Package ‘SRMERS’

January 13, 2026

Type Package

Title Semi-Parametric Shape-Restricted Fixed/Mixed Effect(s) Regression Spline

Version 0.1.1

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Imports splines2, stats, lme4, nloptr, dplyr, MASS, coneproj, Matrix

Description Select the most suitable shape to describe the relationship between the exposure and the outcome among increasing, decreasing, convex, and concave shapes (Yin et al. (2021) <DOI:10.1007/s13571-020-00246-7>); estimate the direct and indirect effects with prior knowledge on the relationship between the mediator and the outcome with binary exposure (Yin et al. (2024) <DOI:10.1007/s13571-024-00336-w>); estimate the direct and indirect effects using linear regression-based approach (VanderWeele (2015, ISBN:9780199325870)).

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

Depends R (>= 4.4.0)

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-01-13 18:30:07 UTC

Contents

`data.sim.fixed` *Simulated dataset for SRMERS FERS example*

Description

Simulated dataset for SRMERS FERS example

Usage

```
data(data.sim.fixed)
```

Format

A dataframe with 245 rows and 14 variables

hormone continuous variable (main x)

age continuous variable (confounder x)

invwt continuous variable (confounder x)

race2 binary variable (confounder x)

race3 binary variable (confounder x)

race4 binary variable (confounder x)

race5 binary variable (confounder x)

season2 binary variable (confounder x)

season3 binary variable (confounder x)

season4 binary variable (confounder x)

smoking1 binary variable (confounder x)

ovum1 binary variable (confounder x)

diabetes1 binary variable (confounder x)

ySim continuous varible (y)

`data.sim.fixed.int` *Simulated dataset for SRMERS FERSInt example*

Description

Simulated dataset for SRMERS FERSInt example

Usage

```
data(data.sim.fixed.int)
```

Format

A dataframe with 500 rows and 15 variables

hormone	continuous variable (mediator)
age	continuous variable (confounder x)
invwt	continuous variable (confounder x)
race2	binary variable (confounder x)
race3	binary variable (confounder x)
race4	binary variable (confounder x)
race5	binary variable (confounder x)
season2	binary variable (confounder x)
season3	binary variable (confounder x)
season4	binary variable (confounder x)
smoking1	binary variable (confounder x)
ovum1	binary variable (confounder x)
diabetes1	binary variable (confounder x)
pesticide1	binary variable (exposure)
ySim	continuous varible (y)

`data.sim.med` *Simulated dataset for SRMERS SRSplineMed, LRMed, LRMed2 example*

Description

Simulated dataset for SRMERS SRSplineMed, LRMed, LRMed2 example

Usage

```
data(data.sim.med)
```

Format

A dataframe with 500 rows and 16 variables

hormone continuous variable (mediator)

age continuous variable (confounder x)

invwt continuous variable (confounder x)

race2 binary variable (confounder x)

race3 binary variable (confounder x)

race4 binary variable (confounder x)

race5 binary variable (confounder x)

season2 binary variable (confounder x)

season3 binary variable (confounder x)

season4 binary variable (confounder x)

smoking1 binary variable (confounder x)

ovum1 binary variable (confounder x)

diabetes1 binary variable (confounder x)

pesticide1 binary variable (exposure)

ySim continuous varible (y)

pesticideCont continuous variable (exposure)

`data.sim.mixed` *Simulated dataset for SRMERS MERS example*

Description

Simulated dataset for SRMERS MERS example

Usage

```
data(data.sim.mixed)
```

Format

A dataframe with 245 rows and 15 variables

cluster categorical variable (random factor)

hormone continuous variable (main x)

age continuous variable (confounder x)

invwt continuous variable (confounder x)

race2 binary variable (confounder x)

race3 binary variable (confounder x)

race4 binary variable (confounder x)

race5 binary variable (confounder x)

season2 binary variable (confounder x)

season3 binary variable (confounder x)

season4 binary variable (confounder x)

smoking1 binary variable (confounder x)

ovum1 binary variable (confounder x)

diabetes1 binary variable (confounder x)

ySim continuous varible (y)

`FERS` *P values for shapes obtained from semi-parametric shape-restricted fixed effect regression splines.*

Description

P values for shapes obtained from semi-parametric shape-restricted fixed effect regression splines.

Usage

```
FERS(
  y,
  xMain,
  xConf = NULL,
  dataset,
  knotType = 2,
  preKnot = NULL,
  nBasis = 5,
  nIter
)
```

Arguments

`y`	The name of the outcome.
`xMain`	The name of the main effect.
`xConf`	The name vector of the confounders.
`dataset`	A data frame.
`knotType`	The knot type: 1=equal-spaced, 2=quantile, 3=pre-specified.
`preKnot`	The pre-specified knots.
`nBasis`	The number of bases.
`nIter`	The number of iterations.

Value

A list of weights of beta distribution and p-values.

Examples

```
shape <- FERS(y = "ySim", xMain = "hormone",
              xConf = c("age", "invwt", "race2", "race3", "race4", "race5",
                     "season2", "season3", "season4", "smoking1", "ovum1", "diabetes1"),
              dataset = data.sim.fixed, nBasis = 5, nIter = 50)
shape
```

`FERSInt` *P values for shapes obtained from semi-parametric shape-restricted fixed effect regression splines with factor-by-curve interaction.*

Description

P values for shapes obtained from semi-parametric shape-restricted fixed effect regression splines with factor-by-curve interaction.

Usage

```
FERSInt(
  y,
  xExp,
  xMed,
  xConf = NULL,
  dataset,
  knotType = 2,
  preKnot = NULL,
  nBasis = 5,
  nIter
)
```

Arguments

`y`	The name of the outcome.
`xExp`	The name of the exposure (must be a binary variable).
`xMed`	The name of the mediator (must be a continuous variable).
`xConf`	The name vector of the confounders.
`dataset`	A data frame.
`knotType`	The knot type: 1=equal-spaced, 2=quantile, 3=pre-specified.
`preKnot`	The pre-specified knots.
`nBasis`	The number of bases.
`nIter`	The number of iterations.

Value

A list of weights of beta distribution and p-values for both exposure groups.

Note

This function has not been validated through simulation studies. Please use with caution. shape <- FERSInt(y = "ySim", xExp = "pesticide1", xMed = "hormone", xConf = c("pesticide1", "age", "invwt", "race2", "race3", "race4", "race5", "season2", "season3", "season4", "smoking1", "ovum1", "diabetes1"), dataset = data.sim.fixed.int, nBasis = 5, nIter = 50) shape

---

`LRMed` *Calculate the CDE, NDE and NIE (linear models, binary exposure).*

Description

Calculate the CDE, NDE and NIE (linear models, binary exposure).

Usage

```
LRMed(data, exposure, mediator, outcome, confounderVec, mValue)
```

Arguments

`data`	A data frame.
`exposure`	The name of the exposure (must be a binary variable).
`mediator`	The name of the mediator (must be a continuous variable).
`outcome`	The name of the outcome (must be a continuous variable).
`confounderVec`	The name vector of the confounders.
`mValue`	The controlled mediator value for CDE estimation.

Value

A list of exposure-outcome model, exposure-mediator model, CDE, NDE and NIE and their asymptotic variances.

Examples

```
medModel <- LRMed(data = data.sim.med,
                  exposure = "pesticide1", mediator = "hormone", outcome = "ySim",
                  confounderVec = c("age", "invwt", "race2", "race3", "race4", "race5",
                                    "season2", "season3", "season4", "smoking1", "ovum1",
                                     "diabetes1"),
                  mValue = 0.15)
medModel
```

`LRMed2` *Calculate the CDE, NDE and NIE (linear models, continuous exposure).*

Description

Calculate the CDE, NDE and NIE (linear models, continuous exposure).

Usage

```
LRMed2(
  data,
  exposure,
  mediator,
  outcome,
  confounderVec,
  mValue,
  eValueLow,
  eValueHigh
)
```

Arguments

`data`	A data frame.
`exposure`	The name of the exposure (must be a continuous variable).
`mediator`	The name of the mediator (must be a continuous variable).
`outcome`	The name of the outcome (must be a continuous variable).
`confounderVec`	The name vector of the confounders.
`mValue`	The controlled mediator value for CDE estimation.
`eValueLow`	The low reference level of exposure.
`eValueHigh`	The high reference level of exposure.

Value

A list of exposure-outcome model, exposure-mediator model, CDE, NDE and NIE and their asymptotic variances.

Examples

```
medModel <- LRMed2(data = data.sim.med,
                   exposure = "pesticideCont", mediator = "hormone", outcome = "ySim",
                   confounderVec = c("age", "invwt", "race2", "race3", "race4", "race5",
                                   "season2", "season3", "season4", "smoking1", "ovum1",
                                     "diabetes1"),
                   mValue = 0.15, eValueLow = 0.1, eValueHigh = 1.1)
medModel
```

`MERS` *P values for shapes obtained from semi-parametric shape-restricted mixed effects regression splines.*

Description

P values for shapes obtained from semi-parametric shape-restricted mixed effects regression splines.

Usage

```
MERS(
  y,
  xMain,
  xConf = NULL,
  xRand,
  dataset,
  knotType = 2,
  preKnot = NULL,
  nBasis = 5,
  nIter
)
```

Arguments

`y`	The name of the outcome.
`xMain`	The name of the main effect.
`xConf`	The name vector of the confounders.
`xRand`	The name of the random effect.
`dataset`	A data frame.
`knotType`	The knot type: 1=equal-spaced, 2=quantile, 3=pre-specified.
`preKnot`	The pre-specified knots.
`nBasis`	The number of bases.
`nIter`	The number of iterations.

Value

A list of weights of beta distribution and p-values.

Examples

```
shape <- MERS(y = "ySim", xMain = "hormone",
             xConf = c("age", "invwt", "race2", "race3", "race4", "race5",
                    "season2", "season3", "season4", "smoking1", "ovum1", "diabetes1"),
             xRand = "cluster",
             dataset = data.sim.mixed, nBasis = 5, nIter = 50)
shape
```

SRSplineMed *Calculate the CDE, NDE and NIE.*

Description

Calculate the CDE, NDE and NIE.

Usage

```
SRSplineMed(
  data,
  nBasis,
  exposure,
  mediator,
  outcome,
  confounderVec,
  shapeExp,
  shapeNonExp,
  mValue,
  varAsymp = FALSE
)
```

Arguments

`data`	A data frame.
`nBasis`	The number of bases.
`exposure`	The name of the exposure (must be a binary variable).
`mediator`	The name of the mediator (must be a continuous variable).
`outcome`	The name of the outcome (must be a continuous variable).
`confounderVec`	The name vector of the confounders.
`shapeExp`	The shape of mediator in exposure group ("increasing", "decreasing", "convex", or "concave").
`shapeNonExp`	The shape of mediator in non-exposure group ("increasing", "decreasing", "convex", or "concave").
`mValue`	The controlled mediator value for CDE estimation.
`varAsymp`	Whether to output the asymptotic variance (T/F)

Value

A list of exposure-outcome model, exposure-mediator model, knot sequence, coefficient vector of exposure spline, coefficient vector of non-exposure spline, residuals, sds and coefficients, CDE, NDE and NIE and their asymptotic variances.

Examples

```
medModel <- SRSplineMed(data = data.sim.med, nBasis = 5,
                        exposure = "pesticide1", mediator = "hormone", outcome = "ySim",
                    confounderVec = c("age", "invwt", "race2", "race3", "race4", "race5",
                                      "season2", "season3", "season4", "smoking1", "ovum1",
                                             "diabetes1"),
                        shapeExp = "concave", shapeNonExp = "increasing", mValue = 0.15,
                        varAsymp = TRUE)
medModel
```

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