Package ‘HDBRR’

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**Description**

Ridge regression provides biased estimators of the regression parameters with lower variance. The HDBRR ("High Dimensional Bayesian Ridge Regression") function fits Bayesian Ridge regression without MCMC, this one uses the SVD or QR decomposition for the posterior computation.

**Usage**

```r
HDBRR(y, X, n0 = 5, p0 = 5, s20 = NULL, d20 = NULL, h = 0.5,
intercept = TRUE, vpapp = TRUE, npts = NULL, c = NULL,
corpred = NULL, method = c("svd","qr"), bigmat = TRUE, ncores = 2)
```

```r
## S3 method for class 'HDBRR'
summary(object, all.coef = FALSE, crit = log(4), ...)
```

```r
## S3 method for class 'HDBRR'
plot(x, crit = log(4), ...)
```

```r
## S3 method for class 'HDBRR'
predict(object, ...)
```

```r
## S3 method for class 'summary.HDBRR'
print(x, ...)
```

**Arguments**

- **y** The data vector (numeric, n) NAs allowed.
- **X** Design Matrix of dimension n x p.
- **n0, p0** $n0/2$ and $p0/2$ are the shape parameter of the Gamma Inverse prior assigned to the residual variance and the shape parameter of the Gamma Inverse prior assigned to the Beta's variance respectively. The default value for $n0/2$ and $p0/2$ parameter is 5.
- **s20, d20** $(n0s20)/2$ and $(p0d20)/2$ are the scale parameter of the Gamma Inverse prior assigned to the residual variance and the scale parameter of the Gamma Inverse prior assigned to the Beta's variance respectively. The default value for the s20 and d20 is NULL. If the scale is not specified a value is calculated with h and quantiles.
- **h** (numeric, 0<h<1) shrinkage factor. Only used if the hyper-parameters are not specified; If h -> 0 then we have greater shrinkage, this is, $\beta$ -> 0. If h -> 1 then we have less shrinkage.
intercept  Logic value. The default value for the intercept is TRUE.
vpapp    Logic value. Compute an approximation of the predictive variance. The default value for the vpapp is TRUE.
npts     Number (integer) of points used to evaluate the u’s density for the numeric approach. The default value for the npts parameter is 200.
c        ratio of Gaussian densities (Spike/Slab) in the prior mixture density of each Beta for variable selection.
corpred  The method for the compute of the correlation, there are two methods, Empirical Bayes ("eb") and Bayesian ("b") method. The default value for the parameter corpred is NULL. If the values is NULL then the corr and edf values will be NULL.
method   Options for the posterior computation. There are two methods available: "qr" decomposition of X*t(X) and "svd" decomposition of matrix X. The default value for the method is SVD decomposition.
bigmat   Use of the bigstatsr package. The default value for bigmat is TRUE.
ncores   Number of the cores for computation. The default value for the ncores is 2, you can detect your number of cores with detectCores() and use it (iOS and Linux).
object   A HDBRR object, typically generated by a call to HDBRR.
all.coef Logical. Should results be returned for all ridge regression penalty parameters (all.coef = TRUE), or only those whose log(bayes factor)>crit.
crit     Numerical. The lower bound of the log Bayes factor in favour to include a variable in the model. The default value for crit is log(4).
...      Additional arguments to be passed to or from other methods.
x        A HDBRR object, typically generated by a call to HDBRR (for the print.HDBRR and plot.HDBRR functions) or an object of class summary.HDBRR (for the print.summary.HDBRR function).

Details

Ridge regression is a useful tool to deal with colinerity in the homocesastic linear regression model providing biased estimators of the regression parameters with lower variance than the least square estimators. The model

\[ y = X\beta + \epsilon \]

where \( \epsilon \) vector is assumed Normal with mean vector 0 and covariance matrix \( \sigma^2I_n \). For further details see the vignettes in the package.

Value

List containing the following components:

betahat Vector (numeric, p) with the betas estimates.
yhat    Vector (numeric, n) with the y’s estimates.
sdyhat   Vector (numeric, n) with the standard deviation of the predicts values.
sdpred Vector (numeric, n) with the standard deviation of predict variances.
varb Vector (numeric, p) with the beta’s variance.
sigshat Value (numeric) of the residual variance estimate.
sigbshat Value (numeric) of the Beta’s variance estimate.
u Vector (numeric, npts) with the u’s values.
postu Vector (numeric, npts) with the values of the u posterior.
what Value (numeric) of u estimated.
umode Value (numeric) of the posterior mode of u.
whichNa Value (integer) of NAs in the y vector.
phat Vector (numeric, p), selection probability of x_i.
delta Used in the variable selection.
edf Value (numeric) of the effective degrees of freedom for regression.
corr Vector (numeric, n) of the correlation between y_i estimates and y_i.

Author(s)
Sergio Perez-Elizalde, Blanca E. Monroy-Castillo, Paulino Perez-Rodriguez, Jose Crossa.

Examples

## Not run:

data("phenowheat")
mod <- lmer(pheno$HD~pheno$env+(1|pheno$Line))
y <- unlist(ranef(mod))
n <- length(y)
X <- scale(X, scale=F)
fitall <- HDBRR(y,X/sqrt(ncol(X)),intercept = FALSE, corpred = "eb", c = 100)
fitall
sumarry(fitall, crit = 0)
plot(fitall, crit = 0)
predict(fitall)

## End(Not run)

matop

Description

Compute the SVD or QR decomposition of the matrix X.

Usage

matop(y, X, method = c("svd", "qr"), bigmat = TRUE)
Arguments

- **y**: The data vector (numeric, n) NAs allowed.
- **X**: Design Matrix of dimension n x p.
- **method**: Options for the posterior computation. Two methods, "qr" and "svd" decomposition. The default value for the method is SVD decomposition.
- **bigmat**: Use of the bigstatsr package. The default value for bigmat is TRUE.

Details

Use the bigstatsr package when \( p >> n \). Auxiliary in the HDBRR function.

Value

If the method used is svd then the list containing the following components:

- **y**: The data vector (numeric, n) NAs allowed.
- **X**: Design Matrix of dimension n x p.
- **D**: A vector containing the singular values of \( X \), of length \( \min(n, p) \).
- **L**: A matrix whose columns contain the left singular vectors of \( X \).
- **R**: A matrix whose columns contain the right singular vectors of \( X \).
- **ev**: A vector containing the square of **D**.
- **Ly**: The cross-product between the matrix **L** and vector **y**.
- **n**: Number of rows of **X**.
- **p**: Number of columns of **X**.

If the method used is qr then the list containing the following components:

- **y**: The data vector (numeric, n) NAs allowed.
- **X**: Design Matrix of dimension n x p.
- **R**: An upper triangular matrix of dimension n x p.
- **n**: Number of rows of **X**.
- **p**: Number of columns of **X**.

Author(s)

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See Also

qr, svd
Examples

```r
n <- 30
p <- 100
X <- matrix(rnorm(n*(p-1),1,1/p),nrow = n,ncol = p-1)
Beta <- sample(1:p,p-1,rep = FALSE)
Beta <- c(1,Beta)
y <- cbind(rep(1,n),X) %*% Beta+rnorm(n,0,1)
matop(y, X, bigmat = TRUE)
```

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**phenowheat**

**Description**

The final number of SNPs included in the NCCR linkage map was 7594. The markers were centered and standardized. Phenotypic evaluation of the NCCR population was performed during two growing seasons (2010-2011 and 2011-2012) in locations in the Po Valley representative of the target environments where durum wheat is grown: Cadriano in the 2010-2011 growing season (Cad11) and the 2011-2012 growing season (Cad12); Poggio Renatico in the 2010-2011 growing season (Pr11) and Argelato in the 2011-2012 growing season (Arg12).

**Source**

International Maize and Wheat Improvement Center (CIMMYT), Mexico.

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**phenowheat**

**Description**

This contain data from a multiparental durum wheat (Triticum turgidum L. spp. duram) trial consisting of 334 lines evaluated in a country-year combination. This population is characterized for Grain Yield (GY), grain volume weight (GVW), 1000-kernel weight (GWT) and heading date (HD) in the four environments. For further details see the vignettes in the package.

**Usage**

```r
data(phenowheat)
```

**Format**

1. phenoMatrix phenowheat.pheno contains the phenotypic data.
2. X The matrix phenowheat.X contains the Genotypic data.
Description

Is a matrix (338 x 7594) with a balanced, four-way multiparental cross population was developed from four elite durum wheat cultivars (Neodur, Claudio, Colosseo, and Rascon/Tarro) that were chosen as diverse contributors of different alleles of agronomic relevance.

Source

International Maize and Wheat Improvement Center (CIMMYT), Mexico.
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