EFSCENSOR) ~ strata(arm2)",
           seed = 13, ...)
```

**Arguments**

|         |   |
|---------|---|
| exprSet | an ExpressionSet class contains minimum of exprs (expression matrix) of genomic data such as gene expression and phenoData (AnnotatedDataFrame of end point data). Please refer to Biobase for details on how to create such an ExpressionSet expression set. |
| geneSet | a GeneSetCollection class with minimum of setName and geneIDs for each GeneSet. Please refer to <i>GSEABase</i> for how to create such a GeneSetCollection class.   |
| lamda   | a predefined fraction of 0 to 1: the fraction of variation retained in the selected orthogonal projections  |
| nboots  | number of bootstrap samples, default=100  |
| model   | a character string to define model  |
| seed    | seed of random number generator   |
| ...     | control arguments to be used in Cox propotional hazard model, default control arguments is used if they are not supplied directly   |

**Details**

The function performs POST analysis for association of gene set with time to event endpoint in Cox proportional hazard model framework.

**Value**

a data frame with 5 columns

|         |  |
|---------|--|
| GeneSet | Gene set id  |
| Nprobe  | numbe of probes in the ExpressionSet annotated to the gene set |
| Nproj   | number of projected vectors included in the POST analysis      |
| Stat    | statistic of quadratic form                                    |
| p.value | p value of generalized Chi-square approximation                |

**Author(s)**

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**Examples**

```
## load data
data(sampExprSet)
data(sampGeneSet)
test<-POSTcoxph(exprSet=sampExprSet,
                geneSet=sampGeneSet,
                lamda=0.95,
                seed=13,
                nboots=100,
                model='Surv(time, censor) ~ ')
```

POSTglm

*POST of Generalized Linear Model***Description**

Perform POST analysis with linear model

**Usage**

```
POSTglm (exprSet, geneSet, lamda = 0.95, seed = 13, nboots = 100,
        model = "Group ~ ", family = binomial(link = "logit"), ...)
```

**Arguments**

|         |   |
|---------|---|
| exprSet | an ExpressionSet class contains minimum of exprs (expression matrix) of genomic data such as gene expression and phenoData (AnnotatedDataFrame of end point data). Please refer to Biobase for details on how to create such an ExpressionSet expression set. |
| geneSet | a GeneSetCollection class with minimum of setName and geneIDs for each GeneSet. Please refer to <i>GSEABase</i> for how to create such a GeneSetCollection class.   |
| lamda   | a predefined fraction of 0 to 1: the fraction of variation retained in the selected orthogonal projections  |
| seed    | seed of random number generator   |
| nboots  | number of bootstrap samples, default=100  |
| model   | a character string to define the model  |
| family  | a description of the error distribution and link function to be used in the model. For glm, this can be a character string naming a family function, a family function or the result of a call to a family function.  |
| ...     | control arguments to be passed to generalized linear model, default control argument are used if they are not supplied directly   |

**Details**

The function performs POST analysis for association of gene sets with phenotype in generalized linear model framework.

**Value**

a data frame with 5 columns

|         |  |
|---------|--|
| GeneSet | Gene set id  |
| Nprobe  | numbe of probes in the ExpressionSet annotated to the gene set |
| Nproj   | number of projected vectors included in the POST analysis      |
| Stat    | statistic of quadratic form                                    |
| p.value | p value of generalized Chi-square approximation                |

**Author(s)**

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**Examples**

```
## load data
data(smpExprSet)
data(smpGeneSet)
test<-POSTglm(exprSet=smpExprSet,
              geneSet=smpGeneSet,
              lamda=0.95,
              seed=13,
              nboots=100,
              model='Group ~ ',
              family=binomial(link = "logit"))
```

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|            |                                  |
|------------|----------------------------------|
| smpExprSet | <i>Example of Expression Set</i> |
|------------|----------------------------------|

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**Description**

an ExpressionSet class contains minimum of exprs (expression matrix) of gene expression and phenoData (AnnotatedDataFrame of end point data).

**Usage**

```
data(smpExprSet)
```

**Value**

an simulated ExpressionSet contains conceptual data of 60 expression features for 40 subjects. The phenotype data has 4 columns for the same 40 subjects.

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sampGeneSet

*Example of Expression Set*

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**Description**

a Gene Set Collection contains minimum of GeneSet definition.

**Usage**

```
data(sampGeneSet)
```

**Value**

a gene set collection of 4 gene sets with 60 unique probes

# Index

\*Topic **misc**

sampExprSet, [5](#)

sampGeneSet, [6](#)

\*Topic **package**

POST-package, [2](#)

POST-package, [2](#)

POSTcoxph, [3](#)

POSTglm, [4](#)

sampExprSet, [5](#)

sampGeneSet, [6](#)