

Package ‘CompMix’

July 21, 2025

Type Package

Title A Comprehensive Toolkit for Environmental Mixtures Analysis
(‘CompMix’)

Version 0.1.0

Description Quantitative characterization of the health impacts associated with exposure to chemical mixtures has received considerable attention in current environmental and epidemiological studies. ‘CompMix’ package allows practitioners to estimate the health impacts from exposure to chemical mixtures data through various statistical approaches, including Lasso, Elastic net, Bayesian kernel machine regression (BKMR), hierNet, Quantile g-computation, Weighted quantile sum (WQS) and Random forest. Hao W, Cathey A, Aung M, Boss J, Meeker J, Mukherjee B. (2024) “Statistical methods for chemical mixtures: a practitioners guide”. <[DOI:10.1101/2024.03.03.24303677](https://doi.org/10.1101/2024.03.03.24303677)>.

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Imports Matrix, mvtnorm, gglasso, higglasso, hierNet, glmnet,
SuperLearner, bkmr, qqcomp, gWQS, pROC, randomForest, devtools

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NeedsCompilation no

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Description

A comprehensive toolkit for environmental mixtures analysis

Usage

```
Comp.Mix(
  y,
  x,
  z = NULL,
  y.type,
  test.pct = 0.5,
  var.select = NULL,
  interaction = NULL,
  interaction.exp.cov = NULL,
  covariates.forcein = NULL,
  bkmr.pip = 0.5,
  bkmr.iter = 500,
  formula = NULL,
  expnms = NULL,
  seed = 1234,
  verbose = TRUE
)
```

Arguments

| | |
|---------------------|---|
| y | A vector of either continuous or binary values to indicate the health outcome |
| x | A matrix of numeric values to indicate the chemical mixtures |
| z | A matrix of numeric values to indicate the covariates |
| y.type | A character value of either "continuous" or "binary" |
| test.pct | A numeric scalar between 0 and 1 to indicate the proportion allocated as test samples |
| var.select | A logical value to indicate whether to perform variable selection |
| interaction | A logical value (TRUE/FALSE) to indicate whether to include pairwise interaction terms between all the chemical mixtures x |
| interaction.exp.cov | A logical value (TRUE/FALSE) to indicate whether to include pairwise interaction terms between all the chemical mixtures x and covariates z. If interaction.exp.cov=TRUE, interaction=TURE or interaction=FALSE will be ignored |
| covariates.forcein | A logical value (TRUE/FALSE) to indicate whether to force in any covariates |

| | |
|------------------------|---|
| <code>bkmr.pip</code> | A numeric scalar between 0 and 1 to indicate the cutoff for the posterior inclusion probability in BKMR |
| <code>bkmr.iter</code> | A positive integer to indicate the number of MCMC iterations for bkmr |
| <code>formula</code> | the formula for qgcomp and wqs |
| <code>exnms</code> | a vector of characters for names of exposure variables |
| <code>seed</code> | an integer value for seed |
| <code>verbose</code> | a logical value to show information |

Value

A list object which may contain up to 8 cases

Case 1 variable selection on main effects for exposures and confounders

Each case may contain some of the following elements

betaest a numeric vector of coefficients for the exposures

z_betaest a numeric vector of coefficients for the covariates

sse A positive scalar to indicate sum of squares error

corr A numeric scalar between -1 and 1 to indicate correlation coefficient

Author(s)

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Examples

```
dat <- lmi_simul_dat(n=1000,p=20,q=5,
  block_idx=c(1,1,2,2,3,1,1,1,1,1,2,2,2,2,3,3,3,3,3,3),
  within_rho=0.6,btw_rho=0.1,R2=0.2,
  effect_size=1,effect_size_i=1,
  cancel_effect = FALSE)
#Example 1: The users would like to perform variable selections
#on main effects of exposures and covariates, and outcome, exposures and
#covariates are entered. For any individual interactions that the users would
#like to include in the models, they can add those into the covariate z.
res_ex1 <- Comp.Mix(y.type="continuous",y=dat$y, x=dat$x, z=dat$z, test.pct=0.5,
  var.select = TRUE, interaction = FALSE, interaction.exp.cov = FALSE,
  covariates.forcein = FALSE,
  bkmr.pip=0.5, seed=2023)
```

lmi_simul_dat

*Simulate data from linear model with interactions***Description**

Simulate data from linear model with interactions

Usage

```
lmi_simul_dat(
  n,
  p,
  q,
  block_idx = c(1, 1, 2, 2, 3, 1, 1, 1, 1, 1, 2, 2, 2, 2, 3, 3, 3, 3, 3, 3),
  sigma2_x = 1,
  within_rho = 0.6,
  btw_rho = 0.2,
  R2 = 0.8,
  effect_size = 1,
  effect_size_i = 1,
  cancel_effect = TRUE
)
```

Arguments

| | |
|---------------|---|
| n | a positive integer to indicate sample size |
| p | a positive integer to specify the number of exposures |
| q | a positive integer to specify the number of non-zero effects |
| block_idx | a vector of positive integers to indicate the block IDs. The length of the vector is p. |
| sigma2_x | a positive numeric scalar for variance of the covariates |
| within_rho | a numeric scalar between 0 and 1 for the within block correlation |
| btw_rho | a numeric scalar between 0 and 1 for the between block correlation |
| R2 | a numeric scalar for R-squared |
| effect_size | a numeric scalar for effect size for main effect |
| effect_size_i | a numeric scalar for effect size for interaction effect |
| cancel_effect | a logic value to indicate whether there is effect cancelation |

Value

a list object of the following

x covariate matrix of dimension n by p

n sample size

p number of covariates
sigma2_x variance
within_rho within block correlation
btw_rho between block correlation
block_idx block indices

Author(s)

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| | |
|---------------|---|
| simul_x_block | <i>Simulate covariate matrix with block structure</i> |
|---------------|---|

Description

Simulate covariate matrix with block structure

Usage

```
simul_x_block(n, p, block_idx, sigma2_x = 1, within_rho = 0.6, btw_rho = 0.2)
```

Arguments

n a positive integer to indicate sample size
p a positive integer to specify the number of covariates
block_idx a vector of positive integers to indicate the block IDs. The length of the vector is p.
sigma2_x a positive numeric scalar for variance of the covariates
within_rho a numeric scalar between 0 and 1 for the within block correlation
btw_rho a numeric scalar between 0 and 1 for the between block correlation

Value

a list object of the following

- x** covariate matrix of dimension n by p
- n** sample size
- p** number of covariates
- sigma2_x** variance
- within_rho** within block correlation
- btw_rho** between block correlation
- block_idx** block indices

Author(s)

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Examples

```
dat <- simul_x_block(n = 1000, p = 10, block_idx = rep(1:4,length=10))
```

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