

Package ‘ROBRT’

August 9, 2022

Title R package for conducting robust phylogenetic regression

Version 0.0.0.9000

Description ROBRT includes a suite of functions for conducting L1, L2, M, S, and MM regression for phylogenetic data

License `use_mit_license()`, `use_gpl3_license()` or friends to pick a license

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

R topics documented:

Conduct.MatrixTransformation_PGLS	1
Conduct.PhylogeneticRegression_PGLS_L1	2
Conduct.PhylogeneticRegression_PGLS_L2	3
Conduct.PhylogeneticRegression_PGLS_M	4
Conduct.PhylogeneticRegression_PGLS_MM	5
Conduct.PhylogeneticRegression_PGLS_S	6
Conduct.PhylogeneticRegression_PIC_L1	7
Conduct.PhylogeneticRegression_PIC_L2	8
Conduct.PhylogeneticRegression_PIC_M	9
Conduct.PhylogeneticRegression_PIC_MM	10
Conduct.PhylogeneticRegression_PIC_S	11
Conduct.Robust_PhylogeneticRegression	12
Conduct.Robust_PhylogeneticRegression_PGLS	13
Conduct.Robust_PhylogeneticRegression_PIC	14

Conduct.MatrixTransformation_PGLS

Conduct.MatrixTransformation_PGLS: function to compute the phylogenetic transformation matrix that can be used to transform input trait values

Description

This function returns a matrix that can be used to transform input trait values in phylogenetic space

Usage

```
Conduct.MatrixTransformation_PGLS(handle.Phylogeny)
```

Arguments

```
handle.Phylogeny
```

Phylogeny object that is used to generate the matrix.P (phylogenetic transform matrix)

Value

matrix.P Matrix used for phylogenetic transformation of input trait data

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1]

#####
# transform to PGLS #
#####
Conduct.MatrixTransformation_PGLS(handle.Phylogeny = handle.Phylogeny)
```

Conduct.PhylogeneticRegression_PGLS_L1

Conduct.PhylogeneticRegression_PGLS_L1: function to conduct phylogenetic regression using PGLS and L1 estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PGLS_L1(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

`handle.Phylogeny`
Phylogeny object that is used to compute PGLS

`vector.Trait_X` Vector containing values for independent (predictor) trait X

`vector.Trait_Y` Vector containing values for dependant (response) trait y

Value

`handle.PGLS_L1` Object containing results of L1 regression for PGLS

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent

#####
# conduct S phylogenetic regression #
#####
Conduct.PhylogeneticRegression_PGLS_L1(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.TraitVal
```

Conduct.PhylogeneticRegression_PGLS_L2

Conduct.PhylogeneticRegression_PGLS_L2: function to conduct phylogenetic regression using PGLS and L2 estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PGLS_L2(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PGLS

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependant (response) trait y

Value

handle.PGLS_L2 Object containing results of L2 regression for PGLS

Examples

```
#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent

#####
# conduct S phylogenetic regression #
#####
Conduct.PhylogeneticRegression_PGLS_L2(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.TraitVal
```

Conduct.PhylogeneticRegression_PGLS_M

Conduct.PhylogeneticRegression_PGLS_M: function to conduct phylogenetic regression using PGLS and M estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PGLS_M(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PGLS

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependant (response) trait y

Value

handle.PGLS_M Object containing results of M regression for PGLS

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent

#####
# conduct M phylogenetic regression #
#####
Conduct.PhylogeneticRegression_PGLS_MM(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.TraitValue_X, vector.Trait_Y = vector.TraitValue_Y)
```

Conduct.PhylogeneticRegression_PGLS_MM

Conduct.PhylogeneticRegression_PGLS_MM: function to conduct phylogenetic regression using PGLS and MM estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PGLS_MM(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PGLS

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependant (response) trait y

Value

handle.PGLS_MM Object containing results of MM regression for PGLS

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent

#####
# conduct MM phylogenetic regression #
#####
Conduct.PhylogeneticRegression_PGLS_MM(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.TraitVal
```

Conduct.PhylogeneticRegression_PGLS_S

Conduct.PhylogeneticRegression_PGLS_S: function to conduct phylogenetic regression using PGLS and S estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PGLS_S(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PGLS

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependant (response) trait y

Value

handle.PGLS_S Object containing results of S regression for PGLS

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent

#####
# conduct S phylogenetic regression #
#####
Conduct.PhylogeneticRegression_PGLS_S(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.TraitValue_X, vector.Trait_Y = vector.TraitValue_Y)
```

Conduct.PhylogeneticRegression_PIC_L1

Conduct.PhylogeneticRegression_PIC_L1: function to conduct phylogenetic regression using PIC and L1 estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PIC_L1(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PICs

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

Value

handle.PIC_L1 Object containing results of L1 regression for PIC

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(L1pack)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent

#####
# Conduct L1 phylogenetic regression #
#####
summary(Conduct.PhylogeneticRegression_PIC_L1(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.T
```

Conduct.PhylogeneticRegression_PIC_L2

Conduct.PhylogeneticRegression_PIC_L2: function to conduct phylogenetic regression using PIC and L2 estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PIC_L2(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PICs

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependant (response) trait y

Value

handle.PIC_L2 Object containing results of L2 regression for PIC

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent

#####
# Conduct L2 phylogenetic regression #
#####
summary(Conduct.PhylogeneticRegression_PIC_L2(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.T
```

Conduct.PhylogeneticRegression_PIC_M

Conduct.PhylogeneticRegression_PIC_M: function to conduct phylogenetic regression using PIC and M estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PIC_M(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PICs

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

Value

handle.PIC_M Object containing results of M regression for PIC

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent

#####
# Conduct M phylogenetic regression #
#####
summary(Conduct.PhylogeneticRegression_PIC_M(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.Tr

handle.RESULTS_M <- Conduct.PhylogeneticRegression_PIC_M(handle.Phylogeny = handle.Phylogeny, vector.Trait_X
f.robftest(handle.RESULTS_M, var = "vector.PIC_X")$p.value
```

Conduct.PhylogeneticRegression_PIC_MM

Conduct.PhylogeneticRegression_PIC_MM: function to conduct phylogenetic regression using PIC and MM estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PIC_MM(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PICs

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

Value

handle.PIC_MM Object containing results of MM regression for PIC

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent

#####
# conduct MM phylogenetic regression #
#####
summary(Conduct.PhylogeneticRegression_PIC_MM(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.T
```

Conduct.PhylogeneticRegression_PIC_S

Conduct.PhylogeneticRegression_PIC_S: function to conduct phylogenetic regression using PIC and S estimator

Description

This function returns a regression object that can be read using standard R functions (summary, lm, etc.)

Usage

```
Conduct.PhylogeneticRegression_PIC_S(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y
)
```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PICs

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

Value

handle.PIC_S Object containing results of S regression for PIC

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent

#####
# conduct S phylogenetic regression #
#####
summary(Conduct.PhylogeneticRegression_PIC_S(handle.Phylogeny = handle.Phylogeny, vector.Trait_X = vector.Tr
```

Conduct.Robust_PhylogeneticRegression

Conduct.Robust_PhylogeneticRegression: function to conduct robust phylogenetic regression using L2, L1, S, M, and/or MM for PGLS or PIC

Description

This function returns a list of robust phylogenetic regression results for L2, L1, S, M, and/or MM using PGLS or PIC

Usage

```
Conduct.Robust_PhylogeneticRegression(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y,
  vector.Estimators,
  string.Method
)
```

Arguments

handle.Phylogeny Phylogeny object that is used to compute PGLS or PIC

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

vector.Estimators Vector where each element is a string that is "L1", "L2", "S", "M", or "MM"

string.Method String specifying whether "PGLS" or "PIC" for phylogenetic regression

Value

list.RESULTS List containing regression results for each estimator included in vector.Estimators

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,1] # traits are independent
vector.Estimators <- c("L2")

#####
# conduct robust regression #
#####
Conduct.Robust_PhylogeneticRegression(handle.Phylogeny = handle.Phylogeny,
                                     string.Method = "PGLS",
                                     vector.Trait_X = vector.TraitValue_X,
                                     vector.Trait_Y = vector.TraitValue_Y,
                                     vector.Estimators = vector.Estimators)

Conduct.Robust_PhylogeneticRegression(handle.Phylogeny = handle.Phylogeny,
                                     string.Method = "PIC",
                                     vector.Trait_X = vector.TraitValue_X,
                                     vector.Trait_Y = vector.TraitValue_Y,
                                     vector.Estimators = vector.Estimators)
```

Conduct.Robust_PhylogeneticRegression_PGLS

Conduct.Robust_PhylogeneticRegression_PGLS: function to conduct robust phylogenetic regression using L2, L1, S, M, and/or MM

Description

This function returns a list of robust phylogenetic regression results for L2, L1, S, M, and/or MM

Usage

```
Conduct.Robust_PhylogeneticRegression_PGLS(
  handle.Phylogeny,
```

```

    vector.Trait_X,
    vector.Trait_Y,
    vector.Estimators
  )

```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PGLS

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

vector.Estimators
Vector where each element is a string that is "L1", "L2", "S", "M", or "MM"

Value

list.RESULTS List containing regression results for each estimator included in vector.Estimators

Conduct.Robust_PhylogeneticRegression_PIC

Conduct.Robust_PhylogeneticRegression_PIC: function to conduct robust phylogenetic regression using L2, L1, S, M, and/or MM

Description

This function returns a list of robust phylogenetic regression results for L2, L1, S, M, and/or MM

Usage

```

Conduct.Robust_PhylogeneticRegression_PIC(
  handle.Phylogeny,
  vector.Trait_X,
  vector.Trait_Y,
  vector.Estimators
)

```

Arguments

handle.Phylogeny
Phylogeny object that is used to compute PICs

vector.Trait_X Vector containing values for independent (predictor) trait X

vector.Trait_Y Vector containing values for dependent (response) trait y

vector.Estimators
Vector where each element is a string that is "L1", "L2", "S", "M", or "MM"

Value

list.RESULTS List containing regression results for each estimator included in vector.Estimators

Examples

```
#####
# load depends #
#####
library(geiger)
library(ROBRT)
library(phytools)
library(MASS)
library(L1pack)
library(robust)

#####
# simulate tree and trait data #
#####
handle.Phylogeny <- sim.bdtree(b = 1, n = 10)
vector.TraitValue_X <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent
vector.TraitValue_Y <- sim.char(handle.Phylogeny, par=1, model="BM", root=0)[,,1] # traits are independent
vector.Estimators <- c("L2", "L1", "M", "MM", "S")

#####
# conduct S phylogenetic regression #
#####
handle.RESULTS_PIC <- Conduct.Robust_PhylogeneticRegression_PIC(handle.Phylogeny = handle.Phylogeny,
                                                                vector.Trait_X = vector.TraitValue_X,
                                                                vector.Trait_Y = vector.TraitValue_Y,
                                                                vector.Estimators = vector.Estimators)
```