

Package: CompMix (via r-universe)

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Type Package

Title A Comprehensive Toolkit for Environmental Mixtures Analysis

Version 1.1.0

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. Methods and recommendations are described in Hao et al. (2025) <[doi:10.1289/EHP15305](https://doi.org/10.1289/EHP15305)>.

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Imports Matrix, mvtnorm, hierNet, glmnet, SuperLearner, bkmr, qgcomp, gWQS, pROC, randomForest

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Comp.Mix	<i>A comprehensive toolkit for environmental mixtures analysis</i>
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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,  
  sl.validation = 0.4,  
  sl.rep = 5,  
  sl.max_iter = 1000,  
  sl.tol = 1e-05,  
  formula = NULL,  
  expnms = NULL,  
  seed = 1234,  
  verbose = TRUE  
)
```

Arguments

y	A vector of either continuous or binary values specifying the health outcome
x	A matrix of numeric values specifying the chemical mixtures
z	A matrix of numeric values specifying the covariates
y.type	A character value of either "continuous" or "binary"
test.pct	A numeric scalar between 0 and 1 specifying the proportion allocated as test samples

<code>var.select</code>	A logical value to indicate whether to perform variable selection
<code>interaction</code>	A logical value (TRUE/FALSE) specifying whether to include pairwise interaction terms between all the chemical mixtures x
<code>interaction.exp.cov</code>	A logical value (TRUE/FALSE) specifying whether to include pairwise interaction terms between all the chemical mixtures x and covariates z . If <code>interaction.exp.cov=TRUE</code> , <code>interaction=TURE</code> or <code>interaction=FALSE</code> will be ignored
<code>covariates.forcein</code>	A logical value (TRUE/FALSE) specifying whether to force in any covariates
<code>bkmr.pip</code>	A numeric scalar between 0 and 1 specifying the cutoff for the posterior inclusion probability in BKMR
<code>bkmr.iter</code>	A positive integer specifying the number of MCMC iterations for bkmr
<code>sl.validation</code>	A positive proportion specifying the fraction of data used for validation when estimating Super Learner weights
<code>sl.rep</code>	A positive integer specifying the number of replicates used when estimating Super Learner weights
<code>sl.max_iter</code>	A positive integer specifying the maximum number of iterations allowed when estimating Super Learner weights
<code>sl.tol</code>	A positive numeric value specifying the convergence tolerance when estimating Super Learner weight
<code>formula</code>	the formula for <code>qgcomp</code> and <code>wqs</code>
<code>expnms</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

<code>within_rho</code>	a numeric scalar between 0 and 1 for the within block correlation
<code>btw_rho</code>	a numeric scalar between 0 and 1 for the between block correlation
<code>R2</code>	a numeric scalar for R-squared
<code>effect_size</code>	a numeric scalar for effect size for main effect
<code>effect_size_i</code>	a numeric scalar for effect size for interaction effect
<code>cancel_effect</code>	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)

Wei Hao <weihao@umich.edu>

<code>simul_x_block</code>	<i>Simulate covariate matrix with block structure</i>
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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

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

Wei Hao <weihao@umich.edu>

Examples

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

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