

Package: HhP (via r-universe)

August 27, 2024

Title Hierarchical Heterogeneity Analysis via Penalization

Version 1.0.0

Description In medical research, supervised heterogeneity analysis has important implications. Assume that there are two types of features. Using both types of features, our goal is to conduct the first supervised heterogeneity analysis that satisfies a hierarchical structure. That is, the first type of features defines a rough structure, and the second type defines a nested and more refined structure. A penalization approach is developed, which has been motivated by but differs significantly from penalized fusion and sparse group penalization. Reference: Ren, M., Zhang, Q., Zhang, S., Zhong, T., Huang, J. & Ma, S. (2022). "Hierarchical cancer heterogeneity analysis based on histopathological imaging features". *Biometrics*, <[doi:10.1111/biom.13426](https://doi.org/10.1111/biom.13426)>.

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Encoding UTF-8

Imports MASS, Matrix, fmrs, methods

LazyData true

LazyLoad yes

RoxygenNote 7.1.2

Depends R (>= 3.5.0)

Suggests knitr, rmarkdown

VignetteBuilder knitr, rmarkdown

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-11-23 11:30:11 UTC

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evaluation.sum	<i>Hierarchical Heterogeneity Regression Analysis.</i>
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Description

The main function for Transfer learning for tensor graphical models.

Usage

```
evaluation.sum(n,q,p,admmres, abic.n, admmres2, Beta0, bic.var)
```

Arguments

n	The sample size.
q	The dimension of type 1 features.
p	The dimension of type 2 features.
admmres	The results corresponding to lambda1.
abic.n	The BIC values.
admmres2	The results corresponding to lambda1.
Beta0	The true values of beta.
bic.var	The BIC values.

Value

A result list including: evaluating indicator

`example.data.GGM`

Some example data

Description

Some example data

Format

A list.

Source

Simulated data

Examples

```
data(example.data.GGM)
```

`example.data.reg`

Some example data

Description

Some example data

Format

A list.

Source

Simulated data

Examples

```
data(example.data.reg)
```

genelambda.obo *Generate tuning parameters*

Description

Generating a sequence of the tuning parameters (lambda1 and lambda2).

Usage

```
genelambda.obo(nlambda1=20, lambda1_max=0.5, lambda1_min=0.1,
               nlambda2=5, lambda2_max=1.5, lambda2_min=0.1)
```

Arguments

nlambda1	The numbers of lambda 1.
lambda1_max	The maximum values of lambda 1.
lambda1_min	The minimum values of lambda 1.
nlambda2	The numbers of lambda 2.
lambda2_max	The maximum values of lambda 2.
lambda2_min	The minimum values of lambda 2.

Value

A sequence of the tuning parameters (lambda1, lambda2, and lambda3).

Author(s)

Mingyang Ren

Examples

```
lambda <- genelambda.obo()
lambda
```

gen_int_beta *Hierarchical Heterogeneity Regression Analysis.*

Description

The main function for Transfer learning for tensor graphical models.

Usage

```
gen_int_beta(n, p, q, whole.data, subgroup=c(2,4),
             ridge = FALSE, gr.init=10, lambda.min=0.0001)
```

Arguments

n	The sample size.
p	The dimension of type 2 features.
q	The dimension of type 1 features.
whole.data	The input data analyzed (a list including the response and design matrix).
subgroup	When using fmrs to generate initial value, the initial value parameter of fmrs is given. Randomly divide this number of groups into several groups.
ridge	The logical variable, whether or not to yield initial values using ridge regression.
gr.init	The subgroup number of initial values using ridge regression.
lambda.min	The tuning parameter using ridge regression, the default is 0.0001.

Value

A result list.

Author(s)

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References

Mingyang Ren, Qingzhao Zhang, Sanguo Zhang, Tingyan Zhong, Jian Huang, Shuangge Ma. 2022. Hierarchical Cancer Heterogeneity Analysis Based On Histopathological Imaging Features. *Bio-metrics*, <DOI: 10.1111/biom.13544>.

Examples

```
library(HhP)
library(Matrix)
library(MASS)
library(fmrs)
data(example.data.reg)
n = example.data.reg$n
q = example.data.reg$q
p = example.data.reg$p

beta.init.list = gen_int_beta(n, p, q, example.data.reg)
beta.init = beta.init.list$beta.init
lambda = genelambda.obo()
result = HhP.reg(lambda, example.data.reg, n, q, p, beta.init)
index.list = evaluation.sum(n,q,p, result$admmres, result$ablc.n,
                           result$admmres2, example.data.reg$Beta0, result$bic.var)
index.list$err.s
```

HhP.reg

Hierarchical Heterogeneity Regression Analysis.

Description

The main function for Transfer learning for tensor graphical models.

Usage

```
HhP.reg(lambda, whole.data, n, q, p, beta.init,  
        merge.all=FALSE, trace=FALSE, selection.sub=FALSE)
```

Arguments

lambda	The sequences of the tuning parameters (lambda1 and lambda2).
whole.data	The input data analyzed (a list including the response and design matrix).
n	The sample size.
q	The dimension of type 1 features.
p	The dimension of type 2 features.
beta.init	The Initial values of regression coefficients.
merge.all	the logical variable, the default is F.
trace	the logical variable, whether or not to output the number of identified subgroups during the search for parameters.
selection.sub	the logical variable, the default is F.

Value

A result list.

Author(s)

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References

Mingyang Ren, Qingzhao Zhang, Sanguo Zhang, Tingyan Zhong, Jian Huang, Shuangge Ma. 2022. Hierarchical Cancer Heterogeneity Analysis Based On Histopathological Imaging Features. *Bio-metrics*, <DOI: 10.1111/biom.13544>.

Examples

```
library(HhP)
library(Matrix)
library(MASS)
library(fmrs)
data(example.data.reg)
n = example.data.reg$n
q = example.data.reg$q
p = example.data.reg$p

beta.init.list = gen_int_beta(n, p, q, example.data.reg)
beta.init = beta.init.list$beta.init
lambda = genelambda.obo()
result = HhP.reg(lambda, example.data.reg, n, q, p, beta.init)
index.list = evaluation.sum(n,q,p, result$admmres, result$abic.n,
                             result$admmres2, example.data.reg$Beta0, result$bic.var)
index.list$err.s
```

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