

# Package ‘HomUHet’

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**Title** Identifying and Separating Homogeneous and Heterogeneous Predictors

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**Depends** glmnet, gglasso, dplyr, R (>= 4.0.3)

**Imports** mvtnorm, stats

**Description** This package contains functions to identify and separate predictors with homogeneous or heterogeneous effects across datasets.

**License** GPL (>=3)

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

## R topics documented:

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HomUHet	<i>fit a two-step penalized regression model</i>
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### Description

This function outputs the names of predictors with homogeneous or heterogeneous predictors across multiple data sets, the estimates of predictors, and solution plots

### Usage

```
HomUHet(data, solution_path_plot = FALSE)
```

### Arguments

data	The input dataframe containing observations from all studies where the first column is the study label, the second column is the response variable and the following columns are the predictors.
solution_path_plot	TRUE if outputting solution path plots is desired

### Value

	the names of identified predictors and their estimated effects
Homo	a character string of names of homogeneous predictors
Heter	a character string of N=names of heterogeneous predictors
coefficients	a data frame containing estimated coefficients of the homogeneous and heterogeneous predictors in K studies

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HomUHet.sim	<i>simulate multiple data sets with both homogeneous and heterogeneous effects from the predictors</i>
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### Description

this function simulate data

### Usage

```
HomUHet.sim(
  Pred_type = c("Gaussian", "SNP"),
  J,
  K,
  beta = NULL,
  rho = 0.5,
  sigma = 2,
  level = c("l", "m", "e"),
  nlower = 50,
  nupper = 300,
  allele_freq
)
```

**Arguments**

Pred_type	the predictor type; choose between Gaussian or SNP
J	the number of predictors.
K	the number of studies.
beta	the K x J coefficient matrix
rho	a number between 0 and 1. controlling the degree of correlation between predictors
sigma	a positive number. controlling the added noise to the simulated response variable
level	the level of heterogeneity. ignored if "beta" is supplied. "l" stands for low, "m" stands for medium, and "h" stands for high.
nlower	the lower bound of the K sample sizes
nupper	the upper bound of the K sample sizes
allele_freq	a J-length vector containing the allele frequencies for the J SNPs. ignored if Pred_type="Gaussian"

**Value**

the simulated data

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HomUHet_data	<i>simulated data to be used as demonstration for HomUHet package</i>
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**Description**

A dataset containing observations of 4 studies and 500 predictors

**Usage**

```
HomUHet_data
```

**Format**

A data frame with 444 rows and 502 variables:

**Study\_label** integers indicating the study number

**y** the response variable ...

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