

# Package ‘conformalInference’

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conformalInference-package

*Tools for conformal inference in regression*

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## Description

A collection of tools for distribution-free inference for regression problems using the theory of conformal prediction.

## Details

Conformal inference is a framework for converting any pre-chosen estimator of the regression function into prediction intervals with finite-sample validity, under essentially no assumptions on the data-generating process (aside from the the assumption of i.i.d. observations). The main functions in this package for computing such prediction intervals are [conformal.pred](#) (shorter intervals, but more expensive) and [conformal.pred.split](#) (wider intervals, but much more efficient).

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conformal.pred

*Conformal prediction intervals.*

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## Description

Compute prediction intervals using conformal inference.

## Usage

```
conformal.pred(x, y, x0, train.fun, predict.fun, alpha = 0.1, w = NULL,
  mad.train.fun = NULL, mad.predict.fun = NULL, num.grid.pts = 100,
  grid.factor = 1.25, verbose = FALSE)
```

## Arguments

<code>x</code>	Matrix of features, of dimension (say) $n \times p$ .
<code>y</code>	Vector of responses, of length (say) $n$ .
<code>x0</code>	Matrix of features, each row being a point at which we want to form a prediction interval, of dimension (say) $n_0 \times p$ .
<code>train.fun</code>	A function to perform model training, i.e., to produce an estimator of $E(Y X)$ , the conditional expectation of the response variable $Y$ given features $X$ . Its input arguments should be <code>x</code> : matrix of features, <code>y</code> : vector of responses, and <code>out</code> : the output produced by a previous call to <code>train.fun</code> , at the <i>same</i> features <code>x</code> . The function <code>train.fun</code> may (optionally) leverage this returned output for efficiency purposes. See details below.

<code>predict.fun</code>	A function to perform prediction for the (mean of the) responses at new feature values. Its input arguments should be <code>out</code> : output produced by <code>train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions.
<code>alpha</code>	Miscoverage level for the prediction intervals, i.e., intervals with coverage $1-\alpha$ are formed. Default for <code>alpha</code> is 0.1.
<code>w</code>	Weights, in the case of covariate shift. This should be a vector of length $n+n_0$ , giving the weights (i.e., ratio of test to training feature densities), at each of $n+n_0$ the training and test points. Default is <code>NULL</code> , which means that we take all weights to be 1.
<code>mad.train.fun</code>	A function to perform training on the absolute residuals i.e., to produce an estimator of $E(R X)$ where $R$ is the absolute residual $R =  Y - m(X) $ , and $m$ denotes the estimator produced by <code>train.fun</code> . This is used to scale the conformal score, to produce a prediction interval with varying local width. The input arguments to <code>mad.train.fun</code> should be <code>x</code> : matrix of features, <code>y</code> : vector of absolute residuals, and <code>out</code> : the output produced by a previous call to <code>mad.train.fun</code> , at the <i>same</i> features <code>x</code> . The function <code>mad.train.fun</code> may (optionally) leverage this returned output for efficiency purposes. See details below. The default for <code>mad.train.fun</code> is <code>NULL</code> , which means that no training is done on the absolute residuals, and the usual (unscaled) conformal score is used. Note that if <code>mad.train.fun</code> is non- <code>NULL</code> , then so must be <code>mad.predict.fun</code> (next).
<code>mad.predict.fun</code>	A function to perform prediction for the (mean of the) absolute residuals at new feature values. Its input arguments should be <code>out</code> : output produced by <code>mad.train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions. The default for <code>mad.predict.fun</code> is <code>NULL</code> , which means that no local scaling is done for the conformal score, i.e., the usual (unscaled) conformal score is used.
<code>num.grid.pts</code>	Number of grid points used when forming the conformal intervals (each grid point is a trial value for the interval). Default is 100.
<code>grid.factor</code>	Expansion factor used to define the grid for the conformal intervals, i.e., the grid points are taken to be equally spaced in between $-\text{grid.factor} \cdot \max(\text{abs}(y))$ and $\text{grid.factor} \cdot \max(\text{abs}(y))$ . Default is 1.25. In this case (and with exchangeable data, thus unity weights) the restriction of the trial values to this range costs at most $1/(n+1)$ in coverage. See details below.
<code>verbose</code>	Should intermediate progress be printed out? Default is <code>FALSE</code> .

## Details

For concreteness, suppose that we want to use the predictions from forward stepwise regression at steps 1 through 5 in the path. In this case, there are  $m = 5$  internal tuning parameter values to `predict.fun`, in the notation used above, and each of the returned matrices `pred`, `lo`, and `up` will have 5 rows (one corresponding to each step of the forward stepwise path). The code is structured in this way so that we may define a single pair of functions `train.fun` and `predict.fun`, over a set of  $m = 5$  tuning parameter values, instead of calling the conformal function separately  $m = 5$  times.

The third argument to `train.fun`, as explained above, is the output produced by a previous call to `train.fun`, but importantly, at the *same* features `x`. The function `train.fun` may (optionally) leverage this returned output for efficiency purposes. Here is how it is used, in this function: when successively querying several trial values for the prediction interval, denoted, say, `y0[j]`,  $j = 1, 2, 3, \dots$ , we set the `out` argument in `train.fun` to be the result of calling `train.fun` at the previous trial value `y0[j-1]`. Note of course that the function `train.fun` can also choose to ignore the returned output `out`, and most default training functions made available in this package will do so, for simplicity. An exception

is the training function produced by `lm.funs`. This will use this output efficiently: the first time it trains by regressing onto a matrix of features  $x$ , it computes an appropriate Cholesky factorization; each successive time it is asked to train by regressing onto the same matrix  $x$ , it simply uses this Cholesky factorization (rather than recomputing one). The analogous explanation and discussion here applies to the `out` argument used by `mad.train.fun`.

If the data (training and test) are assumed to be exchangeable, the basic assumption underlying conformal prediction, then the probability that a new response value will lie outside of  $[-\max(\text{abs}(y)), \max(\text{abs}(y))]$ , where  $y$  is the vector of training responses, is  $1/(n+1)$ . Thus the restriction of the trials values to  $[-\text{grid.factor} \cdot \max(\text{abs}(y)), \text{grid.factor} \cdot \max(\text{abs}(y))]$ , for all choices  $\text{grid.factor} \geq 1$ , will lead to a loss in coverage of at most  $1/(n+1)$ . This was also noted in "Trimmed Conformal Prediction for High-Dimensional Models" by Chen, Wang, Ha, Barber (2016) (who use this basic fact as motivation for proposing more refined trimming methods).

## Value

A list with the following components: `pred`, `lo`, `up`, `fit`. The first three are matrices of dimension  $m \times n_0$ , and the last is a matrix of dimension  $m \times n$ . Recall that  $n_0$  is the number of rows of  $x_0$ , and  $m$  is the number of tuning parameter values internal to `predict.fun`. In a sense, each of the  $m$  columns really corresponds to a different prediction function; see details below. Hence, the rows of the matrices `pred`, `lo`, `up` give the predicted value, and lower and upper confidence limits (from conformal inference), respectively, for the response at the  $n_0$  points given in  $x_0$ . The rows of `fit` give the fitted values for the  $n$  points given in  $x$ .

## References

See "Algorithmic Learning in a Random World" by Vovk, Gammerman, Shafer (2005) as the definitive reference for conformal prediction; see also "Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018) for another description; and "Conformal Prediction Under Covariate Shift" by Barber, Candes, Ramdas, Tibshirani (2019) for the weighted extension.

## See Also

[conformal.pred.jack](#), [conformal.pred.split](#), [conformal.pred.roo](#)

## Examples

```
## Lasso: use a fixed sequence of 100 lambda values

# Generate some example training data
set.seed(33)
n = 100; p = 120; s = 10
x = matrix(rnorm(n*p),n,p)
beta = c(rnorm(s),rep(0,p-s))
y = x %*% beta + rnorm(n)

# Generate some example test data
n0 = 50
x0 = matrix(rnorm(n0*p),n0,p)
y0 = x0 %*% beta + rnorm(n0)

# Grab a fixed lambda sequence from one call to glmnet, then
# define lasso training and prediction functions
if (!require("glmnet",quietly=TRUE)) {
  stop("Package glmnet not installed (required for this example)!")
}
```

```

}
out.gnet = glmnet(x,y,nlambda=100,lambda.min.ratio=1e-3)
lambda = out.gnet$lambda
funs = lasso.funs(lambda=lambda)

# Conformal inference, and jackknife and split conformal versions
out.conf = conformal.pred(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict, verb=TRUE)

out.jack = conformal.pred.jack(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

out.split = conformal.pred.split(x, y, x0, alpha=0.1, seed=0,
  train.fun=funs$train, predict.fun=funs$predict)

y0.mat = matrix(rep(y0,ncol(out.conf$lo)),nrow=n0)
cov.conf = colMeans(out.conf$lo <= y0.mat & y0.mat <= out.conf$up)
len.conf = colMeans(out.conf$up - out.conf$lo)
err.conf = colMeans((y0.mat - out.conf$pred)^2)

cov.jack = colMeans(out.jack$lo <= y0.mat & y0.mat <= out.jack$up)
len.jack = colMeans(out.jack$up - out.jack$lo)
err.jack = colMeans((y0.mat - out.jack$pred)^2)

cov.split = colMeans(out.split$lo <= y0.mat & y0.mat <= out.split$up)
len.split = colMeans(out.split$up - out.split$lo)
err.split = colMeans((y0.mat - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac,newdata=list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

# Plot average coverage
plot(log(lambda),cov.conf,type="o",pch=20,ylim=c(0,1),
  xlab="log(lambda)",ylab="Avg coverage",
  main=paste0("Conformal + lasso (fixed lambda sequence):",
    "\nAverage coverage"))
points(log(lambda),cov.jack,type="o",pch=20,col=3)
points(log(lambda),cov.split,type="o",pch=20,col=4)
abline(h=cov.orac,lty=2,col=2)
legend("bottomleft",col=c(1,3,4,2),lty=c(1,1,1,2),
  legend=c("Conformal","Jackknife conformal",
    "Split conformal","Oracle"))

# Plot average length
plot(log(lambda),len.conf,type="o",pch=20,
  ylim=range(len.conf,len.jack,len.split,len.orac),
  xlab="log(lambda)",ylab="Avg length",
  main=paste0("Conformal + lasso (fixed lambda sequence):",
    "\nAverage length"))
points(log(lambda),len.jack,type="o",pch=20,col=3)
points(log(lambda),len.split,type="o",pch=20,col=4)

```

```

abline(h=len.orac,lty=2,col=2)
legend("topleft",col=c(1,3,4,2),lty=c(1,1,1,2),
      legend=c("Conformal","Jackknife conformal",
               "Split conformal","Oracle"))

# Plot test error
plot(log(lambda),err.conf,type="o",pch=20,
     ylim=range(err.conf,err.jack,err.split,err.orac),
     xlab="log(lambda)",ylab="Test error",
     main=paste0("Conformal + lasso (fixed lambda sequence):",
                 "\nTest error"))
points(log(lambda),err.jack,type="o",pch=20,col=3)
points(log(lambda),err.split,type="o",pch=20,col=4)
abline(h=err.orac,lty=2,col=2)
legend("topleft",col=c(1,3,4,2),lty=c(1,1,1,2),
      legend=c("Conformal","Jackknife conformal",
               "Split conformal","Oracle"))

```

---

conformal.pred.jack     *Jackknife conformal prediction intervals.*

---

## Description

Compute prediction intervals using a jackknife variant of conformal inference.

## Usage

```

conformal.pred.jack(x, y, x0, train.fun, predict.fun, alpha = 0.1,
  special.fun = NULL, mad.train.fun = NULL, mad.predict.fun = NULL,
  verbose = FALSE)

```

## Arguments

x	Matrix of features, of dimension (say) $n \times p$ .
y	Vector of responses, of length (say) $n$ .
x0	Matrix of features, each row being a point at which we want to form a prediction interval, of dimension (say) $n_0 \times p$ .
train.fun	A function to perform model training, i.e., to produce an estimator of $E(Y X)$ , the conditional expectation of the response variable $Y$ given features $X$ . Its input arguments should be $x$ : matrix of features, and $y$ : vector of responses.
predict.fun	A function to perform prediction for the (mean of the) responses at new feature values. Its input arguments should be $out$ : output produced by <code>train.fun</code> , and $newx$ : feature values at which we want to make predictions.
alpha	Miscoverage level for the prediction intervals, i.e., intervals with coverage $1 - \alpha$ are formed. Default for $\alpha$ is 0.1.
special.fun	A function to compute leave-one-out fitted values in an efficient manner. For example, for many linear smoothers (e.g., linear regression, smoothing splines,

kernel smoothing — essentially, anything for which the fast leave-one-out cross-validation formula holds), we have the "magic" property:

$$y_i - \hat{f}^{(-i)}(x_i) = \frac{y_i - \hat{f}(x_i)}{1 - S_{ii}},$$

where  $\hat{f}$  is the linear smoother trained on the entire data set  $\hat{f}^{(-i)}$  is the linear smoother trained on all but the  $i$ th data point, and  $S_{ii}$  is the  $i$ th diagonal element of the smoothing matrix. The input arguments to `special.fun` should be `x`: matrix of features, `y`: vector of responses, and `out`: output produced by `train.fun` when run on `x`, `y`. The default for `special.fun` is `NULL`, which means that no special leave-one-out formula is leverage, and the usual (manual) way of computing leave-one-out fitted values is used. Note that if `mad.train.fun` and `mad.predict.fun` are passed, in order to obtain prediction intervals with locally varying width, then `special.fun` will be ignored (since the fast shortcut it offers can no longer be used).

<code>mad.train.fun</code>	A function to perform training on the absolute residuals i.e., to produce an estimator of $E(R X)$ where $R$ is the absolute residual $R =  Y - m(X) $ , and $m$ denotes the estimator produced by <code>train.fun</code> . This is used to scale the conformal score, to produce a prediction interval with varying local width. The input arguments to <code>mad.train.fun</code> should be <code>x</code> : matrix of features, and <code>y</code> : vector of absolute residuals. The default for <code>mad.train.fun</code> is <code>NULL</code> , which means that no training is done on the absolute residuals, and the usual (unscaled) conformal score is used. Note that if <code>mad.train.fun</code> is non- <code>NULL</code> , then so must be <code>mad.predict.fun</code> (next).
<code>mad.predict.fun</code>	A function to perform prediction for the (mean of the) absolute residuals at new feature values. Its input arguments should be <code>out</code> : output produced by <code>mad.train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions. The default for <code>mad.predict.fun</code> is <code>NULL</code> , which means that no local scaling is done for the conformal score, i.e., the usual (unscaled) conformal score is used.
<code>verbose</code>	Should intermediate progress be printed out? Default is <code>FALSE</code> .
<code>alpha</code>	Miscoverage level for the prediction intervals, i.e., intervals with coverage $1 - \alpha$ are formed. Default for <code>alpha</code> is 0.1.

## Details

For concreteness, suppose that we want to use the predictions from forward stepwise regression at steps 1 through 5 in the path. In this case, there are  $m = 5$  internal tuning parameter values to `predict.fun`, in the notation used above, and each of the returned matrices `pred`, `lo`, and `up` will have 5 rows (one corresponding to each step of the forward stepwise path). The code is structured in this way so that we may defined a single pair of functions `train.fun` and `predict.fun`, over a set of  $m = 5$  tuning parameter values, instead of calling the conformal function separately  $m = 5$  times.

## Value

A list with the following components: `pred`, `lo`, `up`, `fit`. The first three are matrices of dimension  $m \times n_0$ , and the last is a matrix of dimension  $m \times n$ . Recall that  $n_0$  is the number of rows of `x0`, and  $m$  is the number of tuning parameter values internal to `predict.fun`. In a sense, each of the  $m$  columns really corresponds to a different prediction function; see details below. Hence, the rows of the matrices `pred`, `lo`, `up` give the predicted value, and lower and upper confidence limits, respectively, for the response at the  $n_0$  points given in `x0`. The predicted values are computed based on the entire training set, and the confidence limits are computed using jackknife conformal inference. The rows of `fit` give the fitted values for the  $n$  points given in `x`.

## References

"Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018).

## See Also

[conformal.pred](#), [conformal.pred.split](#), [conformal.pred.roo](#)

## Examples

```
## See examples for conformal.pred function
```

---

conformal.pred.roo	<i>In-sample split conformal prediction intervals.</i>
--------------------	--

---

## Description

Compute prediction intervals, having valid in-sample coverage, using rank-one-out (ROO) split conformal inference.

## Usage

```
conformal.pred.roo(x, y, train.fun, predict.fun, alpha = 0.1,
  mad.train.fun = NULL, mad.predict.fun = NULL, split = NULL,
  seed = NULL, verbose = FALSE)
```

## Arguments

<code>x</code>	Matrix of features, of dimension (say) $n \times p$ .
<code>y</code>	Vector of responses, of length (say) $n$ .
<code>train.fun</code>	A function to perform model training, i.e., to produce an estimator of $E(Y X)$ , the conditional expectation of the response variable $Y$ given features $X$ . Its input arguments should be <code>x</code> : matrix of features, and <code>y</code> : vector of responses.
<code>predict.fun</code>	A function to perform prediction for the (mean of the) responses at new feature values. Its input arguments should be <code>out</code> : output produced by <code>train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions.
<code>alpha</code>	Miscoverage level for the prediction intervals, i.e., intervals with coverage $1 - \alpha$ are formed. Default for <code>alpha</code> is 0.1.
<code>mad.train.fun</code>	A function to perform training on the absolute residuals i.e., to produce an estimator of $E(R X)$ where $R$ is the absolute residual $R =  Y - m(X) $ , and $m$ denotes the estimator produced by <code>train.fun</code> . This is used to scale the conformal score, to produce a prediction interval with varying local width. The input arguments to <code>mad.train.fun</code> should be <code>x</code> : matrix of features, and <code>y</code> : vector of absolute residuals. The default for <code>mad.train.fun</code> is <code>NULL</code> , which means that no training is done on the absolute residuals, and the usual (unscaled) conformal score is used. Note that if <code>mad.train.fun</code> is non- <code>NULL</code> , then so must be <code>mad.predict.fun</code> (see next).



<code>mad.predict.fun</code>	A function to perform prediction for the (mean of the) absolute residuals at new feature values. Its input arguments should be <code>out</code> : output produced by <code>mad.train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions. The default for <code>mad.predict.fun</code> is <code>NULL</code> , which means that no local scaling is done for the conformal score, i.e., the usual (unscaled) conformal score is used.
<code>split</code>	Indices that define the data-split to be used (i.e., the indices define the first half of the data-split). Default is <code>NULL</code> , in which case the split is chosen randomly.
<code>seed</code>	Integer to be passed to <code>set.seed</code> before defining the random data-split to be used. Default is <code>NULL</code> , which effectively sets no seed. If both <code>split</code> and <code>seed</code> are passed, the former takes priority and the latter is ignored.
<code>verbose</code>	Should intermediate progress be printed out? Default is <code>FALSE</code> .

### Details

For concreteness, suppose that we want to use the predictions from forward stepwise regression at steps 1 through 5 in the path. In this case, there are  $m = 5$  internal tuning parameter values to `predict.fun`, in the notation used above, and each of the returned matrices `pred`, `lo`, `up`, `fit` will have 5 columns (one for each step of the forward stepwise path). The code is structured in this way so that we may define a single pair of functions `train.fun` and `predict.fun`, over a set of  $m = 5$  tuning parameter values, instead of calling the conformal function separately  $m = 5$  times.

The rank-one-out or ROO variant of split conformal prediction produces intervals with a special in-sample average coverage property. Namely, if we were to observe new response values  $y^*$  at the given feature values  $x$ , then the ROO method produces a prediction band  $\hat{C}(x)$  with the asymptotic in-sample average coverage property

$$\liminf_{n \rightarrow \infty} \frac{1}{n} \sum_{i=1}^n P(Y_i^* \in \hat{C}(X_i)) \geq 1 - \alpha.$$

The usual split conformal band would not necessarily share this in-sample property. Of course, the split conformal band has valid predictive (i.e., out-of-sample) coverage, and the ROO split conformal variant maintains this property as well.

### Value

A list with the following components: `pred`, `lo`, `up`, `fit`, `split`, `fit.all`, `out.all`. The first four are matrices of dimension  $n \times m$ . In a sense, each of the  $m$  columns really corresponds to a different prediction function; see details below. Hence, the rows of the matrices `pred`, `lo`, `up` give the predicted value, and lower and upper confidence limits (from rank-one-out split conformal inference), respectively, for the response at the  $n$  points given in `x`. The rows of the matrix `fit` give the fitted values for the  $n$  points given in `x`. The indices used for the half of the data-split are returned in `split`. Finally, for convenience, the output from running `train.out` on the entire (unsplit) data set `x,y` is stored in `out.all`, and `fit.all` is an  $n \times m$  matrix whose rows store the fitted values from `out.all`.

### References

"Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018).

### See Also

[conformal.pred](#), [conformal.pred.jack](#), [conformal.pred.split](#)

## Examples

```
## Lasso: use a fixed sequence of 100 lambda values

# Generate some example training data
set.seed(33)
n = 200; p = 500; s = 10
x = matrix(rnorm(n*p),n,p)
beta = c(rnorm(s),rep(0,p-s))
y = x %*% beta + rnorm(n)

# Generate some example test data, but using the same x points
n0 = n
x0 = x
y0 = x0 %*% beta + rnorm(n0)

# Grab a fixed lambda sequence from one call to glmnet, then
# define lasso training and prediction functions
if (!require("glmnet",quietly=TRUE)) {
  stop("Package glmnet not installed (required for this example)!")
}
out.gnet = glmnet(x,y,nlambdas=100,lambda.min.ratio=1e-4)
lambda = out.gnet$lambda
funs = lasso.funs(lambda=lambda)

# Rank-one-out conformal inference, and split conformal inference
out.roo = conformal.pred.roo(x, y, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

y0.mat = matrix(rep(y0,ncol(out.roo$lo)),nrow=n0)
cov.roo = colMeans(out.roo$lo <= y0.mat & y0.mat <= out.roo$up)
len.roo = colMeans(out.roo$up - out.roo$lo)
err.roo = colMeans((y0.mat - out.roo$pred)^2)

cov.split = colMeans(out.split$lo <= y0.mat & y0.mat <= out.split$up)
len.split = colMeans(out.split$up - out.split$lo)
err.split = colMeans((y0.mat - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac,newdata=list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

# Plot average coverage
plot(log(lambda),cov.roo,type="o",pch=20,ylim=c(0,1),
  xlab="log(lambda)",ylab="Avg coverage",
  main=paste0("R00 conformal + lasso (fixed lambda sequence):",
    "\nAverage coverage"))
points(log(lambda),cov.split,type="o",pch=20,col=4)
abline(h=cov.orac,lty=2,col=2)
```

```

legend("bottomleft",col=c(1,4,2),lty=c(1,1,2),
      legend=c("R00 conformal","Split conformal","Oracle"))

# Plot average length
plot(log(lambda),len.roo,type="o",pch=20,
     ylim=range(len.roo,len.split,len.orac),
     xlab="log(lambda)",ylab="Avg length",
     main=paste0("Split conformal + lasso (fixed lambda sequence):",
                 "\nAverage length"))
points(log(lambda),len.split,type="o",pch=20,col=4)
abline(h=len.orac,lty=2,col=2)
legend("bottomleft",col=c(1,4,2),lty=c(1,1,2),
      legend=c("R00 conformal","Split conformal","Oracle"))

# Plot test error
plot(log(lambda),err.roo,type="o",pch=20,
     ylim=range(err.roo,err.split,err.orac),
     xlab="log(lambda)",ylab="Test error",
     main=paste0("Split conformal + lasso (fixed lambda sequence):",
                 "\nTest error"))
points(log(lambda),err.split,type="o",pch=20,col=4)
abline(h=err.orac,lty=2,col=2)
legend("bottomleft",col=c(1,4,2),lty=c(1,1,2),
      legend=c("R00 conformal","Split conformal","Oracle"))

```

---

conformal.pred.split    *Split conformal prediction intervals.*

---

## Description

Compute prediction intervals using split conformal inference.

## Usage

```

conformal.pred.split(x, y, x0, train.fun, predict.fun, alpha = 0.1,
  w = NULL, mad.train.fun = NULL, mad.predict.fun = NULL,
  split = NULL, seed = NULL, verbose = FALSE)

```

## Arguments

x	Matrix of features, of dimension (say) $n \times p$ .
y	Vector of responses, of length (say) $n$ .
x0	Matrix of features, each row being a point at which we want to form a prediction interval, of dimension (say) $n_0 \times p$ .
train.fun	A function to perform model training, i.e., to produce an estimator of $E(Y X)$ , the conditional expectation of the response variable $Y$ given features $X$ . Its input arguments should be $x$ : matrix of features, and $y$ : vector of responses.
predict.fun	A function to perform prediction for the (mean of the) responses at new feature values. Its input arguments should be $out$ : output produced by <code>train.fun</code> , and $newx$ : feature values at which we want to make predictions.
alpha	Miscoverage level for the prediction intervals, i.e., intervals with coverage $1 - \alpha$ are formed. Default for $\alpha$ is 0.1.

<code>w</code>	Weights, in the case of covariate shift. This should be a vector of length $n+n_0$ , giving the weights (i.e., ratio of test to training feature densities), at each of $n+n_0$ the training and test points. Default is NULL, which means that we take all weights to be 1.
<code>mad.train.fun</code>	A function to perform training on the absolute residuals i.e., to produce an estimator of $E(R X)$ where $R$ is the absolute residual $R =  Y - m(X) $ , and $m$ denotes the estimator produced by <code>train.fun</code> . This is used to scale the conformal score, to produce a prediction interval with varying local width. The input arguments to <code>mad.train.fun</code> should be <code>x</code> : matrix of features, and <code>y</code> : vector of absolute residuals. The default for <code>mad.train.fun</code> is NULL, which means that no training is done on the absolute residuals, and the usual (unscaled) conformal score is used. Note that if <code>mad.train.fun</code> is non-NULL, then so must be <code>mad.predict.fun</code> (see next).
<code>mad.predict.fun</code>	A function to perform prediction for the (mean of the) absolute residuals at new feature values. Its input arguments should be <code>out</code> : output produced by <code>mad.train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions. The default for <code>mad.predict.fun</code> is NULL, which means that no local scaling is done for the conformal score, i.e., the usual (unscaled) conformal score is used.
<code>split</code>	Indices that define the data-split to be used (i.e., the indices define the first half of the data-split, on which the model is trained). Default is NULL, in which case the split is chosen randomly.
<code>seed</code>	Integer to be passed to <code>set.seed</code> before defining the random data-split to be used. Default is NULL, which effectively sets no seed. If both <code>split</code> and <code>seed</code> are passed, the former takes priority and the latter is ignored.
<code>verbose</code>	Should intermediate progress be printed out? Default is FALSE.

## Details

For concreteness, suppose that we want to use the predictions from forward stepwise regression at steps 1 through 5 in the path. In this case, there are  $m = 5$  internal tuning parameter values to `predict.fun`, in the notation used above, and each of the returned matrices `pred`, `lo`, `up`, `fit` will have 5 columns (one for each step of the forward stepwise path). The code is structured in this way so that we may define a single pair of functions `train.fun` and `predict.fun`, over a set of  $m = 5$  tuning parameter values, instead of calling the conformal function separately  $m = 5$  times.

## Value

A list with the following components: `pred`, `lo`, `up`, `fit`, `split`. The first three are matrices of dimension  $n_0 \times m$ , and the fourth is a matrix of dimension  $n \times m$ . Recall that  $n_0$  is the number of rows of `x0`, and  $m$  is the number of tuning parameter values internal to `predict.fun`. In a sense, each of the  $m$  columns really corresponds to a different prediction function; see details below. Hence, the rows of the matrices `pred`, `lo`, `up` give the predicted value, and lower and upper confidence limits (from split conformal inference), respectively, for the response at the  $n_0$  points given in `x0`. The rows of `fit` give the fitted values for the  $n$  points given in `x`. Finally, `split` contains the indices used for the first half of the data-split.

## References

See "Algorithmic Learning in a Random World" by Vovk, Gammerman, Shafer (2005) as the definitive reference for conformal prediction; see also "Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018) for another description; and "Con-

formal Prediction Under Covariate Shift" by Barber, Candes, Ramdas, Tibshirani (2019) for the weighted extension.

### See Also

[conformal.pred](#), [conformal.pred.jack](#), [conformal.pred.roo](#)

---

glmnet.funs

*Elastic net, lasso, ridge regression training and prediction functions.*

---

### Description

Construct training and prediction functions for the elastic net, the lasso, or ridge regression, based on the [glmnet](#) package, over a sequence of (given or internally computed) lambda values.

### Usage

```
elastic.funs(gamma = 0.5, standardize = TRUE, intercept = TRUE,
             lambda = NULL, nlambda = 50, lambda.min.ratio = 1e-04,
             cv = FALSE, cv.rule = c("min", "1se"))
```

```
lasso.funs(standardize = TRUE, intercept = TRUE, lambda = NULL,
           nlambda = 50, lambda.min.ratio = 1e-04, cv = FALSE,
           cv.rule = c("min", "1se"))
```

```
ridge.funs(standardize = TRUE, intercept = TRUE, lambda = NULL,
           nlambda = 50, lambda.min.ratio = 1e-04, cv = FALSE,
           cv.rule = c("min", "1se"))
```

### Arguments

- |                        |   |
|------------------------|---|
| gamma                  | Mixing parameter (between 0 and 1) for the elastic net, where 0 corresponds to ridge regression, and 1 to the lasso. Default is 0.5.  |
| standardize, intercept | Should the data be standardized, and should an intercept be included? Default for both is TRUE.   |
| lambda                 | Sequence of lambda values over which training is performed. This must be in decreasing order, and — this argument should be used with caution! When used, it is usually best to grab the sequence constructed by one initial call to glmnet (see examples). Default is NULL, which means that the nlambda, lambda.min.ratio arguments will define the lambda sequence (see next). |
| nlambda                | Number of lambda values over which training is performed. In particular, the lambda sequence is defined by nlambda log-spaced values between lambda.max and lambda.min.ratio * lambda.max, where lambda.max is the smallest value of lambda at which the solution has all zero components, and lambda.min.ratio is a small fraction (see next). Default is 50.                    |
| lambda.min.ratio       | Small fraction that gets used in conjunction with nlambda to specify a lambda sequence (see above). Default is 1e-4.  |

cv	Should 10-fold cross-validation be used? If TRUE, then prediction is done with either the (usual) min rule, or the 1se rule. See the cv.rule argument, below. If FALSE (the default), then prediction is done over the same lambda sequence as that used for training.
cv.rule	If the cv argument is TRUE, then cv.rule determines which rule should be used for the predict function, either "min" (the usual rule) or "1se" (the one-standard-error rule). See the glmnet help files for details. Default is "min".

## Details

This function is based on the packages [glmnet](#) and [plyr](#). If these packages are not installed, then the function will abort. The functions [lasso.funs](#) and [ridge.funs](#) are convenience functions, they simply call [elastic.funs](#) with  $\gamma = 1$  and  $\gamma = 0$ , respectively.

## Value

A list with three components: [train.fun](#), [predict.fun](#), [active.fun](#). The third function is designed to take the output of [train.fun](#), and reports which features are active for each fitted model contained in this output.

## See Also

[lars.funs](#) for stepwise, least angle regression, and lasso path training and prediction functions.

## Examples

```
## Elastic net: use a fixed sequence of 100 lambda values

# Generate some example training data
set.seed(11)
n = 200; p = 500; s = 10
x = matrix(rnorm(n*p),n,p)
beta = c(rnorm(s),rep(0,p-s))
y = x %*% beta + rnorm(n)

# Generate some example test data
n0 = 1000
x0 = matrix(rnorm(n0*p),n0,p)
y0 = x0 %*% beta + rnorm(n0)

# Grab a fixed lambda sequence from one call to glmnet, then
# define elastic net training and prediction functions
if (!require("glmnet",quietly=TRUE)) {
  stop("Package glmnet not installed (required for this example)!")
}
out.gnet = glmnet(x,y,alpha=0.9,nlambda=100,lambda.min.ratio=1e-4)
lambda = out.gnet$lambda
funs = elastic.funs(gamma=0.9,lambda=lambda)

# Split conformal inference
out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

y0.mat = matrix(rep(y0,ncol(out.split$lo)),nrow=n0)
cov.split = colMeans(out.split$lo <= y0.mat & y0.mat <= out.split$up)
len.split = colMeans(out.split$up - out.split$lo)
```

```

err.split = colMeans((y0.mat - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac, list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

# Plot average coverage
plot(log(lambda), cov.split, type="o", pch=20, ylim=c(0,1),
  xlab="log(lambda)", ylab="Avg coverage",
  main=paste0("Split conformal + elastic net (fixed lambda sequence):",
    "\nAverage coverage"))
abline(h=cov.orac, lty=2, col=2)
legend("bottomleft", col=1:2, lty=1:2,
  legend=c("Split conformal", "Oracle"))

# Plot average length
plot(log(lambda), len.split, type="o", pch=20,
  ylim=range(len.split, len.orac),
  xlab="log(lambda)", ylab="Avg length",
  main=paste0("Split conformal + elastic net (fixed lambda sequence):",
    "\nAverage length"))
abline(h=len.orac, lty=2, col=2)
legend("topleft", col=1:2, lty=1:2,
  legend=c("Split conformal", "Oracle"))

# Plot test error
plot(log(lambda), err.split, type="o", pch=20,
  ylim=range(err.split, err.orac),
  xlab="log(lambda)", ylab="Test error",
  main=paste0("Split conformal + elastic net (fixed lambda sequence):",
    "\nTest error"))
abline(h=err.orac, lty=2, col=2)
legend("topleft", col=1:2, lty=1:2,
  legend=c("Split conformal", "Oracle"))

#####

cat("Type return to continue ...\n")
tmp = readLines(n=1)

## Elastic net: alternate way, use a dynamic sequence of 100 lambda values

# Elastic net training and prediction functions
funs = elastic.funs(gamma=0.9, nlambdas=100)

# Split conformal inference
out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

y0.mat = matrix(rep(y0, ncol(out.split$lo)), nrow=n0)
cov.split = colMeans(out.split$lo <= y0.mat & y0.mat <= out.split$up)
len.split = colMeans(out.split$up - out.split$lo)

```

```

err.split = colMeans((y0.mat - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac, list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

# Plot average coverage
plot(log(length(cov.split):1), cov.split, type="o", pch=20, ylim=c(0,1),
  xlab="log(lambda rank) (i.e., log(1)=0 is smallest)",
  ylab="Avg coverage",
  main=paste0("Split conformal + elastic net (dynamic lambda sequence):",
    "\nAverage coverage"))
abline(h=cov.orac, lty=2, col=2)
legend("bottomleft", col=1:2, lty=1:2,
  legend=c("Split conformal", "Oracle"))

# Plot average length
plot(log(length(len.split):1), len.split, type="o", pch=20,
  ylim=range(len.split, len.orac),
  xlab="log(lambda rank) (i.e., log(1)=0 is smallest)",
  ylab="Avg length",
  main=paste0("Split conformal + elastic net (dynamic lambda sequence):",
    "\nAverage length"))
abline(h=len.orac, lty=2, col=2)
legend("topleft", col=1:2, lty=1:2,
  legend=c("Split conformal", "Oracle"))

# Plot test error
plot(log(length(err.split):1), err.split, type="o", pch=20,
  ylim=range(err.split, err.orac),
  xlab="log(lambda rank) (i.e., log(1)=0 is smallest)", ylab="Test error",
  main=paste0("Split conformal + elastic net (dynamic lambda sequence):",
    "\nTest error"))
abline(h=err.orac, lty=2, col=2)
legend("topleft", col=1:2, lty=1:2,
  legend=c("Split conformal", "Oracle"))

#####

cat("Type return to continue ...\n")
tmp = readLines(n=1)

## Elastic net: cross-validate over a sequence of 100 lambda values

# Elastic net training and prediction functions
funs = elastic.funs(gamma=0.9, nlambdas=100, cv=TRUE)

# Split conformal inference
out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

cov.split = mean(out.split$lo <= y0 & y0 <= out.split$up)

```



```

len.split = mean(out.split$up - out.split$lo)
err.split = mean((y0 - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac, list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

tab = matrix(c(cov.split, len.split, err.split,
  cov.orac, len.orac, err.orac), ncol=2)
colnames(tab) = c("Split conformal", "Oracle")
rownames(tab) = c("Avg coverage", "Avg length", "Test error")
tab

```

---

lars.funs	<i>Forward stepwise, least angle regression, and lasso training and prediction functions.</i>
-----------	---

---

## Description

Construct training and prediction functions for forward stepwise, least angle regression net, or the lasso path, based on the [lars](#) package, over a given number of steps.

## Usage

```

lars.funs(type = c("stepwise", "lar", "lasso"), normalize = TRUE,
  intercept = TRUE, max.steps = 20, cv = FALSE, cv.rule = c("min",
    "lse"), use.Gram = TRUE)

```

## Arguments

type	One of "stepwise", "lar", or "lasso", indicating which path algorithm should be run. Default is "stepwise".
normalize, intercept	Should the features be normalized (to have unit L2 norm), and should an intercept be included? Default for both is TRUE.
max.steps	Number of steps down the path to be taken before quitting. Default is 20. Prediction is done over steps 1 through max.steps, unless
cv	Should 10-fold cross-validation be used? If TRUE, then prediction is done with either the (usual) min rule, or the lse rule. See the cv.rule argument, below. If FALSE (the default), then prediction is done over all path steps taken.
cv.rule	If the cv argument is TRUE, then cv.rule determines which rule should be used for the predict function, either "min" (the usual rule) or "lse" (the one-standard-error rule). Default is "min".
use.Gram	Should the Gram matrix (cross product of feature matrix) be stored? Default is TRUE. But storing the Gram matrix may be costly when p (number of columns of feature matrix) is large, say, large compared to n (number rows of feature matrix), so in this case, you may want to choose FALSE.

## Details

This function is based on the packages [lars](#) and [plyr](#). If these packages are not installed, then the function will abort.

## Value

A list with three components: train.fun, predict.fun, active.fun. The third function is designed to take the output of train.fun, and reports which features are active for each fitted model contained in this output.

## See Also

[glmnet.funs](#) for elastic net, lasso, and ridge regression training and prediction functions, defined over a sequence of lambda values.

## Examples

```
## Forward stepwise: use 30 path steps

# Generate some example training data
set.seed(33)
n = 100; p = 120; s = 10
x = matrix(rnorm(n*p),n,p)
beta = c(rnorm(s),rep(0,p-s))
y = x %*% beta + rnorm(n)

# Generate some example test data
n0 = 50
x0 = matrix(rnorm(n0*p),n0,p)
y0 = x0 %*% beta + rnorm(n0)

# Stepwise training and prediction functions
funs = lars.funs(type="stepwise",max.steps=30)

# Split conformal inference
out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

y0.mat = matrix(rep(y0,ncol(out.split$lo)),nrow=n0)
cov.split = colMeans(out.split$lo <= y0.mat & y0.mat <= out.split$up)
len.split = colMeans(out.split$up - out.split$lo)
err.split = colMeans((y0.mat - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac, list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

# Plot average coverage
plot(1:length(cov.split),cov.split,type="o",pch=20,ylim=c(0,1),
  xlab="Number of path steps",ylab="Avg coverage",
  main=paste0("Split conformal + stepwise:\nAverage coverage"))
```

```

abline(h=cov.orac,lty=2,col=2)
legend("bottomright",col=1:2,lty=1:2,
      legend=c("Split conformal","Oracle"))

# Plot average length
plot(1:length(len.split),len.split,type="o",pch=20,
     ylim=range(len.split,len.orac),
     xlab="Number of path steps",ylab="Avg length",
     main=paste0("Split conformal + stepwise:\nAverage length"))
abline(h=len.orac,lty=2,col=2)
legend("topright",col=1:2,lty=1:2,
      legend=c("Split conformal","Oracle"))

# Plot test error
plot(1:length(err.split),err.split,type="o",pch=20,
     ylim=range(err.split,err.orac),
     xlab="Number of path steps",ylab="Test error",
     main=paste0("Split conformal + stepwise:\nTest error"))
abline(h=err.orac,lty=2,col=2)
legend("topright",col=1:2,lty=1:2,
      legend=c("Split conformal","Oracle"))

#####

cat("Type return to continue ...\n")
tmp = readLines(n=1)

## Forward stepwise: cross-validate over 30 path steps

# Stepwise training and prediction functions
funs = lars.funs(type="stepwise",max.steps=30,cv=TRUE,cv.rule="1se")

# Split conformal inference
out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

cov.split = mean(out.split$lo <= y0 & y0 <= out.split$up)
len.split = mean(out.split$up - out.split$lo)
err.split = mean((y0 - out.split$pred)^2)

# Compare to parametric intervals from oracle linear regression
lm.orac = lm(y~x[,1:s])
out.orac = predict(lm.orac, list(x=x0[,1:s]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

tab = matrix(c(cov.split,len.split,err.split,
  cov.orac,len.orac,err.orac),ncol=2)
colnames(tab) = c("Split conformal","Oracle")
rownames(tab) = c("Avg coverage","Avg length","Test error")
tab

```

---

lm.funs	<i>Linear regression training and prediction functions, and special leave-one-out fitting function.</i>
---------	---

---

## Description

Construct the training and prediction functions for linear regression, and a special function to quickly compute leave-one-out fitted values.

## Usage

```
lm.funs(intercept = TRUE, lambda = 0)
```

## Arguments

intercept	Should an intercept be included in the linear model? Default is TRUE.
lambda	A value or sequence of lambda values to be used in ridge regression. Default is 0, which means ordinary linear regression.

## Details

The train.fun function constructed here leverages an optional third argument (in addition to the usual x,y): out, whose default is NULL. If non-NULL, it is assumed to be the result of a previous call to train.fun, on the *same* features x as we are currently considering. This is done for efficiency, and to perform the regression, it uses the saved Cholesky decomposition instead of computing a new one from scratch.

## Value

A list with four components: train.fun, predict.fun, special.fun, active.fun. The last function is designed to take the output of train.fun, and reports which features are active for each fitted model contained in this output. Trivially, here, all features are generically active in ridged linear models.

## Examples

```
## Linear regression: classical setting

# Generate some example training data
set.seed(33)
n = 100; p = 10
x = matrix(rnorm(n*p),n,p)
beta = rnorm(p)
y = x %*% beta + rnorm(n)

# Generate some example test data
n0 = 50
x0 = matrix(rnorm(n0*p),n0,p)
y0 = x0 %*% beta + rnorm(n0)

# Linear regression training and prediction functions
funs = lm.funs()

# Conformal inference, and split conformal inference
```

```

out.conf = conformal.pred(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict, verb=TRUE)

out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

cov.conf = mean(out.conf$lo <= y0 & y0 <= out.conf$up)
len.conf = mean(out.conf$up - out.conf$lo)
err.conf = mean((y0 - out.conf$pred)^2)

cov.split = mean(out.split$lo <= y0 & y0 <= out.split$up)
len.split = mean(out.split$up - out.split$lo)
err.split = mean((y0 - out.split$pred)^2)

# Compare to parametric intervals from linear regression
lm.orac = lm(y~x[,1:p])
out.orac = predict(lm.orac, list(x=x0[,1:p]),
  interval="predict", level=0.9)

cov.orac = mean(out.orac[, "lwr"] <= y0 & y0 <= out.orac[, "upr"])
len.orac = mean(out.orac[, "upr"] - out.orac[, "lwr"])
err.orac = mean((y0 - out.orac[, "fit"])^2)

tab = matrix(c(cov.conf, len.conf, err.conf,
  cov.split, len.split, err.split,
  cov.orac, len.orac, err.orac), ncol=3)
colnames(tab) = c("Conformal", "Split conformal", "Oracle")
rownames(tab) = c("Avg coverage", "Avg length", "Test error")
tab

plot(y0, ylim=c(min(out.conf$lo, out.split$lo, out.orac[, "lwr"]),
  max(out.conf$up, out.split$up, out.orac[, "upr"])),
  main="Linear regression: prediction intervals")
segments(1:n0, out.conf$lo, 1:n0, out.conf$up)
segments(1:n0+0.2, out.split$lo, 1:n0+0.2, out.split$up, col=4)
segments(1:n0-0.2, out.orac[, "lwr"], 1:n0-0.2, out.orac[, "upr"], lty=2, col=2)
legend("topleft", col=c(1, 4, 2), lty=c(1, 1, 2),
  legend=c("Conformal", "Split conformal", "Oracle"))

```

loco

*Variable importance via mean (or median) excess test error***Description**

Compute confidence intervals for mean (or median) excess test error due to dropping a variable

**Usage**

```
loco(x, y, train.fun, predict.fun, active.fun, alpha = 0.1,
  bonf.correct = TRUE, split = NULL, seed = NULL, verbose = FALSE)
```

**Arguments**

**x** Matrix of features, of dimension (say)  $n \times p$ .

<code>y</code>	Vector of responses, of length (say) $n$ .
<code>train.fun</code>	A function to perform model training, i.e., to produce an estimator of $E(Y X)$ , the conditional expectation of the response variable $Y$ given features $X$ . Its input arguments should be <code>x</code> : matrix of features, and <code>y</code> : vector of responses.
<code>predict.fun</code>	A function to perform prediction for the (mean of the) responses at new feature values. Its input arguments should be <code>out</code> : output produced by <code>train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions.
<code>active.fun</code>	A function which takes the output of <code>train.fun</code> , and reports which features are active for each fitted model contained in this output. Its only input argument should be <code>out</code> : output produced by <code>train.fun</code> .
<code>alpha</code>	Miscoverage level for the confidence intervals, i.e., intervals with coverage $1 - \alpha$ are formed. Default for <code>alpha</code> is 0.1.
<code>bonf.correct</code>	Should a Bonferroni correction be applied to the p-values and confidence intervals? Default is TRUE.
<code>split</code>	Indices that define the data-split to be used (i.e., the indices define the first half of the data-split, on which the model is trained). Default is NULL, in which case the split is chosen randomly.
<code>seed</code>	Integer to be passed to <code>set.seed</code> before defining the random data-split to be used. Default is NULL, which effectively sets no seed. If both <code>split</code> and <code>seed</code> are passed, the former takes priority and the latter is ignored.
<code>verbose</code>	Should intermediate progress be printed out? Default is FALSE.

## Details

In leave-one-covariate-out or LOCO inference, the training data is split in two parts, and the first part is used to train a model, or some number of models across multiple tuning steps (e.g., indexed by different tuning parameter values  $\lambda$  in the lasso, or different steps along the forward stepwise path). For each model, each variable is left out one at a time from the first part of the data, and the entire training procedure is repeated without this variable in consideration. Residuals are computed on both from the original fitted model, and the refitted model without the variable in consideration. A pairwise difference between the latter and former residuals is computed, and either a Z-test, sign test, or Wilcoxon signed rank test is performed to test either the mean or median difference here being zero. The Z-test is of course approximately valid under the conditions needed for the CLT; the sign test is distribution-free and exact in finite samples (only assumes continuity of the underlying distribution); the Wilcoxon signed rank test is also distribution-free and exact in finite samples, but may offer more power (it assumes both continuity and symmetry of the underlying distribution).

A couple other important notes: p-values here are from a one-sided test of the target parameter (mean or median excess test error) being equal to zero versus greater than zero. Confidence intervals are from inverting the two-sided version of this test.

## Value

A list with the following components: `inf.z`, `inf.sign`, `inf.wilcox`, `active`, `master`, `bonf.correct`. The first three are lists, containing the results of LOCO inference with the Z-test, sign test, and Wilcoxon signed rank test, respectively. More details on these tests are given below. These lists have one element per tuning step inherent to the training and prediction functions, `train.fun` and `predict.fun`. The fourth returned component `active` is a list, with one element per tuning step, that reports which features are active in the corresponding fitted model. The fifth returned component `master` collects all active features across all tuning steps, for easy reference. The last component signals whether a Bonferroni correction has been applied.

## References

"Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018).

## Examples

```
## Use lasso + CV to choose a model, then test variable importance in the
## selected model

# Generate some example training data
set.seed(33)
n = 200; p = 500; s = 5
x = matrix(rnorm(n*p),n,p)
beta = 2*c(rnorm(s),rep(0,p-s))
y = x %*% beta + rnorm(n)

# Lasso training and prediction functions, using cross-validation over 100
# values of lambda, with the 1se rule
funs = lasso.funs(nlambda=100,cv=TRUE,cv.rule="1se")

# Split-sample LOCO analysis
out.loco = loco(x, y, alpha=0.1, train.fun=funs$train, predict.fun=funs$predict,
  active.fun=funs$active.fun, verbose=TRUE)
out.loco

# Plot the Wilcoxon intervals
ylim = range(out.loco$inf.wilcox[[1]][,2:3])
J = length(out.loco$active[[1]])
plot(c(), c(), xlim=c(1,J), ylim=ylim, xaxt="n",
  main="LOCO analysis from lasso + CV model",
  xlab="Variable", ylab="Confidence interval")
axis(side=1, at=1:J, labels=FALSE)
for (j in 1:J) {
  axis(side=1, at=j, labels=out.loco$active[[1]][j], cex.axis=0.75,
    line=0.5*j%2)
}
abline(h=0)
segments(1:J, out.loco$inf.wilcox[[1]][,2],
  1:J, out.loco$inf.wilcox[[1]][,3],
  col="red", lwd=2)
```

---

loco.roo

---

*Variable importance via excess test error*


---

## Description

Compute prediction intervals for the excess test error due to dropping a variable, measured in-sample and having valid in-sample coverage

## Usage

```
loco.roo(x, y, train.fun, predict.fun, vars = 0, alpha = 0.1,
  mad.train.fun = NULL, mad.predict.fun = NULL, split = NULL,
  seed = NULL, out.roo = NULL, verbose = FALSE)
```

## Arguments

<code>x</code>	Matrix of variables, of dimension (say) $n \times p$ .
<code>y</code>	Vector of responses, of length (say) $n$ .
<code>train.fun</code>	A function to perform model training, i.e., to produce an estimator of $E(Y X)$ , the conditional expectation of the response variable $Y$ given features $X$ . Its input arguments should be <code>x</code> : matrix of features, and <code>y</code> : vector of responses.
<code>predict.fun</code>	A function to perform prediction for the (mean of the) responses at new feature values. Its input arguments should be <code>out</code> : output produced by <code>train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions.
<code>vars</code>	A list specifying the variables (indices between 1 and $p$ ) to for which variable importance should be investigated. Alternatively, if set equal to 0, the default, then all variables are investigated.
<code>alpha</code>	Miscoverage level for the prediction intervals, i.e., intervals with coverage $1 - \alpha$ are formed. Default for <code>alpha</code> is 0.1.
<code>mad.train.fun</code>	A function to perform training on the absolute residuals i.e., to produce an estimator of $E(R X)$ where $R$ is the absolute residual $R =  Y - m(X) $ , and $m$ denotes the estimator produced by <code>train.fun</code> . This is used to scale the conformal score, to produce a prediction interval with varying local width. The input arguments to <code>mad.train.fun</code> should be <code>x</code> : matrix of features, and <code>y</code> : vector of absolute residuals. The default for <code>mad.train.fun</code> is <code>NULL</code> , which means that no training is done on the absolute residuals, and the usual (unscaled) conformal score is used. Note that if <code>mad.train.fun</code> is non- <code>NULL</code> , then so must be <code>mad.predict.fun</code> (see next).
<code>mad.predict.fun</code>	A function to perform prediction for the (mean of the) absolute residuals at new feature values. Its input arguments should be <code>out</code> : output produced by <code>mad.train.fun</code> , and <code>newx</code> : feature values at which we want to make predictions. The default for <code>mad.predict.fun</code> is <code>NULL</code> , which means that no local scaling is done for the conformal score, i.e., the usual (unscaled) conformal score is used.
<code>split</code>	Indices that define the data-split to be used (i.e., the indices define the first half of the data-split). Note that this split is common both to <code>conformal.pred.roo</code> (whether already run, or to be run internally, see below) and the excess error intervals computed by this function. Default is <code>NULL</code> , in which case the split is chosen randomly.
<code>seed</code>	Integer to be passed to <code>set.seed</code> before defining the random data-split to be used. Default is <code>NULL</code> , which effectively sets no seed. If both <code>split</code> and <code>seed</code> are passed, the former takes priority and the latter is ignored.
<code>out.roo</code>	Output from running <code>conformal.pred.roo</code> on the given data set; default is <code>NULL</code> , which means that <code>conformal.pred.roo</code> will be run internally in order to compute in-sample prediction intervals. If <code>out.roo</code> is <code>NULL</code> , then the data-split common to <code>conformal.pred.roo</code> and this function will be determined by the <code>split</code> or <code>seed</code> arguments. If non- <code>NULL</code> , then the common data-split will be determined by that recorded in <code>out.roo</code> , and the <code>split</code> and <code>seed</code> arguments will be (silently) ignored.
<code>verbose</code>	Should intermediate progress be printed out? Default is <code>FALSE</code> .

## Details

For concreteness, suppose that we want to use the predictions from forward stepwise regression at steps 1 through 5 in the path. In this case, there are  $m = 5$  internal tuning parameter values to `predict.fun`, in the notation used above, and each of the returned matrices `pred`, `lo`, `up`, `fit` will have



5 columns (one for each step of the forward stepwise path). The code is structured in this way so that we may defined a single pair of functions `train.fun` and `predict.fun`, over a set of  $m = 5$  tuning parameter values, instead of calling the conformal function separately  $m = 5$  times.

### Value

A list with the following components: `lo`, `up`, `vars`, `split`, `out.roo`. The third component is a list of variables that were tested (i.e., dropped one at a time, to compute excess error). The first two are arrays. The indices used for the half of the data-split are returned in `split`. Finally, for convenience, the output from running `conformal.pred.roo` is stored in `out.roo`.

### References

"Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018).

### Examples

```
## Use lasso + CV to choose a model, then test variable importance in the
## selected model

# Generate some example training data
set.seed(11)
n = 200; p = 500; s = 10
x = matrix(rnorm(n*p),n,p)
beta = 8*c(rnorm(s),rep(0,p-s))
y = x %*% beta + rnorm(n)

# Lasso training and prediction functions, using cross-validation over 100
# values of lambda, with the 1se rule
funs = lasso.funs(nlambda=100,cv=TRUE,cv.rule="1se")

# In-sample rank-one-out conformal inference
out.roo = conformal.pred.roo(x, y, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

# Look at which variables were nonzero in the lasso + CV model fit to the whole
# data set
out.all = out.roo$out.all
vars = which(coef(out.all$glmnet.fit, s=out.all$lambda.1se) != 0)

# Look at error inflation due to variable dropping, among vars
out.loco = loco.roo(x, y, alpha=0.1, vars=vars,
  train.fun=funs$train, predict.fun=funs$predict, verbose=TRUE)

# Compute "c-values", the proportion of intervals that have a left endpoint
# less than or equal to 0
cvals = colMeans(out.loco$lo[, ,1] <= 0)
names(cvals) = vars
cvals

xlab = "Sample number"
ylab = "Interval"

# For each dropped variable in consideration, plot the intervals
for (j in 1:length(vars)) {
```

```

plot(c(),c(),xlim=c(1,n),ylim=range(c(out.loco$lo[,j,1],out.loco$up[,j,1])),
     xlab=xlab,ylab=ylob,main=sprintf("Variable %i, c-value = %0.3f",
                                     vars[j], cvals[j]))
cols = ifelse(out.loco$lo[,j,1] <= 0, 1, 3)
segments(1:n,out.loco$lo[,j,1],1:n,out.loco$up[,j,1],col=cols)
abline(h=0, lty=2, lwd=2, col=2)
}

```

---

plot.sim

*Plot function for sim object.*


---

## Description

Plot the results of a set of simulations, stored in an object of class sim (produced by sim.master).

## Usage

```

## S3 method for class 'sim'
plot(x, method.nums = 1:length(x$ave.cov),
     method.names = NULL, cols = 1:8, log = "", xlim = NULL,
     se = FALSE, main = NULL, cex.main = 1.25,
     xlab = "Relative optimism", legend.pos = c("bottomleft", "", ""),
     make.pdf = FALSE, fig.dir = ".", file.prefix = "", h = 6,
     w = 6, mar = NULL, ...)

```

---

print.loco

*Print function for loco object.*


---

## Description

Summary and print the results of a set of simulations, stored an object of class sim (produced by sim.master).

## Usage

```

## S3 method for class 'loco'
print(x, test = c("wilcox", "sign", "z", "all"),
     digits = 3, ...)

```

## Arguments

x	The loco object.
test	One of "z", "sign", "wilcox", or "all", describing which test results to show. If "z", then the results from only Z-tests are displayed; if "sign", then only sign tests; if "wilcox", then only Wilcoxon tests. If "all", then the results from all tests are displayed. Default is "wilcox".
digits	Number of digits to display. Default is 3.
...	Other arguments (currently not used).

---

print.sim	<i>Print function for sim object.</i>
-----------	---------------------------------------

---

### Description

Summarize and print the results of a set of simulations, stored an object of class sim (produced by sim.master).

### Usage

```
## S3 method for class 'sim'
print(x, type = c("err", "len", "all"), se = TRUE,
      digits = 3, ...)
```

### Arguments

x	The sim object.
type	One of "all", "err", or "len" describing the type of summary to be used. If "err", then for each method, the tuning parameter value that gives the best average test error is selected, and the coverage and length properties at this tuning parameter value are report. If "len", then the analogous thing is done, but for the tuning parameter value that gives the best average length. If "all", then the average coverage, length, and test error results are shown across all tuning parameter values. Default is "err".
se	Should standard errors be displayed (in parantheses)? For each metric, this is defined as the standard deviation divided by the square root of the number of simulation repetitions. Default is TRUE.
digits	Number of digits to display. Default is 3.
...	Other arguments (currently not used).

---

print.tex	<i>Print function for latex-style tables.</i>
-----------	---

---

### Description

Print a given table in format digestable by latex.

### Usage

```
## S3 method for class 'tex'
print(tab, tab.se = NULL, digits = 3, file = NULL,
      align = "l")
```

---

`rf.funs`*Random forests training and prediction functions.*

---

### Description

Construct training and prediction functions for random forests.

### Usage

```
rf.funs(ntree = 500, varfrac = 0.333, replace = TRUE,  
        obsfrac = ifelse(replace, 1, 0.632), nodesize = 5)
```

### Arguments

<code>ntree</code>	Number of trees to grow. Default is 500.
<code>varfrac</code>	Determines the number of variables used as candidates at each split: this is $\text{floor}(\text{varfrac} * p)$ , where $p$ is the total number of variables. Default is 0.333.
<code>replace</code>	Should sampling of observations done with or without replacement? Default is FALSE.
<code>obsfrac</code>	Determines the number of observations used by each tree: this is $\text{floor}(\text{obsfrac} * n)$ , where $n$ is the number of training observations. Default is 1 when <code>replace</code> is TRUE, and 0.632 when <code>replace</code> is FALSE.
<code>nodesize</code>	Sought size of terminal nodes, in growing each tree. Default is 5.

### Details

This function is based on the packages [randomForest](#) and [plyr](#). If these packages are not installed, then the function will abort.

### Value

A list with three components: `train.fun`, `predict.fun`, `active.fun`. The third function is designed to take the output of `train.fun`, and reports which features are active for the fitted model contained in this output.

### Examples

```
## See examples for sam.funs function
```

sam.funs

*Sparse additive models training and prediction functions.***Description**

Construct training and prediction functions for sparse additive models, based on the [SAM](#) package, over a sequence of (given or internally computed) lambda values.

**Usage**

```

sam.funs(m = 3, lambda = NULL, nlambda = 30,
        lambda.min.ratio = 0.005)

```

**Arguments**

m	Number of spline functions to be used in the additive expansion of each variable. Default is 3.
lambda	Sequence of lambda values over which training is performed. This must be in decreasing order, and — this argument should be used with caution! When used, it is usually best to grab the sequence constructed by one initial call to SAM (see examples). Default is NULL, which means that the nlambda, lambda.min.ratio arguments will define the lambda sequence (see next).
nlambda	Number of lambda values over which training is performed. In particular, the lambda sequence is defined by nlambda log-spaced values between lambda.max and lambda.min.ratio * lambda.max, where lambda.max is the smallest value of lambda at which the solution has all zero components, and lambda.min.ratio is a small fraction (see next). Default is 30.

**Details**

This function is based on the packages [SAM](#) and [plyr](#). If these packages are not installed, then the function will abort.

**Value**

A list with three components: train.fun, predict.fun, active.fun. The third function is designed to take the output of train.fun, and reports which features are active for each fitted model contained in this output.

**Examples**

```

## Sparse additive models: high-dimensional example

# Use the sim.xy function to get a data set with additive structure
set.seed(11)
n = 200; n0 = 200; p = 500; s = 10
obj = sim.xy(n+n0, p, mean.fun="additive", m=4, s=s, snr=3)
x = obj$x[1:n,]
y = obj$y[1:n]
x0 = obj$x[(n+1):(n+n0),]
y0 = obj$y[(n+1):(n+n0)]

```

```

# Grab a fixed lambda sequence from one call to samQL, then define the sparse
# additive models training and prediction functions
if (!require("SAM",quietly=TRUE)) {
  stop("Package SAM not installed (required for this example)!")
}
out.sam = samQL(x,y,nlambda=50,lambda.min.ratio=1e-5)
lambda = out.sam$lambda
my.sam.funs = sam.funs(m=5,lambda=lambda)

# Random forest training and prediction functions
if (!require("randomForest",quietly=TRUE)) {
  stop("Package randomForest not installed (required for this example)!")
}
my.rf.funs = rf.funs(ntree=500)

# Split conformal inference with sparse additive models and random forest
out.sam = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=my.sam.funs$train, predict.fun=my.sam.funs$predict)

out.rf = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=my.rf.funs$train, predict.fun=my.rf.funs$predict)

y0.mat = matrix(rep(y0,ncol(out.sam$lo)),nrow=n0)
cov.sam = colMeans(out.sam$lo <= y0.mat & y0.mat <= out.sam$up)
len.sam = colMeans(out.sam$up - out.sam$lo)
err.sam = colMeans((y0.mat - out.sam$pred)^2)

cov.rf = mean(out.rf$lo <= y0 & y0 <= out.rf$up)
len.rf = mean(out.rf$up - out.rf$lo)
err.rf = mean((y0 - out.rf$pred)^2)

# Plot average coverage
plot(log(lambda),cov.sam,type="o",pch=20,ylim=c(0,1),
  xlab="log(lambda)",ylab="Avg coverage",
  main=paste0("Split conformal + Spam, RF:\nAverage coverage"))
abline(h=cov.rf,lty=2,col=4)
legend("bottomright",col=c(1,4),lty=1:2,
  legend=c("Spam","Random forest"))

# Plot average length
plot(log(lambda),len.sam,type="o",pch=20,
  ylim=range(len.sam,len.rf),
  xlab="log(lambda)",ylab="Avg length",
  main=paste0("Split conformal + Spam, RF:\nAverage length"))
abline(h=len.rf,lty=2,col=4)
legend("topleft",col=c(1,4),lty=1:2,
  legend=c("Spam","Random forest"))

# Plot test error
plot(log(lambda),err.sam,type="o",pch=20,
  ylim=range(err.sam,err.rf),
  xlab="log(lambda)",ylab="Test error",
  main=paste0("Split conformal + Spam, RF:\nTest error"))
abline(h=err.rf,lty=2,col=4)
legend("topleft",col=c(1,4),lty=1:2,
  legend=c("Spam","Random forest"))

```

sim.master

*Master function for running simulations.*

## Description

Run a set of simulations with the specified configuration.

## Usage

```
sim.master(n, p, conformal.pred.funs, n0 = n, in.sample = FALSE,
  nrep = 20, seed = NULL, verbose = FALSE, file = NULL,
  file.rep = 5, x.dist = c("normal", "binom", "sn", "mix"),
  cor = c("none", "pair", "auto", "rand"), rho = 0.5, k = 5,
  standardize = TRUE, mean.fun = c("linear", "additive", "rotated"),
  m = 4, sparsity = c("strong", "weak"), s = round(log(p)),
  weak.decay = 0.5, mu.seed = NULL, error.dist = c("normal", "unif",
  "t", "sn"), sigma = 1, bval = 3, snr = NULL,
  sigma.type = c("const", "var"), df = 3, alpha = 5,
  omitted.vars = FALSE)
```

## Arguments

- |   |  |
|---|--|
| n, p  | Number of observations and features, respectively.   |
| conformal.pred.funs   | A list containing conformal inference functions to use. Each function here must take three arguments: x, y, x0 — and no more. These will typically be defined with a wrapper around, e.g., <a href="#">conformal.pred</a> or <a href="#">conformal.pred.split</a> . See examples below.  |
| n0  | The number of points at which to make predictions. Default is n.   |
| in.sample   | Should the original x points be used for predictions (within each repetition)? If TRUE, then the n0 argument (above) is ignored. Default is FALSE.   |
| nrep  | Number of repetitions over which to average results. Default is 20.  |
| seed  | Seed to be set for the overall random number generation, i.e., set before repetitions are begun (for reproducibility of the simulation results). Default is NULL, which effectively sets no seed.  |
| verbose   | Should intermediate progress be printed out? Default is FALSE.   |
| file, file.rep  | Name of a file to which simulation results will be saved (using saveRDS), and a number of repetitions after which intermediate results will be saved. Setting file to NULL is interpreted to mean that no simulations results should be saved; setting file.rep to 0 is interpreted to mean that simulations results should be saved at the very end, i.e., no intermediate saving. Defaults are NULL and 5, respectively. |
| x.dist, cor, rho, k, standardize, mean.fun, m, sparsity, s, weak.decay, error.dist, sigma, bval, snr, sigma.type, df, alpha, omitted.vars | Arguments to pass to <a href="#">sim.xy</a> , see the latter's help file for details.  |

**Value**

A list with the following components.

- `ave.cov`, `ave.len`, `ave.err`: lists of length `m`, where `m` denotes the number of conformal methods evaluated (i.e., the length of the list `conformal.pred.funs`). Each element of `ave.cov` corresponds to a conformal method considered, and is a vector whose length is equal to the number of tuning parameters internal to this method, containing the empirical coverages of conformal intervals, averaged across the repetitions. The lists `ave.len` and `ave.err` are analogous, except they contain the average lengths of conformal intervals, and average test errors, respectively.
- `ave.opt`, `ave.tim`: lists of length `m`, analogous to `ave.cov`, `ave.len`, and `ave.err` (see above), but where `ave.opt` contains the average (relative) optimism of the methods, a unitless measure of model complexity defined by  $(\text{test error} - \text{training error}) / (\text{test error})$ ; and `ave.tim` contains the average runtimes (in seconds) of the methods.
- `sd.cov`, `sd.len`, `sd.err`, `sd.opt`, `sd.tim`: same as above, but containing deviations, rather than averages, across the repetitions.
- `cov`, `len`, `err`, `opt`, `tim`: lists of length `m`, reporting the full set of metrics across repetitions (rather than averages or standard deviations).
- `lev`: a matrix of dimension `nrep` x `n0`, reporting the leverage scores of the test points, across the repetitions.
- `ave.best.err`, `ave.best.len`: matrices of dimension `5` x `m`, providing a summary of the average coverage, length, error, optimism, and time metrics (see description above), but at only one particular tuning parameter value for each method considered — this is the tuning parameter value that either gives the best average error, or best average length.
- `sd.best.err`, `sd.best.len`: matrices of dimension `5` x `m`, providing a summary of the standard deviation of coverage, length, error, optimism, and time metrics for each method's best tuning parameter value (analogous to the construction of `ave.best.err` and `ave.best.len`).

**References**

"Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018).

**See Also**

[sim.xy](#)

**Examples**

```
## Linear regression: test out conformal intervals and parametric intervals
## across a variety of settings

## Not run:
# Set some overall simulation parameters
n = 100; p = 10 # Numbers of observations and features
s = 10 # Number of truly relevant features
n0 = 100 # Number of points at which to make predictions
nrep = 50 # Number of repetitions for a given setting
sigma = 1 # Marginal error standard deviation
alpha = 0.1 # Miscoverage level

# Define conformal inference functions: these are basically just wrappers
# around a particular instantiation of conformal.pred or conformal.pred.split,
```



```

# i.e., particular training and prediction functions
my.lm.funs = lm.funs()
my.conf.fun = function(x, y, x0) {
  conformal.pred(x,y,x0,alpha=alpha,verb="\t\t",
    train.fun=my.lm.funs$train,
    predict.fun=my.lm.funs$predict)
}
my.split.fun = function(x, y, x0) {
  conformal.pred.split(x,y,x0,alpha=alpha,
    train.fun=my.lm.funs$train,
    predict.fun=my.lm.funs$predict)
}

# Hack together our own "conformal" inference function, really, just one that
# returns the parametric intervals
my.param.fun = function(x, y, x0) {
  lm.obj = lm(y~x)
  mat = predict(lm.obj,list(x=x0),interval="predict",level=1-alpha)
  # Return proper outputs in proper formatting
  return(list(pred=mat[, "fit", drop=F], lo=mat[, "lwr", drop=F],
    up=mat[, "upr", drop=F], fit=matrix(lm.obj$fit, ncol=1)))
}

# Now put together a list with our three conformal inference functions
conformal.pred.funs = list(my.conf.fun, my.split.fun, my.param.fun)
names(conformal.pred.funs) = c("Conformal", "Split conformal", "Parametric")

# Set some path, where we can save the rds files containing sim results
path = "."

# Simulation setting A: classical setup --- linear (fully supported) mean
# function; normal, homoskedastic errors; and normal, uncorrelated features
cat("=====\n")
cat("          SETTING A          \n")
cat("=====\n")
simA = sim.master(n, p, conformal.pred.funs, n0=n0, nrep=nrep, verb=TRUE,
  file=paste0(path, "simA.rds"), x.dist="normal", cor="none",
  mean.fun="linear", s=s, error.dist="normal", sigma=sigma, snr=snr,
  sigma.type="const")

# Simulation setting B: now, nonlinear mean, and t2 errors
cat("=====\n")
cat("          SETTING B          \n")
cat("=====\n")
simB = sim.master(n, p, conformal.pred.funs, n0=n0, nrep=nrep, verb=TRUE,
  file=paste0(path, "simB.rds"), x.dist="normal", cor="none",
  mean.fun="additive", m=4, s=s, error.dist="t", df=2, sigma=sigma, snr=snr,
  sigma.type="const")

# Simulation setting C: now, nonlinear mean, heteroskedastic t2 errors, and
# auto-correlated mix of x variables
cat("=====\n")
cat("          SETTING C          \n")
cat("=====\n")
simC = sim.master(n, p, conformal.pred.funs, n0=n0, nrep=nrep, verb=TRUE,
  file=paste0(path, "simC.rds"), x.dist="mix", cor="auto", k=5,
  mean.fun="linear", s=s, error.dist="t", df=2, sigma=sigma, snr=snr,

```

```
sigma.type="var")

## End(Not run)
```

sim.xy

*Features and responses generation.*

## Description

Generate a feature matrix  $x$ , and response vector  $y$ , following a specified setup.

## Usage

```
sim.xy(n, p, x.dist = c("normal", "binom", "sn", "mix"),
  cor = c("none", "pair", "auto", "rand"), rho = 0.5, k = 5,
  standardize = TRUE, mean.fun = c("linear", "additive", "rotated"),
  m = 4, sparsity = c("strong", "weak"), s = round(log(p)),
  weak.decay = 0.5, mu.seed = NULL, error.dist = c("normal", "unif",
  "t", "sn"), sigma = 1, bval = 3, snr = NULL,
  sigma.type = c("const", "var"), df = 3, alpha = 5,
  omitted.vars = FALSE)
```

## Arguments

<code>n</code> , <code>p</code>	The dimensions, as in $n \times p$ , of the feature matrix $x$ . Note that $n$ is also the length of the response vector $y$ .
<code>x.dist</code>	One of "normal", "binom", "sn", "mix", indicating the distribution for the entries of $x$ . In the first three cases, the columns of $x$ are filled out with i.i.d. normal, standard binomial, or skewed normal (with skewness parameter $\alpha = 5$ ) draws, respectively. The third option requires the <a href="#">sn</a> package. In the last case, "mix", each column of $x$ is drawn with equal probability from the above three distributions. Default is "normal".
<code>cor</code>	One of "none", "pair", "auto", "rand", indicating the type of correlation among columns of $x$ . If "pair", then $x$ is post-multiplied by the symmetric square root of the $p \times p$ matrix whose diagonals are 1 and off diagonals are $\rho$ (see parameter below). If "auto", then each column of $x$ is taken to be a random convex combination of its old value and the previous $k$ (see parameter) columns. If "rand", then each column of $x$ is taken to be a random convex combination of its old value and a randomly $k$ other columns. Default is "none".
<code>rho</code>	If <code>cor</code> is "pair", then this specifies the pairwise correlation. Default is 0.5.
<code>k</code>	If <code>cor</code> is "auto" or "rand", then this specifies the number of other columns that are used in the lagged or random convex combinations (see above). Default is 5.
<code>standardize</code>	Should the columns of $x$ be standardized (i.e., centered, and scaled to have variance 1)? Default is TRUE.
<code>mean.fun</code>	One of "linear", "additive", or "rotated", indicating the functional dependence of the mean on the variables. If "additive", then the mean vector $\mu$ is constructed to be an additive function of B-splines of the variables, where each variable is expanded into $df$ B-splines (with knots spaced evenly over the range of observed measurements of the variable). If "rotated", then $\mu$ is set to be randomly rotated version of such an additive function. Default is "linear".

m	Number of B-splines per variable in the "additive" or "rotated" cases for mean.fun; default is 4. Ignored when mean.fun is "linear".
sparsity	Either "strong" or "weak". In the former case, s (see below) randomly chosen variables of the p total contribute to mu, with coefficients randomly set to +1 or -1. In the latter case, still s variable contribute to mu, as before, but now the remaining p-s variables contribute in a weak sense, in that their coefficients are randomly set to +1 or -1 times a successively increasing power of the weak.decay factor (see below). In the "additive" or "rotated" cases for mean.fun, the above should be interpreted in the appropriate groupwise sense, e.g., s groups of spline functions are randomly chosen, each group corresponding to the expansion of a single variable.
s	Number indicating the level of sparsity. Note that the choice $s = p$ would correspond to a fully dense model. Default is $\text{round}(\log(p))$ .
weak.decay	Number controlling the decay of the weak coefficients, in the case sparsity is "weak", as their magnitudes get set to a successive power of weak.decay. Default is 0.5.
mu.seed	Seed to be set before generation of the mean vector mu (ensures that the mean is the same, over multiple calls to this function). Default is NULL, which effectively sets no seed.
error.dist	One of "normal", "unif", "t", "sn", indicating the error distribution, where the last option "sn" is for the skewed normal, and requires the <a href="#">sn</a> package. Default is "normal".
sigma	Standard deviation of errors. When the error distribution does not have a second moment (i.e., t-distribution with 1 or 2 df), then sigma represents the MAD. Default is 1.
bval	Magnitude of nonzero coefficients in the model for mu as a linear function of x (or as a linear function of B-splines of x in the "additive" and "rotated" cases for mean.fun). Default is 3. This is overridden if the snr parameter is specified (see next).
snr	The signal-to-noise ratio, specifically $\text{var}(\mu)/\sigma^2$ , where $\sigma^2$ is the variance of the errors (see previous). The mean will be scaled to meet the desired signal-to-noise ratio.
sigma.type	Either "const" or "var", indicating constant or varying error variance. In the latter case, the error standard deviation sigma is multiplied by $1 + \text{abs}(\mu)/\text{mean}(\text{abs}(\mu))$ (this gives a vector of the same length as mu, i.e., a different standard deviation per component).
df	If error.dist is "t", then this specifies the degrees of freedom of the t-distribution for the errors. Default is 3.
alpha	If error.dist is "sn", then this specifies the skewness parameter (i.e., shape parameter) of the skewed normal distribution for the errors. The location and scale parameters are set so that the resulting distribution always has mean zero and variance 1. Note that $\alpha > 0$ means right-skewed and $\alpha < 0$ means left-skewed. Default is 5.
omitted.vars	Should important (active) variables be omitted from x? Induces correlation between the x and the error terms.

## Details

In the case of an "additive" or "rotated" mean, this function relies on the packages [plyr](#) and [splines](#). If these packages are not installed, then the function will abort.

**Value**

A list with the following components: x, y, and mu.

**References**

"Distribution-Free Predictive Inference for Regression" by Lei, G'Sell, Rinaldo, Tibshirani, Wasserman (2018).

**Examples**

```
## See examples for sam.funs function
```

---

smooth.spline.funs	<i>Smoothing spline training and prediction functions, and special leave-one-out fitting function.</i>
--------------------	--

---

**Description**

Construct the training and prediction functions for smoothing splines, at a particular tuning parameter value or df value (either given or chosen by cross-validation), and construct also a special function for computing leave-one-out fitted values. Based on the [smooth.spline](#) function.

**Usage**

```
smooth.spline.funs(df = NULL, spar = NULL, cv = TRUE,
  tol.fact = 1e-06)
```

**Arguments**

df	Desired effective degrees of freedom of the smoothing spline fit. If NULL, then the complexity of the fit controlled either the spar or cv arguments (see below).
spar	Parameter that scales roughly as $\log(\lambda)$ , where $\lambda$ is the parameter multiplying the roughness penalty in the smoothing spline criterion. See the smooth.spline help file for details. If NULL, then the complexity of the fit is chosen by the cv argument (see next).
cv	Either TRUE, indicating that leave-one-out cross-validation should be used to choose the smoothing parameter $\lambda$ , or FALSE, indicating that generalized cross-validation should be used to choose $\lambda$ . Note that this argument is only in effect when both df and spar are NULL.
tol.fact	Factor multiplying the interquartile range of the x values, $IQR(x)$ , to determine a threshold for uniqueness: the x values are binned into bins of size $tol.fact * IQR(x)$ , and values which fall into the same bin are regarded as the same. Default is $1e-6$ .

## Details

Note that the constructed function `special.fun` only serve as an approximation to the exact leave-one-out fits when the `smooth.spline` function merges nearby adjacent  $x$  points (which happens when adjacent  $x$  points are closer than `tol`), since in this case the `smooth.spline` function only returns the leverage scores (diagonal elements of the smoother matrix) on the reduced (merged) data set. Another important note is that the constructed `special.fun` will be formally invalid when cross-validation (or generalized cross-validation) is used to pick the smooth parameter. In both of these cases, `special.fun` does *not* throw a warning, and it is left up to the user to consider using this function wisely.

## Value

A list with four components: `train.fun`, `predict.fun`, `special.fun`, `active.fun`. The last function is designed to take the output of `train.fun`, and reports which features are active for each fitted model contained in this output. Trivially, here, there is only one feature and it is always active.

## Examples

```
## Smoothing splines: some simple univariate examples

# Generate some example training data, clearly heteroskedastic
set.seed(33)
n = 1000
x = runif(n,0,2*pi)
y = sin(x) + x*pi/30*rnorm(n)

# Generate some example test data
n0 = 1000
x0 = runif(n,0,2*pi)
y0 = sin(x0) + x0*pi/30*rnorm(n0)

# Smoothing spline training and prediction functions, where the smoothing
# parameter is chosen via cross-validation
funs = smooth.spline.funs(cv=TRUE)

# Jackknife conformal for out-of-sample prediction intervals (valid on average
# over new x0 values), we can use the special leave-one-out fitting function
out.jack = conformal.pred.jack(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict, special.fun=funs$special)

plot(c(), c(), xlab="x0", ylab="y0", xlim=range(x0),
  ylim=range(c(y0,out.jack$lo,out.jack$up)), col="white",
  main=paste0("Jackknife (out-of-sample) prediction intervals\n",
    sprintf("Average length: %0.3f",mean(out.jack$up-out.jack$lo))))
o = order(x0)
segments(x0[o], out.jack$lo[o], x0[o], out.jack$up[o], col="pink")
lines(x0[o], out.jack$pred[o], lwd=2, col="red")
points(x0, y0, col="gray50")

# Split conformal for out-of-sample prediction intervals (valid on average over
# new x0 values)
out.split = conformal.pred.split(x, y, x0, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict)

plot(c(), c(), xlab="x0", ylab="y0", xlim=range(x0),
```

```

        ylim=range(c(y0,out.split$lo,out.split$up)), col="white",
        main=paste0("Split conformal (out-of-sample) prediction intervals\n",
        sprintf("Average length: %0.3f",mean(out.split$up-out.split$lo))))
o = order(x0)
segments(x0[o], out.split$lo[o], x0[o], out.split$up[o], col="lightgreen")
lines(x0[o], out.split$pred[o], lwd=2, col="darkgreen")
points(x0, y0, col="gray50")

# Rank-one-out split conformal for in-sample prediction intervals (valid on
# averaged over observed x values)
out.roo = conformal.pred.roo(x, y, alpha=0.1,
        train.fun=funs$train, predict.fun=funs$predict)

plot(c(), c(), xlab="x", ylab="y", xlim=range(x),
        ylim=range(c(y,out.roo$lo,out.roo$up)), col="white",
        main=paste0("R00-conformal (in-sample) prediction intervals\n",
        sprintf("Average length: %0.3f",mean(out.roo$up-out.roo$lo))))
o = order(x)
segments(x[o], out.roo$lo[o], x[o], out.roo$up[o], col="lightblue")
lines(x[o], out.roo$fit.all[o], lwd=2, col="blue")
points(x, y, col="gray50")

## Adjust now for heteroskedasticity, by using mad.train.fun and mad.predict.fun

# Jackknife conformal is much slower to run, because we can't use the special
# leave-one-out fitting function anymore
out.jack.local = conformal.pred.jack(x, y, x0, alpha=0.1,
        train.fun=funs$train, predict.fun=funs$predict,
        mad.train.fun=funs$train, mad.predict.fun=funs$predict, verb=TRUE)

plot(c(), c(), xlab="x0", ylab="y0", xlim=range(x0),
        ylim=range(c(y0,out.jack.local$lo,out.jack.local$up)), col="white",
        main=paste0("Jackknife (out-of-sample) prediction intervals\n",
        sprintf("Average length: %0.3f",
        mean(out.jack.local$up-out.jack.local$lo))))
o = order(x0)
segments(x0[o], out.jack.local$lo[o], x0[o], out.jack.local$up[o], col="pink")
lines(x0[o], out.jack.local$pred[o], lwd=2, col="red")
points(x0, y0, col="gray50")

# Split conformal, also using smooth splines (under CV) to train on residuals
out.split.local = conformal.pred.split(x, y, x0, alpha=0.1,
        train.fun=funs$train, predict.fun=funs$predict,
        mad.train.fun=funs$train, mad.predict.fun=funs$predict)

plot(c(), c(), xlab="x0", ylab="y0", xlim=range(x0),
        ylim=range(c(y0,out.split.local$lo,out.split.local$up)), col="white",
        main=paste0("Split conformal (out-of-sample) prediction intervals\n",
        sprintf("Average length: %0.3f",
        mean(out.split.local$up-out.split.local$lo))))
o = order(x0)
segments(x0[o], out.split.local$lo[o], x0[o], out.split.local$up[o],
        col="lightgreen")
lines(x0[o], out.split.local$pred[o], lwd=2, col="darkgreen")
points(x0, y0, col="gray50")

# Rank-one-out split conformal, again using smoothing splines (under CV) to

```

```

# train on residuals
out.roo.local = conformal.pred.roo(x, y, alpha=0.1,
  train.fun=funs$train, predict.fun=funs$predict,
  mad.train.fun=funs$train, mad.predict.fun=funs$predict)

plot(c(), c(), xlab="x", ylab="y", xlim=range(x),
  ylim=range(c(y,out.roo.local$lo,out.roo.local$up)), col="white",
  main=paste0("R00-conformal (in-sample) prediction intervals\n",
    sprintf("Average length: %0.3f",
      mean(out.roo.local$up-out.roo.local$lo))))
o = order(x)
segments(x[o], out.roo.local$lo[o], x[o], out.roo.local$up[o], col="lightblue")
lines(x[o], out.roo.local$fit.all[o], lwd=2, col="blue")
points(x, y, col="gray50")

# The reason the local from rank-one-out method here don't look entirely smooth
# is because they're actually a mishmash of two separate split procedures on
# each half of the data set (so they'd look smooth over the points within each
# half, but not necessarily overall)

```

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