

# Package ‘islasso’

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**Type** Package

**Title** The Induced Smoothed Lasso

**Version** 1.1.1

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**Depends** glmnet, Matrix, R (>= 2.10)

**Description** An implementation of the induced smoothing (IS) idea to lasso regularization models to allow estimation and inference on the model coefficients (currently hypothesis testing only). Linear, logistic, Poisson and gamma regressions with several link functions are implemented. The algorithm is described in the original paper: Cilluffo, G., Sottile, G., La Grutta, S. and Muggeo, V. (2019) The Induced Smoothed lasso: A practical framework for hypothesis testing in high dimensional regression. <doi:10.1177/0962280219842890>, and discussed in a tutorial: Sottile, G., Cilluffo, G., and Muggeo, V. (2019) The R package islasso: estimation and hypothesis testing in lasso regression. <doi:10.13140/RG.2.2.16360.11521>.

**License** GPL (>= 2)

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islasso-package	<i>The Induced Smoothed lasso: A practical framework for hypothesis testing in high dimensional regression</i>
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## Description

This package implements an induced smoothed approach for hypothesis testing in lasso regression.

## Details

Package: islasso  
 Type: Package  
 Version: 1.1.1  
 Date: 2020-02-20  
 License: GPL-2

`islasso` is used to fit generalized linear models with a L1-penalty on (some) regression coefficients. Along with point estimates, the main advantage is to return the full covariance matrix of estimate. The resulting standard errors can be used to make inference in the lasso framework. The main function is `islasso` and the corresponding fitter function `islasso.fit`, and many auxiliary functions are implemented to summarize and visualize results: `summary.islasso`, `predict.islasso`, `coef.islasso`, `fitted.islasso`, `logLik.islasso`, `AIC.islasso`, `deviance.islasso`, `residuals.islasso`.

## Author(s)

Gianluca Sottile based on some preliminary functions by Vito Muggeo.

Maintainer: Gianluca Sottile <gianluca.sottile@unipa.it>

## References

Cilluffo, G, Sottile, G, S, La Grutta, S and Muggeo, VMR (2019). *The Induced Smoothed lasso: A practical framework for hypothesis testing in high dimensional regression*. Statistical Methods in Medical Research, DOI: 10.1177/0962280219842890.

Sottile, G, Cilluffo, G, Muggeo, VMR (2019). *The R package islasso: estimation and hypothesis testing in lasso regression*. Technical Report on ResearchGate. doi:10.13140/RG.2.2.16360.11521.

## Examples

```
set.seed(1)
n <- 100
p <- 100
p1 <- 20 #number of nonzero coefficients
coef.veri <- sort(round(c(seq(.5, 3, l=p1/2), seq(-1, -2, l=p1/2)), 2))
sigma <- 1

coef <- c(coef.veri, rep(0, p-p1))

X <- matrix(rnorm(n*p), n, p)
mu <- drop(X%%coef)
y <- mu + rnorm(n, 0, sigma)

lambda <- 2
o <- islasso(y~1+X, family=gaussian, lambda=lambda)
o
summary(o)
```

---

a ic . islasso

*Optimization for the selection of the tuning parameter*


---

## Description

This function performs a minimization of the AIC/BIC criterion for selecting the tuning parameter in “islasso”.

## Usage

```
aic.islasso(object, method = c("aic", "bic"), interval, y, X,
  intercept = FALSE, family = gaussian(), alpha = 1, offset,
  weights, unpenalized, control = is.control())
```

## Arguments

object	a fitted model object of class "islasso".
method	the criterion to optimize, AIC or BIC.
interval	the lower and upper limits of $\lambda$ wherein the AIC/BIC criterion should be optimized. Can be missing, if object has been obtained via cross-validation (and therefore includes the range of lambdas)
y	if object is missing, the response vector of length n.
X	if object is missing, the design matrix of dimension n * p.

intercept	if object is missing, if TRUE the intercept is added to the model matrix.
family	if object is missing, a description of the error distribution, family=gaussian, family=binomial and family=poisson are implemented with canonical link.
alpha	The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$ . The penalty is defined as $(1 - \alpha)/2 \ \beta\ _2^2 + \alpha \ \beta\ _1.$ <p>alpha=1 is the lasso penalty, and alpha=0 the ridge penalty.</p>
offset	this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
weights	observation weights. Default is 1 for each observation.
unpenalized	a vector used to specify the unpenalized estimators; unpenalized has to be a vector of logicals.
control	a list of parameters for controlling the fitting process (see <code>islasso.control</code> for more details).

### Details

Minimization of the Akaike Information Criterion (AIC) or Bayesian Information Criterion (BIC) is sometimes employed to select the tuning parameter as an alternative to the cross validation. The model degrees of freedom (not necessarily integers as in the plain lasso) used in AIC/BIC are computed as trace of the hat matrix at convergence.

### Value

the optimal lambda value is returned

### Author(s)

Gianluca Sottile

Maintainer: Gianluca Sottile <gianluca.sottile@unipa.it>

### See Also

[islasso.fit](#), [coef.islasso](#), [summary.islasso](#), [residuals.islasso](#), [AIC.islasso](#), [logLik.islasso](#), [fitted.islasso](#), [predict.islasso](#) and [deviance.islasso](#) methods.

### Examples

```
set.seed(1)
n <- 100
p <- 100
p1 <- 20 #number of nonzero coefficients
coef.veri <- sort(round(c(seq(.5, 3, l=p1/2), seq(-1, -2, l=p1/2)), 2))
sigma <- 1

coef <- c(coef.veri, rep(0, p-p1))
```

```

X <- matrix(rnorm(n*p), n, p)
mu <- drop(X**coef)
y <- mu + rnorm(n, 0, sigma)

o <- islasso(y ~ X)

## Not run:
#use the evaluation interval of the fit
lambda_aic <- aic.islasso(o, method="aic")

#overwrites the evaluation interval for lambda
lambda_bic <- aic.islasso(o, interval=c(.1, 30), method="bic")

## End(Not run)

```

---

anova.islasso

*General Linear Hypotheses method for islasso objects*


---

## Description

General linear hypotheses for linear combinations of the regression coefficients in islasso fits

## Usage

```

## S3 method for class 'islasso'
anova(object, A, b, ...)

```

## Arguments

object	a fitted model object of class "islasso".
A	a specification of the linear hypotheses to be tested. Linear functions can be specified by either a single vector (of length p) or by a matrix (of dimension k x p) of one or more linear hypotheses.
b	an optional numeric vector specifying the right hand side of the hypothesis. Can be a scalar.
...	not used.

## Details

For the islasso regression model with coefficients  $\beta$ , the null hypothesis is

$$H_0 : A\beta = b$$

where A and b are known matrix and vector. A can be a vector and b can be a scalar

**Examples**

```

## Not run:
set.seed(1)
n <- 100
p <- 100
p1 <- 10 #number of nonzero coefficients
coef.true <- sort(round(c(seq(.5, 3, l=p1/2), seq(-1, -2, l=p1/2)), 2))
sigma <- 1

coef <- c(coef.true, rep(0, p-p1))

X <- matrix(rnorm(n*p), n, p)
eta <- drop(X %*% coef)
mu <- eta
y <- mu + rnorm(n, 0, sigma)

o <- islasso(y~1+X, family=gaussian)
A <- rbind(rep(c(1,0), c(10, p-10)),
           rep(c(0,1), c(10, p-10)))
anova(o, A)

A <- cbind(diag(10), matrix(0, 10, p-10))
b <- coef.true
anova(o, A, b)

## End(Not run)

```

---

breast

*Breast Cancer microarray experiment*


---

**Description**

This data set details microarray experiment for 52 breast cancer patients. The binary variable `status` is used to indicate whether or not the patient has died of breast cancer (`status = 0` = did not die of breast cancer, `status = 1` = died of breast cancer). The other variables contain the amplification or deletion of the considered genes.

Rather than measuring gene expression, this experiment aims to measure gene amplification or deletion, which refers to the number of copies of a particular DNA sequence within the genome. The aim of the experiment is to find out the key genomic factors involved in aggressive and non-aggressive forms of breast cancer.

The experiment was conducted by the Dr. John Bartlett and Dr. Caroline Witton in the Division of Cancer Sciences and Molecular Pathology of the University of Glasgow at the city's Royal Infirmary.

**Usage**

```
data(breast)
```

**Source**

Dr. John Bartlett and Dr. Caroline Witton, Division of Cancer Sciences and Molecular Pathology, University of Glasgow, Glasgow Royal Infirmary.

**References**

Augugliaro L., Mineo A.M. and Wit E.C. (2013) *dgLARS: a differential geometric approach to sparse generalized linear models*, *Journal of the Royal Statistical Society. Series B.*, Vol 75(3), 471-498.

Wit E.C. and McClure J. (2004) "Statistics for Microarrays: Design, Analysis and Inference" Chichester: Wiley.

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diabetes

*Blood and other measurements in diabetics*

---

**Description**

The diabetes data frame has 442 rows and 3 columns. These are the data used in the Efron et al "Least Angle Regression" paper.

**Format**

This data frame contains the following columns:

**x** a matrix with 10 columns

**y** a numeric vector

**x2** a matrix with 64 columns

**Details**

The x matrix has been standardized to have unit L2 norm in each column and zero mean. The matrix x2 consists of x plus certain interactions.

**Source**

[http://www-stat.stanford.edu/~hastie/Papers/LARS/LeastAngle\\_2002.ps](http://www-stat.stanford.edu/~hastie/Papers/LARS/LeastAngle_2002.ps)

**References**

Efron, Hastie, Johnstone and Tibshirani (2003) "Least Angle Regression" (with discussion) *Annals of Statistics*

---

is.control

*Auxiliary for controlling islasso model fitting*


---

### Description

Auxiliary function for controlling the islasso model fitting.

### Usage

```
is.control(sigma2 = -1, tol = 1e-04, itmax = 500, stand = TRUE,
           trace = 0, nfolds = 5, seed=NULL, debias = FALSE, adaptive = FALSE,
           b0 = NULL, V0 = NULL, c = -1)
```

### Arguments

sigma2	optional. The fixed value of dispersion parameter. If -1 (default) it is estimated from the data
tol	tolerance value to declare convergence, default to 1e-4
itmax	maximum number of iterations, default to 500
stand	if TRUE, the covariates are standardized prior to fitting the model. However the coefficients are always returned on the original scale
trace	Should the iterative procedure be printed? 0: no printing, 1 = compact printing, 2 = enlarged printing.
nfolds	if lambda is unspecified in islasso, the number of folds to be used to perform cross validation. Default to 5, and nfolds>2 is allowed. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. nfolds is ignored if lambda is supplied.
seed	optional, the seed to be used to split the dataframe and to perform cross validation. Useful to make reproducible the results.
debias	experimental, if TRUE, unbiased estimates are also returned.
adaptive	experimental, if TRUE the adaptive LASSO is implemented.
b0	optional, starting values for the regression coefficients. If NULL, the point estimates from glmnet are used.
V0	optional, starting value for the estimates covariance matrix, If NULL, the identity matrix is used.
c	the weight of the mixture in the induced smoothed lasso. c=-1 means to compute it at each step of the iterative algorithm.



---

islasso *The Induced Smoothed lasso*

---

### Description

islasso is used to fit lasso regression models wherein the nonsmooth  $L_1$  norm penalty is replaced by a smooth approximation justified under the induced smoothing paradigm. Simple lasso-type or elastic-net penalties are permitted and Linear, Logistic, Poisson and Gamma responses are allowed.

### Usage

```
islasso(formula, family = gaussian, lambda, alpha=1, data, weights, subset,
        offset, unpenalized, contrasts = NULL, control = is.control())
```

### Arguments

- |             |   |
|-------------|---|
| formula     | an object of class “formula” (or one that can be coerced to that class): the ‘usual’ symbolic description of the model to be fitted.  |
| family      | the assumed response distribution. Gaussian, (quasi) Binomial, (quasi) Poisson, and Gamma are allowed. family=gaussian is implemented with identity link, family=binomial is implemented with logit or probit links, family=poisson is implemented with log link, and family=Gamma is implemented with inverse, log and identity links. |
| lambda      | Value of the tuning parameter in the objective. If missing, the optimal lambda is computed using <code>cv.glmnet</code> .   |
| alpha       | The elastic-net mixing parameter, with $0 \leq \alpha \leq 1$ . The penalty is defined as $(1 - \alpha)/2 \ \beta\ _2^2 + \alpha \ \beta\ _1.$ alpha=1 is the lasso penalty, and alpha=0 the ridge penalty.   |
| data        | an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which islasso is called.                                   |
| weights     | observation weights. Default is 1 for each observation.   |
| subset      | an optional vector specifying a subset of observations to be used in the fitting process.   |
| offset      | this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.  |
| unpenalized | optional. A vector of integers or characters indicating the covariate coefficients not to penalize. The intercept, if included in the model, is <i>always</i> unpenalized.  |
| contrasts   | an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .   |
| control     | a list of parameters for controlling the fitting process (see <code>islasso.control</code> for more details).   |

**Details**

islasso estimates regression models by imposing a lasso-type penalty on some or all regression coefficients. However the nonsmooth  $L_1$  norm penalty is replaced by a smooth approximation justified under the induced smoothing paradigm. The advantage is that reliable standard errors are returned as model output and hypothesis testing on linear combinations of the regression parameters can be carried out straightforwardly via the Wald statistic. Simulation studies provide evidence that the proposed approach controls type-I errors and exhibits good power in different scenarios.

**Value**

A list of

coefficients	a named vector of coefficients
se	a named vector of standard errors
res	the working residuals
fitted.values	the fitted values
linear.predictors	the linear predictors
rank	the estimated degrees of freedom
family	the family object used
deviance	the family deviance
null.deviance	the family null deviance
aic	the Akaike Information Criterion
df.null	the degrees of freedom of a null model
phi	the estimated dispersion parameter
beta.unbias	unbiased coefficients
se.unbias	unbiased standard errors
internal	internal elements
control	the value of the control argument used
model	if requested (the default), the model frame used.
terms	the terms object used.
contrasts	(only where relevant) the contrasts used.
call	the matched call
formula	the formula supplied

**Author(s)**

The main function of the same name was inspired by the R function previously implemented by Vito MR Muggeo. Maintainer: Gianluca Sottile <gianluca.sottile@unipa.it>

## References

Cilluffo, G, Sottile, G, S, La Grutta, S and Muggeo, VMR (2019). *The Induced Smoothed lasso: A practical framework for hypothesis testing in high dimensional regression*. Statistical Methods in Medical Research, DOI: 10.1177/0962280219842890.

Sottile, G, Cilluffo, G, Muggeo, VMR (2019). *The R package islasso: estimation and hypothesis testing in lasso regression*. Technical Report on ResearchGate. doi:10.13140/RG.2.2.16360.11521.

## See Also

[islasso.fit](#), [coef.islasso](#), [summary.islasso](#), [residuals.islasso](#), [AIC.islasso](#), [logLik.islasso](#), [fitted.islasso](#), [predict.islasso](#) and [deviance.islasso](#) methods.

## Examples

```
set.seed(1)
n <- 100
p <- 100
p1 <- 10 #number of nonzero coefficients
coef.veri <- sort(round(c(seq(.5, 3, l=p1/2), seq(-1, -2, l=p1/2)), 2))
sigma <- 1

coef <- c(coef.veri, rep(0, p-p1))

X <- matrix(rnorm(n*p), n, p)
eta <- drop(X%*%coef)

##### gaussian #####
mu <- eta
y <- mu + rnorm(n, 0, sigma)

o <- islasso(y~1+X, family=gaussian)
o
summary(o)
coef(o)
fitted(o)
predict(o, type="response")
plot(o)
residuals(o)
deviance(o)
AIC(o)
logLik(o)

## Not run:
# for the interaction
o <- islasso(y~1+X[,1]*X[,2], family=gaussian)

##### binomial #####
coef <- c(c(1,1,1), rep(0, p-3))
X <- matrix(rnorm(n*p), n, p)
eta <- drop(cbind(1, X)%*%c(1, coef))
```

```

mu <- binomial()$linkinv(eta)
y <- rbinom(n, 100, mu)
y <- cbind(y, 100-y)

o <- islasso(y~X, family=binomial)

##### poisson #####
coef <- c(c(1,1,1), rep(0, p-3))
X <- matrix(rnorm(n*p), n, p)
eta <- drop(cbind(1, X)%*%c(1, coef))
mu <- poisson()$linkinv(eta)
y <- rpois(n, mu)

o <- islasso(y~X, family=poisson)

##### Gamma #####
coef <- c(c(1,1,1), rep(0, p-3))
X <- matrix(rnorm(n*p), n, p)
eta <- drop(cbind(1, X)%*%c(1, coef))
mu <- Gamma(link="log")$linkinv(eta)
shape <- 10
phi <- 1 / shape
y <- rgamma(n, scale = mu / shape, shape = shape)

o <- islasso(y~X, family=Gamma(link="log"))

## End(Not run)

```

---

plot.islasso

*Diagnostics plots for Induced Smoothing Lasso Model*


---

## Description

Diagnostics plots for Induced Smoothing Lasso Model

## Usage

```

## S3 method for class 'islasso'
plot(x, ...)

```

## Arguments

x                    an object of class `islasso`, usually, a result of a call to `islasso`.

...                   other graphical parameters for the plot

## Details

The plot on the top left is a plot of the standard deviance residuals against the fitted values. The plot on the top right is a normal QQ plot of the standardized deviance residuals. The red line is the expected line if the standardized residuals are normally distributed, i.e. it is the line with intercept 0 and slope 1. The bottom two panels are plots of link and variance functions. On the left is squared standardized Pearson residuals against the fitted values. On the right working vector against the linear predictor.

## Examples

```
## Not run:
set.seed(1)
n <- 100
p <- 100
p1 <- 20 #number of nonzero coefficients
coef.veri <- sort(round(c(seq(.5, 3, l=p1/2), seq(-1, -2, l=p1/2)), 2))
sigma <- 1

coef <- c(coef.veri, rep(0, p-p1))

X <- matrix(rnorm(n*p), n, p)
mu <- drop(X%%coef)
y <- mu + rnorm(n, 0, sigma)

lambda <- 2
o <- islasso(y~X, family=gaussian, lambda=lambda)
plot(o)

## End(Not run)
```

---

predict.islasso

*Prediction method for islasso fitted objects*

---

## Description

Prediction method for islasso fitted objects

## Usage

```
## S3 method for class 'islasso'
predict(object, type = c("link", "response",
  "coefficients", "class"), newdata, ...)
```

## Arguments

object            a fitted object of class "islasso".

type	the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and type = "response" gives the predicted probabilities. The coefficients option returns coefficients. Type "class" applies only to "binomial" models, and produces the class label.
newdata	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
...	further arguments passed to or from other methods.

**Value**

An object depending on the type argument

**Examples**

```
## Not run:
set.seed(1)
n <- 100
p <- 100
p1 <- 20 #number of nonzero coefficients
coef.veri <- sort(round(c(seq(.5, 3, l=p1/2), seq(-1, -2, l=p1/2)), 2))
sigma <- 1

coef <- c(coef.veri, rep(0, p-p1))

X <- matrix(rnorm(n*p), n, p)
mu <- drop(X%%coef)
y <- mu + rnorm(n, 0, sigma)
lambda <- 2
o <- islasso(y~X, family=gaussian, lambda=lambda)
predict(o)

###prediction of new dataset
newdata <- matrix(rnorm(n*p), n, p)
predict(o, type="response", newdata=newdata)

## End(Not run)
```

---

Prostate

*Prostate Cancer Data*


---

**Description**

These data come from a study that examined the correlation between the level of prostate specific antigen and a number of clinical measures in men who were about to receive a radical prostatectomy. It is data frame with 97 rows and 9 columns.

**Usage**

```
data(Prostate)
```

**Format**

The data frame has the following components:

```
lcavol log(cancer volume)
lweight log(prostate weight)
age age
lbph log(benign prostatic hyperplasia amount)
svi seminal vesicle invasion
lcp log(capsular penetration)
gleason Gleason score
pgg45 percentage Gleason scores 4 or 5
lpsa log(prostate specific antigen)
```

**Source**

Stamey, T.A., Kabalin, J.N., McNeal, J.E., Johnstone, I.M., Freiha, F., Redwine, E.A. and Yang, N. (1989)

Prostate specific antigen in the diagnosis and treatment of adenocarcinoma of the prostate: II. radical prostatectomy treated patients, *Journal of Urology* **141**(5), 1076–1083.

---

simulXy

*Simulate model matrix and response*

---

**Description**

Simulate model matrix and response from a specified distribution.

**Usage**

```
simulXy(n, p, interc = 0, beta, family = gaussian(), prop =
  0.1, lim.b = c(-3, 3), sigma = 1, size = 1, rho = 0,
  scale = TRUE, seed, X)
```

**Arguments**

n	number of observations.
p	total number of covariates in the model matrix.
interc	the model intercept.
beta	the vector of p coefficients in the linear predictor.

family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. Only gaussian, binomial or poisson are allowed.
prop	if beta is missing, prop represent the quote of non-null coefficients out of p. The default is 0.10 p.
lim.b	if beta is missing, the coefficients come from uniform variates in lim.b. The default is (-3,3).
sigma	if family is 'gaussian', the standard deviation of the response. The default is 1.
size	if family is 'binomial', the number of trials to build the response vector. The default is 1.
rho	correlation value to define the variance covariance matrix to build the model matrix, i.e., $\rho^{ i-j }$ $i, j = 1, \dots, p$ and $i$ different from $j$ . The default is 0.
scale	Should the columns of the mdoel matrix be scaled? The default is TRUE
seed	optional, the seed to generate the data.
X	optional, the model matrix.

### Examples

```
n <- 100
p <- 100
beta <- c(runif(10, -3, 3), rep(0, p-10))
dat <- simulxy(n, p, beta = beta, seed=1234)
```

---

summary.islasso      *summary method for islasso fitted objects*

---

### Description

summary method for islasso fitted objects

### Usage

```
## S3 method for class 'islasso'
summary(object, pval = 1, use.t=FALSE, ...)
```

### Arguments

object	fitted "islasso" object
pval	a threshold p-value value indicating which coefficients should be printed. If $pval = 0.10$ , say, only the variables/coefficients with $p - value \leq 0.10$ are printed. If no variables have a p-value lower than pval the unpenalized variables are printed (e.g., the intercept). Moreover, if no variables are unpenalized the variable associated to the lowest p-value is reported.



```
use.t      if TRUE, the p-values are computed using the t-distribution with residual model
           degrees of freedom
...        not used
```

### **Examples**

```
## Not run:
#continues example from ?islasso
summary(o, pval=.1) #print just the "borderline" significant coefficients

## End(Not run)
```

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