

Package ‘EMSHS’

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Type Package

Title EM Algorithm for Bayesian Shrinkage Approach with Structural Information Incorporated

Version 1.0.0

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Description Fits a Bayesian shrinkage regression model that can incorporate structural information. Changgee Chang, Suprateek Kundu, Qi Long (2018) <doi:10.1111/biom.12882>.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Imports Rdpack

RdMacros Rdpack

NeedsCompilation no

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

Repository CRAN

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EMSHS	<i>EM Estimator for Bayesian Shrinkage approach with Structural Information incorporated</i>
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Description

EMSHS implements the EM algorithm for Bayesian shrinkage approach that incorporates structural information. Users are referred to Chang et al (2018).

Usage

```
EMSHS(y, X, mus, nu, E = NULL, a_sigma = 1, b_sigma = 1, a_omega = 2,
      b_omega = 1, w = 1, eps = 1e-05)
```

Arguments

<code>y</code>	An n by 1 response vector
<code>X</code>	An n by p design matrix
<code>mus</code>	A vector of shrinkage parameters
<code>nu</code>	The adaptivity parameter
<code>E</code>	An e by 2 matrix with edges. Edges must be sorted by the first column and then the second column. A single edge (j,k) must be duplicated with (k,j) in E. NULL if no edge.
<code>a_sigma</code>	The shape parameter of the prior for residual variance.
<code>b_sigma</code>	The rate parameter of the prior for residual variance.
<code>a_omega</code>	The shape parameter of the prior for nonzero omega values.
<code>b_omega</code>	The rate parameter of the prior for nonzero omega values.
<code>w</code>	A weight vector for samples.
<code>eps</code>	The algorithm stops if relative improvement goes below eps.

Value

A list that contains the number of EM iterations (`niter`), the estimated coefficients (`beta`), the estimated residual variance (`sigma`), the estimated shrinkage parameter (`lambda`), and the imputed correlations for the shrinkage parameter (`omega`) is returned.

References

Chang C, Kundu S, Long Q (2018). “Scalable Bayesian Variable Selection for Structured High-dimensional Data.” *Biometrics*.


```
31,22,
22,31,
22,45,
45,22,
45,32,
32,45,
22,21,
21,22,
31,21,
21,31,
21,25,
25,21,
21,18,
18,21,
18,49,
49,18,
49,47,
47,49,
47,37,
37,47,
37,21,
21,37,
18,25,
25,18), nrow = 42, ncol = 2, byrow = TRUE)

# Sort edges by first column then second column

E <- EE[do.call(order, lapply(1:ncol(EE), function(i) EE[,i])),)]

em_edge <- EMSHS(y, X, mus, nu, E,
  a_sigma = 1, b_sigma = 1, a_omega = 2, b_omega = 1,
  w = 1, eps = 1e-5)
```

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