

# Package ‘crs’

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**Title** Categorical Regression Splines

**Description** Regression splines that handle a mix of continuous and categorical (discrete) data often encountered in applied settings. I would like to gratefully acknowledge support from the Natural Sciences and Engineering Research Council of Canada (NSERC, <<https://www.nserc-crsng.gc.ca>>), the Social Sciences and Humanities Research Council of Canada (SSHRC, <<https://www.sshrc-crsh.gc.ca>>), and the Shared Hierarchical Academic Research Computing Network (SHARC-NET, <<https://www.sharcnet.ca>>). We would also like to acknowledge the contributions of the GNU GSL authors. In particular, we adapt the GNU GSL B-spline routine `gsl_bspline.c` adding automated support for quantile knots (in addition to uniform knots), providing missing functionality for derivatives, and for extending the splines beyond their endpoints.

**License** GPL (>= 3)

**URL** <https://github.com/JeffreyRacine/R-Package-crs>

**BugReports** <https://github.com/JeffreyRacine/R-Package-crs/issues>

**Repository** CRAN

**NeedsCompilation** yes

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crs-package	<i>Nonparametric Regression Splines with Continuous and Categorical Predictors</i>
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## Description

This package provides a method for nonparametric regression that combines the (global) approximation power of regression splines for continuous predictors ('x') with the (local) power of kernel methods for categorical predictors ('z'). The user also has the option of instead using indicator bases for the categorical predictors. When the predictors contain both continuous and categorical (discrete) data types, both approaches offer more efficient estimation than the traditional sample-splitting (i.e. 'frequency') approach where the data is first broken into subsets governed by the categorical z.

To cite the **crs** package type: 'citation("crs")' (without the single quotes).

For a listing of all routines in the **crs** package type: 'library(help="crs")'.

For a listing of all demos in the **crs** package type: 'demo(package="crs")'.

For a 'vignette' that presents a getting-started introduction to the **crs** package type: 'vignette("crs\_getting\_started", package = "crs")'.

## Details

For the continuous predictors the regression spline model employs the B-spline basis matrix using the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>).

The `tensor.prod.model.matrix` function is used to construct multivariate tensor spline bases when `basis="tensor"` and uses additive B-splines otherwise (i.e. when `basis="additive"`).

For the discrete predictors the product kernel function is of the ‘Li-Racine’ type (see Li and Racine (2007) for details) which is formed by constructing products of one of the following univariate kernels:

(***z* is discrete/nominal**)  $l(z_i, z, \lambda) = 1$  if  $z_i = z$ , and  $\lambda$  if  $z_i \neq z$ . Note that  $\lambda$  must lie between 0 and 1.

(***z* is discrete/ordinal**)  $l(z_i, z, \lambda) = 1$  if  $|z_i - z| = 0$ , and  $\lambda^{|z_i - z|}$  if  $|z_i - z| \geq 1$ . Note that  $\lambda$  must lie between 0 and 1.

Alternatively, for the ordinal/nominal predictors the regression spline model will use indicator basis functions.

## Author(s)

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I would like to gratefully acknowledge support from the Natural Sciences and Engineering Research Council of Canada (<https://www.nserc-crsng.gc.ca>), the Social Sciences and Humanities Research Council of Canada (<https://www.sshrc-crsh.gc.ca>), and the Shared Hierarchical Academic Research Computing Network (<https://www.sharcnet.ca>).

## References

Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

Ma, S. and J.S. Racine and L. Yang (2015), “Spline Regression in the Presence of Categorical Predictors,” *Journal of Applied Econometrics*, Volume 30, 705-717.

Ma, S. and J.S. Racine (2013), “Additive Regression Splines with Irrelevant Categorical and Continuous Regressors,” *Statistica Sinica*, Volume 23, 515-541.

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clsd

*Categorical Logspline Density*

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## Description

`clsd` computes the logspline density, density derivative, distribution, and smoothed quantiles for a one (1) dimensional continuous variable using the approach of Racine (2013).

**Usage**

```

clsd(x = NULL,
     beta = NULL,
     xeval = NULL,
     basis = "tensor",
     degree = NULL,
     degree.max = 25,
     degree.min = 2,
     deriv = 1,
     deriv.index = 1,
     display.nomad.progress = TRUE,
     display.warnings = TRUE,
     do.gradient = TRUE,
     elastic.diff = 3,
     elastic.max = TRUE,
     er = NULL,
     knots = "quantiles",
     lbound = NULL,
     max.attempts = 25,
     maxit = 10^5,
     method = c("L-BFGS-B", "Nelder-Mead", "BFGS", "CG", "SANN"),
     monotone = TRUE,
     monotone.lb = -250,
     n.integrate = 500,
     nmulti = 1,
     NOMAD = FALSE,
     penalty = NULL,
     quantile.seq = seq(.01, .99, by=.01),
     random.seed = 42,
     segments = NULL,
     segments.max = 100,
     segments.min = 1,
     ubound = NULL,
     verbose = FALSE)

```

**Arguments**

x	a numeric vector of training data
beta	a numeric vector of coefficients (default NULL)
xeval	a numeric vector of evaluation data
basis	a character string (default basis="tensor") indicating whether the additive or tensor product B-spline basis matrix for a multivariate polynomial spline or generalized B-spline polynomial basis should be used
degree	integer/vector specifying the polynomial degree of the B-spline basis for each dimension of the continuous x (default degree=2)

<code>degree.min, degree.max</code>	when <code>elastic.max=FALSE</code> the minimum/maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=2, degree.max=25</code> )
<code>deriv</code>	an integer <code>l</code> (default <code>deriv=1</code> ) specifying whether to compute the univariate <code>l</code> th partial derivative for each continuous predictor (and difference in levels for each categorical predictor) or not and if so what order. Note that if <code>deriv</code> is higher than the spline degree of the associated continuous predictor then the derivative will be zero and a warning issued to this effect
<code>deriv.index</code>	an integer <code>l</code> (default <code>deriv.index=1</code> ) specifying the index (currently only supports 1) of the variable whose derivative is requested
<code>display.nomad.progress</code>	a logical value indicating whether to display the progress of the NOMAD solver (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>do.gradient</code>	a logical value indicating whether or not to use the analytical gradient during optimization (defaults to <code>TRUE</code> )
<code>elastic.max, elastic.diff</code>	a logical value/integer indicating whether to use ‘elastic’ search bounds such that the optimal degree/segment must lie <code>elastic.diff</code> units from the respective search bounds
<code>er</code>	a scalar indicating the fraction of data range to extend the tails (default <code>1/log(n)</code> , see <a href="#">extendrange</a> for further details)
<code>knots</code>	a character string (default <code>knots="quantiles"</code> ) specifying where knots are to be placed. ‘quantiles’ specifies knots placed at equally spaced quantiles (equal number of observations lie in each segment) and ‘uniform’ specifies knots placed at equally spaced intervals
<code>lbound, ubound</code>	lower/upper bound for the support of the density. For example, if there is a priori knowledge that the density equals zero to the left of 0, and has a discontinuity at 0, the user could specify <code>lbound = 0</code> . However, if the density is essentially zero near 0, one does not need to specify <code>lbound</code>
<code>max.attempts</code>	maximum number of attempts to undertake if <code>optim</code> fails for any set of initial parameters for each value of <code>nmulti</code>
<code>maxit</code>	maximum number of iterations used by <code>optim</code>
<code>method</code>	see <code>optim</code> for details
<code>monotone</code>	a logical value indicating whether modify the standard B-spline basis function so that it is tailored for density estimation (default <code>TRUE</code> )
<code>monotone.lb</code>	a negative bound specifying the lower bound on the linear segment coefficients used when ( <code>monotone=FALSE</code> )
<code>n.integrate</code>	the number of evenly spaced integration points on the extended range specified by <code>er</code> (defaults to 500)
<code>nmulti</code>	integer number of times to restart the process of finding extrema of the cross-validation function from different (random) initial points (default <code>nmulti=1</code> )

NOMAD	a logical value which when TRUE calls <code>snomadr</code> to determine the optimal degree and segments
penalty	the parameter to be used in the AIC criterion. The method chooses the number of degrees plus number of segments (knots-1) that maximizes $2 \cdot \log 1 - \text{penalty} \cdot (\text{degree} + \text{segments})$ . The default is to use the penalty parameter of $\log(n)/2$ (2 would deliver standard AIC, $\log(n)$ standard BIC)
quantile.seq	a sequence of numbers lying in $[0, 1]$ on which quantiles from the logspline distribution are obtained
random.seed	seeds the random number generator for initial parameter values when <code>optim</code> is called
segments	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous x (i.e. number of knots minus one) (default segments=1, i.e. Bezier curve)
segments.min, segments.max	when <code>elastic.max=FALSE</code> , the minimum/maximum segments of the B-spline basis for each of the continuous predictors (default segments.min=1, segments.max=100)
verbose	a logical value which when TRUE produces verbose output during optimization

## Details

Typical usages are (see below for a list of options and also the examples at the end of this help file)

```
model <- clsd(x)
```

`clsd` computes a logspline density estimate of a one (1) dimensional continuous variable.

The spline model employs the tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>) and the `tensor.prod.model.matrix` function.

When `basis="additive"` the model becomes additive in nature (i.e. no interaction/tensor terms thus semiparametric not fully nonparametric).

When `basis="tensor"` the model uses the multivariate tensor product basis.

## Value

`clsd` returns a `clsd` object. The generic functions `coef`, `fitted`, `plot` and `summary` support objects of this type (`er=FALSE` plots the density on the sample realizations (default is 'extended range' data), see `er` above, `distribution=TRUE` plots the distribution). The returned object has the following components:

<code>density</code>	estimates of the density function at the sample points
<code>density.er</code>	the density evaluated on the 'extended range' of the data
<code>density.deriv</code>	estimates of the derivative of the density function at the sample points

density.deriv.er	estimates of the derivative of the density function evaluated on the ‘extended range’ of the data
distribution	estimates of the distribution function at the sample points
distribution.er	the distribution evaluated on the ‘extended range’ of the data
xer	the ‘extended range’ of the data
degree	integer/vector specifying the degree of the B-spline basis for each dimension of the continuous x
segments	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous x
xq	vector of quantiles
tau	vector generated by <code>quantile.seq</code> or input by the user (lying in $[0, 1]$ ) from which the quantiles <code>xq</code> are obtained

### Usage Issues

This function should be considered to be in ‘beta’ status until further notice.

If smoother estimates are desired and `degree=degree.min`, increase `degree.min` to, say, `degree.min=3`.

The use of ‘regression’ B-splines can lead to undesirable behavior at the endpoints of the data (i.e. when `monotone=FALSE`). The default ‘density’ B-splines ought to be well-behaved in these regions.

### Author(s)

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### References

Racine, J.S. (2013), “Log spline Mixed Data Density Estimation,” manuscript.

### See Also

[logspline](#)

### Examples

```
## Not run:
## Old Faithful eruptions data histogram and clsd density

library(MASS)
data(faithful)
attach(faithful)

model <- clsd(eruptions)

ylim <- c(0, max(model$density, hist(eruptions, breaks=20, plot=FALSE)$density))

plot(model, ylim=ylim)
```

```

hist(eruptions,breaks=20,freq=FALSE,add=TRUE,lty=2)

rug(eruptions)

summary(model)

coef(model)

## Simulated data

set.seed(42)
require(logspline)

## Example - simulated data

n <- 250
x <- sort(rnorm(n))
f.dgp <- dnorm(x)

model <- clsd(x)

## Standard (cubic) estimate taken from the logspline package
## Compute MSEs

mse.clsd <- mean((fitted(model)-f.dgp)^2)

model.logspline <- logspline(x)

mse.logspline <- mean((dlogspline(x,model.logspline)-f.dgp)^2)

ylim <- c(0,max(fitted(model),dlogspline(x,model.logspline),f.dgp))

plot(model,
      ylim=ylim,
      sub=paste("MSE: logspline = ",format(mse.logspline),", clsd = ",
              format(mse.clsd)),
      lty=3,
      col=3)

xer <- model$xer

lines(xer,dlogspline(xer,model.logspline),col=2,lty=2)
lines(xer,dnorm(xer),col=1,lty=1)

rug(x)

legend("topright",c("DGP",
                   paste("Cubic Logspline Density (package 'logspline', knots = ",
                           model.logspline$nknots,")",sep=""),
                   paste("clsd Density (degree = ", model$degree, ", segments = ",
                           model$segments, ", penalty = ",round(model$penalty,2),")",sep="")),
      lty=1:3,

```

```
      col=1:3,  
      bty="n",  
      cex=0.75)  
  
summary(model)  
  
coef(model)  
  
## Simulate data with known bounds  
  
set.seed(42)  
n <- 10000  
x <- runif(n,0,1)  
  
model <- clsd(x,lbound=0,ubound=1)  
  
plot(model)  
  
## End(Not run)
```

---

cps71

*Canadian High School Graduate Earnings*

---

### Description

Canadian cross-section wage data consisting of a random sample taken from the 1971 Canadian Census Public Use Tapes for male individuals having common education (grade 13). There are 205 observations in total.

### Usage

```
data("cps71")
```

### Format

A data frame with 2 columns, and 205 rows.

**logwage** the first column, of type numeric

**age** the second column, of type integer

### Source

Aman Ullah

### References

Pagan, A. and A. Ullah (1999), *Nonparametric Econometrics*, Cambridge University Press.

## Examples

```
## Example - fit a spline model for log wages as a function of age.

data(cps71)
attach(cps71)

model.crs <- crs(logwage~age,complexity="degree-knots")
plot(age,logwage,cex=0.25,col="grey",
      sub=paste("crs-CV = ", formatC(model.crs$cv.score,format="f",digits=3)))
lines(age,fitted(model.crs),lty=1,col=1)

crs.txt <- paste("crs (R-squared = ",formatC(model.crs$r.squared,format="f",digits=3),")",sep="")
legend(22.5,15,crs.txt,lty=1,col=1,bty="n")

summary(model.crs)
```

---

crs

*Categorical Regression Splines*


---

## Description

crs computes a regression spline estimate of a one (1) dimensional dependent variable on an r-dimensional vector of continuous and categorical ([factor/ordered](#)) predictors (Ma and Racine (2013), Ma, Racine and Yang (2015)).

## Usage

```
crs(...)
## Default S3 method:
crs(xz,
     y,
     basis = c("auto","additive","tensor","glp"),
     complexity = c("degree-knots","degree","knots"),
     data.return = FALSE,
     degree = NULL,
     deriv = 0,
     display.nomad.progress = TRUE,
     display.warnings = TRUE,
     include = NULL,
     kernel = TRUE,
     knots = c("quantiles","uniform","auto"),
     lambda = NULL,
     model.return = FALSE,
     prune = FALSE,
     segments = NULL,
     tau = NULL,
     weights = NULL,
     ...)
```

```

## S3 method for class 'formula'
crs(formula,
     basis = c("auto", "additive", "tensor", "glp"),
     complexity = c("degree-knots", "degree", "knots"),
     cv = c("nomad", "exhaustive", "none"),
     cv.df.min = 1,
     cv.func = c("cv.ls", "cv.gcv", "cv.aic"),
     cv.threshold = 1000,
     data = list(),
     data.return = FALSE,
     degree = NULL,
     degree.max = 10,
     degree.min = 0,
     deriv = 0,
     display.nomad.progress = TRUE,
     display.warnings = TRUE,
     include = NULL,
     initial.mesh.size.integer = "1",
     initial.mesh.size.real = "r1.0e-01",
     kernel = TRUE,
     knots = c("quantiles", "uniform", "auto"),
     lambda = NULL,
     lambda.discrete = FALSE,
     lambda.discrete.num = 100,
     max.bb.eval = 140,
     min.mesh.size.integer = 1,
     min.mesh.size.real = paste(sqrt(.Machine$double.eps)),
     min.frame.size.integer = 1,
     min.frame.size.real = 1,
     model.return = FALSE,
     nmulti = 5,
     opts=list(),
     prune = FALSE,
     random.seed = 42,
     restarts = 0,
     segments = NULL,
     segments.max = 10,
     segments.min = 1,
     singular.ok = FALSE,
     tau = NULL,
     weights = NULL,
     ...)

```

### Arguments

xz	numeric (x) and or nominal/ordinal ( <a href="#">factor/ordered</a> ) predictors (z)
y	a numeric vector of responses.

<code>formula</code>	a symbolic description of the model to be fit
<code>data</code>	an optional data frame containing the variables in the model
<code>basis</code>	a character string (default <code>basis="auto"</code> ) indicating whether the additive or tensor product B-spline basis matrix for a multivariate polynomial spline or generalized B-spline polynomial basis should be used. Note this can be automatically determined by cross-validation if <code>cv="nomad"</code> or <code>cv="exhaustive"</code> and <code>basis="auto"</code> , and is an ‘all or none’ proposition (i.e. interaction terms for all predictors or for no predictors given the nature of ‘tensor products’). Note also that if there is only one predictor this defaults to <code>basis="additive"</code> to avoid unnecessary computation as the spline bases are equivalent in this case
<code>complexity</code>	a character string (default <code>complexity="degree-knots"</code> ) indicating whether model ‘complexity’ is determined by the degree of the spline or by the number of segments (i.e. number of knots minus one). This option allows the user to use cross-validation to select either the spline degree (number of knots held fixed) or the number of knots (spline degree held fixed) or both the spline degree and number of knots  For the continuous predictors the regression spline model employs either the additive or tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library ( <a href="https://www.gnu.org/software/gsl/">https://www.gnu.org/software/gsl/</a> ) and the <code>tensor.prod.model.matrix</code> function
<code>cv</code>	a character string (default <code>cv="nomad"</code> ) indicating whether to use nonsmooth mesh adaptive direct search, exhaustive search, or no search (i.e. use user supplied values for degree, segments, and lambda)
<code>cv.df.min</code>	the minimum degrees of freedom to allow when conducting NOMAD-based cross-validation (default <code>cv.df.min=1</code> )
<code>cv.func</code>	a character string (default <code>cv.func="cv.ls"</code> ) indicating which method to use to select smoothing parameters. <code>cv.gcv</code> specifies generalized cross-validation (Craven and Wahba (1979)), <code>cv.aic</code> specifies expected Kullback-Leibler cross-validation (Hurvich, Simonoff, and Tsai (1998)), and <code>cv.ls</code> specifies least-squares cross-validation
<code>cv.threshold</code>	an integer (default <code>cv.threshold=1000</code> ) for simple problems with no categorical predictors (i.e. <code>kernel=FALSE</code> otherwise <code>optim/snomadr</code> search is necessary) such that, if the number of combinations of degree/segments is less than the threshold and <code>cv="nomad"</code> , instead use exhaustive search ( <code>cv="exhaustive"</code> )
<code>data.return</code>	a logical value indicating whether to return <code>x, z, y</code> or not (default <code>data.return=FALSE</code> )
<code>degree</code>	integer/vector specifying the polynomial degree of the B-spline basis for each dimension of the continuous <code>x</code> (default <code>degree=3</code> , i.e. cubic spline)
<code>degree.max</code>	the maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.max=10</code> )
<code>degree.min</code>	the minimum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=0</code> )
<code>deriv</code>	an integer <code>l</code> (default <code>deriv=0</code> ) specifying whether to compute the univariate <code>l</code> th partial derivative for each continuous predictor (and difference in levels for each categorical predictor) or not and if so what order. Note that if <code>deriv</code> is higher than the spline degree of the associated continuous predictor then the derivative will be zero and a warning issued to this effect

<code>display.nomad.progress</code>	a logical value indicating whether to display the progress of the NOMAD solver (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>include</code>	integer/vector specifying whether each of the nominal/ordinal ( <a href="#">factor/ordered</a> ) predictors in <code>x</code> are included or omitted from the resulting estimate
<code>initial.mesh.size.integer</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>initial.mesh.size.real</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>kernel</code>	a logical value (default <code>kernel=TRUE</code> ) indicating whether to use kernel smoothing or not
<code>knots</code>	a character string (default <code>knots="quantiles"</code> ) specifying where knots are to be placed. 'quantiles' specifies knots placed at equally spaced quantiles (equal number of observations lie in each segment) and 'uniform' specifies knots placed at equally spaced intervals. If <code>knots="auto"</code> , the knot type will be automatically determined by cross-validation
<code>lambda</code>	a vector of bandwidths for each dimension of the categorical <code>z</code>
<code>lambda.discrete</code>	if <code>lambda.discrete=TRUE</code> , the bandwidth will be discretized into <code>lambda.discrete.num+1</code> points and <code>lambda</code> will be chosen from these points
<code>lambda.discrete.num</code>	a positive integer indicating the number of discrete values that <code>lambda</code> can assume - this parameter will only be used when <code>lambda.discrete=TRUE</code>
<code>max.bb.eval</code>	argument passed to the NOMAD solver (default <code>max.bb.eval=140</code> ; see <a href="#">snomadr</a> for further details)
<code>min.mesh.size.integer</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.mesh.size.real</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.frame.size.integer</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.frame.size.real</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>model.return</code>	a logical value indicating whether to return the list of <code>lm</code> models or not when <code>kernel=TRUE</code> (default <code>model.return=FALSE</code> )
<code>nmulti</code>	integer number of times to restart the process of finding extrema of the cross-validation function from different (random) initial points (default <code>nmulti=5</code> )
<code>opts</code>	list of optional arguments to be passed to <a href="#">snomadr</a>
<code>prune</code>	a logical value (default <code>prune=FALSE</code> ) specifying whether the (final) model is to be 'pruned' using a stepwise cross-validation criterion based upon a modified version of <a href="#">stepAIC</a> (see below for details)

random.seed	when it is not missing and not equal to 0, the initial points will be generated using this seed when using <code>frscvNOMAD</code> or <code>krscvNOMAD</code> and <code>nmulti &gt; 0</code>
restarts	integer specifying the number of times to restart the process of finding extrema of the cross-validation function (for the bandwidths only) from different (random) initial points
segments	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous $x$ (i.e. number of knots minus one) (default <code>segments=1</code> , i.e. Bezier curve)
segments.max	the maximum segments of the B-spline basis for each of the continuous predictors (default <code>segments.max=10</code> )
segments.min	the minimum segments of the B-spline basis for each of the continuous predictors (default <code>segments.min=1</code> )
singular.ok	a logical value (default <code>singular.ok=FALSE</code> ) that, when <code>FALSE</code> , discards singular bases during cross-validation (a check for ill-conditioned bases is performed).
tau	if non-null a number in (0,1) denoting the quantile for which a quantile regression spline is to be estimated rather than estimating the conditional mean (default <code>tau=NULL</code> ). Criterion function set by <code>cv.func=</code> are modified accordingly to admit quantile regression.
weights	an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector. If non-NULL, weighted least squares is used with weights 'weights' (that is, minimizing 'sum(w*e^2)'); otherwise ordinary least squares is used.
...	optional arguments

## Details

Typical usages are (see below for a list of options and also the examples at the end of this help file)

```
## Estimate the model and let the basis type be determined by
## cross-validation (i.e. cross-validation will determine whether to
## use the additive, generalized, or tensor product basis)

model <- crs(y~x1+x2)

## Estimate the model for a specified degree/segment/bandwidth
## combination and do not run cross-validation (will use the
## additive basis by default)

model <- crs(y~x1+factor(x2),cv="none",degree=3,segments=1,lambda=.1)

## Plot the mean and (asymptotic) error bounds

plot(model,mean=TRUE,ci=TRUE)

## Plot the first partial derivative and (asymptotic) error bounds
```

```
plot(model,deriv=1,ci=TRUE)
```

crs computes a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and categorical ([factor/ordered](#)) predictors.

The regression spline model employs the tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>) and the `tensor.prod.model.matrix` function.

When `basis="additive"` the model becomes additive in nature (i.e. no interaction/tensor terms thus semiparametric not fully nonparametric).

When `basis="tensor"` the model uses the multivariate tensor product basis.

When `kernel=FALSE` the model uses indicator basis functions for the nominal/ordinal ([factor/ordered](#)) predictors rather than kernel weighting.

When `kernel=TRUE` the product kernel function for the discrete predictors is of the ‘Li-Racine’ type (see Li and Racine (2007) for details).

When `cv="nomad"`, numerical search is undertaken using Nonsmooth Optimization by Mesh Adaptive Direct Search (Abramson, Audet, Couture, Dennis, Jr., and Le Digabel (2011)).

When `kernel=TRUE` and `cv="exhaustive"`, numerical search is undertaken using `optim` and the box-constrained L-BFGS-B method (see `optim` for details). The user may restart the algorithm as many times as desired via the `restarts` argument (default `restarts=0`). The approach ascends from `degree=0` (or `segments=0`) through `degree.max` and for each value of `degree` (or `segments`) searches for the optimal bandwidths. After the most complex model has been searched then the optimal `degree/segments/lambda` combination is selected. If any element of the optimal `degree` (or `segments`) vector coincides with `degree.max` (or `segments.max`) a warning is produced and the user ought to restart their search with a larger value of `degree.max` (or `segments.max`).

Note that the default `plot` method for a `crs` object provides some diagnostic measures, in particular, a) residuals versus fitted values (useful for checking the assumption that  $E(u|x)=0$ ), b) a normal quantile-quantile plot which allows residuals to be assessed for normality (`qqnorm`), c) a scale-location plot that is useful for checking the assumption that the errors are iid and, in particular, that the variance is homogeneous, and d) ‘Cook’s distance’ which computes the single-case influence function. See below for other arguments for the `plot` function for a `crs` object.

Note that setting `prune=TRUE` produces a final ‘pruning’ of the model via a stepwise cross-validation criterion achieved by modifying `stepAIC` and replacing `extractAIC` with `extractCV` throughout the function. This option may be enabled to remove potentially superfluous bases thereby improving the finite-sample efficiency of the resulting model. Note that if the cross-validation score for the pruned model is no better than that for the original model then the original model is returned with a warning to this effect. Note also that this option can only be used when `kernel=FALSE`.

## Value

`crs` returns a `crs` object. The generic functions `fitted` and `residuals` extract (or generate) estimated values and residuals. Furthermore, the functions `summary`, `predict`, and `plot` (options `mean=FALSE`, `deriv=i` where  $i$  is an integer, `ci=FALSE`, `persp.rgl=FALSE`, `plot.behavior=c("plot", "plot-data", "data")`, `plot.errors.method=c("asymptotic", "bootstrap")`, `plot.errors.boot.num=99`, `plot.errors.type=c("standard")`, `plot.errors.alpha=0.05`, `xtrim=0.0`, `xq=0.5`) support objects of this type. The returned object has the following components:

<code>fitted.values</code>	estimates of the regression function (conditional mean) at the sample points or evaluation points
<code>lwr, upr</code>	lower/upper bound for a 95% confidence interval for the <code>fitted.values</code> (conditional mean) obtained from <code>predict.lm</code> via the argument <code>interval="confidence"</code> . When plotting with <code>plot.errors.method="bootstrap"</code> , bootstrap-based bounds are used instead for mean plots. Bootstrap derivative bounds in <code>plot.crs</code> currently fall back to asymptotic bounds.
<code>residuals</code>	residuals computed at the sample points or evaluation points
<code>degree</code>	integer/vector specifying the degree of the B-spline basis for each dimension of the continuous <code>x</code>
<code>segments</code>	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous <code>x</code>
<code>include</code>	integer/vector specifying whether each of the nominal/ordinal ( <code>factor/ordered</code> ) predictors <code>z</code> are included or omitted from the resulting estimate if <code>kernel=FALSE</code> (see below)
<code>kernel</code>	a logical value indicating whether kernel smoothing was used ( <code>kernel=TRUE</code> ) or not
<code>lambda</code>	vector of bandwidths used if <code>kernel=TRUE</code>
<code>call</code>	a symbolic description of the model
<code>r.squared</code>	coefficient of determination (Doksum and Samarov (1995))
<code>model.lm</code>	an object of <code>'class' 'lm'</code> if <code>kernel=FALSE</code> or a list of objects of <code>'class' 'lm'</code> if <code>kernel=TRUE</code> (accessed by <code>model.lm[[1]]</code> , <code>model.lm[[2]]</code> , ...). By way of example, if <code>foo</code> is a <code>crs</code> object and <code>kernel=FALSE</code> , then <code>foo\$model.lm</code> is an object of <code>'class' 'lm'</code> , while objects of <code>'class' 'lm'</code> return the <code>model.frame</code> in <code>model.lm\$model</code> which can be accessed via <code>foo\$model.lm\$model</code> where <code>foo</code> is the <code>crs</code> object (the model frame <code>foo\$model.lm\$model</code> contains the B-spline bases underlying the estimate which might be of interest). Again by way of example, when <code>kernel=TRUE</code> then <code>foo\$model.lm[[1]]\$model</code> contains the model frame for the first unique combination of categorical predictors, <code>foo\$model.lm[[2]]\$model</code> the second and so forth (the weights will potentially differ for each model depending on the value(s) of <code>lambda</code> )
<code>deriv.mat</code>	a matrix of derivatives (or differences in levels for the categorical <code>z</code> ) whose order is determined by <code>deriv=</code> in the <code>crs</code> call
<code>deriv.mat.lwr</code>	a matrix of 95% coverage lower bounds for <code>deriv.mat</code>
<code>deriv.mat.upr</code>	a matrix of 95% coverage upper bounds for <code>deriv.mat</code>
<code>hatvalues</code>	the <code>hatvalues</code> for the estimated model
<code>P.hat</code>	the kernel probability estimates corresponding to the categorical predictors in the estimated model

### Usage Issues

Note that when `kernel=FALSE` `summary` supports the option `sigtest=TRUE` that conducts an F-test for significance for each predictor.

**Author(s)**

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**See Also**

[smooth.spline](#), [loess](#), [npreg](#)

**Examples**

```
set.seed(42)
## Example - simulated data
n <- 1000
num.eval <- 50
x1 <- runif(n)
x2 <- runif(n)
z <- rbinom(n,1,.5)
dgp <- cos(2*pi*x1)+sin(2*pi*x2)+z
z <- factor(z)
y <- dgp + rnorm(n,sd=.5)

## Estimate a model with specified degree, segments, and bandwidth
model <- crs(y~x1+x2+z,degree=c(5,5),
             segments=c(1,1),
             lambda=0.1,
             cv="none",
             kernel=TRUE)
```

```

summary(model)

## Perspective plot
x1.seq <- seq(min(x1),max(x1),length=num.eval)
x2.seq <- seq(min(x2),max(x2),length=num.eval)
x.grid <- expand.grid(x1.seq,x2.seq)
newdata <- data.frame(x1=x.grid[,1],x2=x.grid[,2],
                     z=factor(rep(0,num.eval**2),levels=c(0,1)))
z0 <- matrix(predict(model,newdata=newdata),num.eval,num.eval)
newdata <- data.frame(x1=x.grid[,1],x2=x.grid[,2],
                     z=factor(rep(1,num.eval),levels=c(0,1)))
z1 <- matrix(predict(model,newdata=newdata),num.eval,num.eval)
zlim=c(min(z0,z1),max(z0,z1))
persp(x=x1.seq,y=x2.seq,z=z0,
      xlab="x1",ylab="x2",zlab="y",zlim=zlim,
      ticktype="detailed",
      border="red",
      theta=45,phi=45)
par(new=TRUE)
persp(x=x1.seq,y=x2.seq,z=z1,
      xlab="x1",ylab="x2",zlab="y",zlim=zlim,
      theta=45,phi=45,
      ticktype="detailed",
      border="blue")

## Partial regression surface plot
plot(model,mean=TRUE,ci=TRUE)
## Not run:
## A plot example where we extract the partial surfaces, confidence
## intervals etc. automatically generated by plot(mean=TRUE,...) but do
## not plot, rather save for separate use.
pdat <- plot(model,mean=TRUE,ci=TRUE,plot.behavior="data")

## Column 1 is the (evaluation) predictor ([,1]), 2-4 ([,-1]) the mean,
## lwr, and upr (note the returned value is a 'list' hence pdat[[1]] is
## data for the first predictor, pdat[[2]] the second etc). Note that
## matplot() can plot this nicely.
matplot(pdat[[1]][,1],pdat[[1]][,-1],
        xlab=names(pdat[[1]][1]),ylab=names(pdat[[1]][2]),
        lty=c(1,2,2),col=c(1,2,2),type="l")

## End(Not run)

```

## Description

crsiv computes nonparametric estimation of an instrumental regression function  $\varphi$  defined by conditional moment restrictions stemming from a structural econometric model:  $E[Y - \varphi(Z, X)|W] =$

0, and involving endogenous variables  $Y$  and  $Z$ , exogenous variables  $X$ , and instruments  $W$ . The function  $\varphi$  is the solution of an ill-posed inverse problem.

When `method="Tikhonov"`, `crsiv` uses the approach of Darolles, Fan, Florens and Renault (2011) modified for regression splines (Darolles et al use local constant kernel weighting). When `method="Landweber-Fridman"`, `crsiv` uses the approach of Horowitz (2011) using the regression spline methodology implemented in the `crs` package.

## Usage

```
crsiv(y, ...)

## Default S3 method:
crsiv(y,
      z,
      w,
      x = NULL,
      zeval = NULL,
      weval = NULL,
      xeval = NULL,
      alpha = NULL,
      alpha.max = 1e-01,
      alpha.min = 1e-10,
      alpha.tol = .Machine$double.eps^0.25,
      constant = 0.5,
      deriv = 0,
      display.nomad.progress = TRUE,
      display.warnings = TRUE,
      iterate.diff.tol = 1.0e-08,
      iterate.max = 1000,
      method = c("Landweber-Fridman", "Tikhonov"),
      opts = list("MAX_BB_EVAL"=10000,
                  "EPSILON"=.Machine$double.eps,
                  "INITIAL_MESH_SIZE"="r1.0e-01",
                  "MIN_MESH_SIZE"=paste("r", sqrt(.Machine$double.eps), sep=""),
                  "MIN_FRAME_SIZE"=paste("r", 1, sep=""),
                  "DISPLAY_DEGREE"=0),
      penalize.iteration = TRUE,
      smooth.residuals = TRUE,
      start.from = c("Eyz", "EEyz"),
      starting.values = NULL,
      stop.on.increase = TRUE,
      ...)
```

## Arguments

<code>y</code>	a one (1) dimensional numeric or integer vector of dependent data, each element $i$ corresponding to each observation (row) $i$ of <code>z</code>
<code>z</code>	a $p$ -variate data frame of endogenous predictors. The data types may be continuous, discrete (unordered and ordered factors), or some combination thereof

w	a $q$ -variate data frame of instruments. The data types may be continuous, discrete (unordered and ordered factors), or some combination thereof
x	an $r$ -variate data frame of exogenous predictors. The data types may be continuous, discrete (unordered and ordered factors), or some combination thereof
zeval	a $p$ -variate data frame of endogenous predictors on which the regression will be estimated (evaluation data). By default, evaluation takes place on the data provided by z
weval	a $q$ -variate data frame of instruments on which the regression will be estimated (evaluation data). By default, evaluation takes place on the data provided by w
xeval	an $r$ -variate data frame of exogenous predictors on which the regression will be estimated (evaluation data). By default, evaluation takes place on the data provided by x
alpha	a numeric scalar that, if supplied, is used rather than numerically solving for alpha, when using method="Tikhonov"
alpha.max	maximum of search range for $\alpha$ , the Tikhonov regularization parameter, when using method="Tikhonov"
alpha.min	minimum of search range for $\alpha$ , the Tikhonov regularization parameter, when using method="Tikhonov"
alpha.tol	the search tolerance for optimize when solving for $\alpha$ , the Tikhonov regularization parameter, when using method="Tikhonov"
constant	the constant to use when using method="Landweber-Fridman"
deriv	an integer l (default deriv=0) specifying whether to compute the univariate lth partial derivative for each continuous predictor (and difference in levels for each categorical predictor) or not and if so what order. Note that if deriv is higher than the spline degree of the associated continuous predictor then the derivative will be zero and a warning issued to this effect (see important note below)
display.nomad.progress	a logical value indicating whether to display the progress of the NOMAD solver (default display.nomad.progress=TRUE)
display.warnings	a logical value indicating whether to display warnings (default display.warnings=TRUE)
iterate.diff.tol	the search tolerance for the difference in the stopping rule from iteration to iteration when using method="Landweber-Fridman" (disable by setting to zero)
iterate.max	an integer indicating the maximum number of iterations permitted before termination occurs when using method="Landweber-Fridman"
method	the regularization method employed (default "Landweber-Fridman", see Horowitz (2011); see Darolles, Fan, Florens and Renault (2011) for details for "Tikhonov")
opts	arguments passed to the NOMAD solver (see <a href="#">snomad</a> for further details)
penalize.iteration	a logical value indicating whether to penalize the norm by the number of iterations or not (default TRUE)

<code>smooth.residuals</code>	a logical value (defaults to TRUE) indicating whether to optimize bandwidths for the regression of $y - \varphi(z)$ on $w$ or for the regression of $\varphi(z)$ on $w$ during iteration
<code>start.from</code>	a character string indicating whether to start from $E(Y z)$ (default, "Eyz") or from $E(E(Y z) z)$ (this can be overridden by providing <code>starting.values</code> below)
<code>starting.values</code>	a value indicating whether to commence Landweber-Fridman assuming $\varphi_{-1} = \text{starting.values}$ (proper Landweber-Fridman) or instead begin from $E(y z)$ (defaults to NULL, see details below)
<code>stop.on.increase</code>	a logical value (defaults to TRUE) indicating whether to halt iteration if the stopping criterion (see below) increases over the course of one iteration (i.e. it may be above the iteration tolerance but increased)
<code>...</code>	additional arguments supplied to <code>crs</code>

## Details

Tikhonov regularization requires computation of weight matrices of dimension  $n \times n$  which can be computationally costly in terms of memory requirements and may be unsuitable (i.e. unfeasible) for large datasets. Landweber-Fridman will be preferred in such settings as it does not require construction and storage of these weight matrices while it also avoids the need for numerical optimization methods to determine  $\alpha$ , though it does require iteration that may be equally or even more computationally demanding in terms of total computation time.

When using `method="Landweber-Fridman"`, an optimal stopping rule based upon  $\|E(y|w) - E(\varphi_k(z, x)|w)\|^2$  is used to terminate iteration. However, if local rather than global optima are encountered the resulting estimates can be overly noisy. To best guard against this eventuality set `nmulti` to a larger number than the default `nmulti=5` for `crs` when using `cv="nomad"` or instead use `cv="exhaustive"` if possible (this may not be feasible for non-trivial problems).

Note that for subsequent Landweber-Fridman iterations, a "warm start" strategy is employed. The optimal parameters (spline degree, number of segments, and bandwidths or inclusion indicators) from the previous iteration are used as starting values for the current iteration. The user-supplied `nmulti` is respected for all iterations. For iterations after the first successful one, these optimal parameters serve as the first of the multiple initial points (a warm start), while any remaining restarts are cold starts. If `nmulti` is not explicitly supplied by the user, it defaults to the `crs` default (5) for the first iteration and to 1 for all subsequent iterations. This strategy provides a balance between computational efficiency and robustness, allowing the NOMAD solver to refine the structural parameters as the residuals evolve incrementally while still guarding against local optima.

When using `method="Landweber-Fridman"`, iteration will terminate when either the change in the value of  $\|(E(y|w) - E(\varphi_k(z, x)|w))/E(y|w)\|^2$  from iteration to iteration is less than `iterate.diff.tol` or we hit `iterate.max` or  $\|(E(y|w) - E(\varphi_k(z, x)|w))/E(y|w)\|^2$  stops falling in value and starts rising.

When your problem is a simple one (e.g. univariate  $Z$ ,  $W$ , and  $X$ ) you might want to avoid `cv="nomad"` and instead use `cv="exhaustive"` since exhaustive search may be feasible (for `degree.max` and `segments.max` not overly large). This will guarantee an exact solution for each iteration (i.e. there will be no errors arising due to numerical search).

`demo(crsiv)`, `demo(crsiv_exog)`, and `demo(crsiv_exog_persp)` provide flexible interactive demonstrations similar to the example below that allow you to modify and experiment with parameters such as the sample size, method, and so forth in an interactive session.

### Value

`crsiv` returns a `crsiv` object (which inherits from the `crs` class). The generic functions `print`, `summary`, `fitted`, `residuals`, `predict`, and `plot` support objects of this type.

For the `plot` function, the options include `plot.data=FALSE` (a logical value indicating whether to plot the data as a scatter plot), `deriv=FALSE` (a logical value indicating whether to plot the derivative of the structural function rather than the function itself), `ci=FALSE` (a logical value indicating whether to overlay derivative confidence bounds when available), and `xtrim=0.0` (a scalar in  $[\emptyset, 0.5)$  used to trim the plotted support of  $z$  by quantiles). Note that the `plot` method for `crsiv` objects currently only supports univariate endogenous predictors  $z$ .

See `crs` for details on the return object components.

In addition to the standard `crs` components, `crsiv` returns components `phi` and either `alpha` when `method="Tikhonov"` or `phi`, `phi.mat`, `num.iterations`, `norm.stop`, `norm.value` and `convergence` when `method="Landweber-Fridman"`.

### Note

Using the option `deriv=` computes (effectively) the analytical derivative of the estimated  $\varphi(Z, X)$  and not that using `crsivderiv`, which instead uses the method of Florens and Racine (2012). Though both are statistically consistent, practitioners may desire one over the other hence we provide both.

### Note

This function should be considered to be in ‘beta test’ status until further notice.

### Author(s)

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### References

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### See Also

npreg, crs

### Examples

```
## Not run:
## This illustration was made possible by Samuele Centorrino
## <samuele.centorrino@univ-tlse1.fr>

set.seed(42)
n <- 1500

## The DGP is as follows:

## 1)  $y = \phi(z) + u$ 

## 2)  $E(u|z) \neq 0$  (endogeneity present)

## 3) Suppose there exists an instrument  $w$  such that  $z = f(w) + v$  and
##  $E(u|w) = 0$ 

## 4) We generate  $v$ ,  $w$ , and generate  $u$  such that  $u$  and  $z$  are
## correlated. To achieve this we express  $u$  as a function of  $v$  (i.e.  $u =$ 
##  $\gamma v + \epsilon$ )

v <- rnorm(n,mean=0,sd=0.27)
eps <- rnorm(n,mean=0,sd=0.05)
u <- -0.5*v + eps
w <- rnorm(n,mean=0,sd=1)

## In Darolles et al (2011) there exist two DGPs. The first is
##  $\phi(z)=z^2$  and the second is  $\phi(z)=\exp(-\text{abs}(z))$  (which is
## discontinuous and has a kink at zero).

fun1 <- function(z) { z^2 }
fun2 <- function(z) { exp(-abs(z)) }

z <- 0.2*w + v

## Generate two y vectors for each function.

y1 <- fun1(z) + u
y2 <- fun2(z) + u
```

```

## You set y to be either y1 or y2 (ditto for phi) depending on which
## DGP you are considering:

y <- y1
phi <- fun1

## Create an evaluation dataset sorting on z (for plotting)

evaldata <- data.frame(y,z,w)
evaldata <- evaldata[order(evaldata$z),]

## Compute the non-IV regression spline estimator of E(y|z)

model.noniv <- crs(y~z,opts=opts)
mean.noniv <- predict(model.noniv,newdata=evaldata)

## Compute the IV-regression spline estimator of phi(z)

## Setting cv.threshold = 0 forces NOMAD search instead of exhaustive search
## when no categorical predictors are present. This avoids unnecessary
## evaluation of all degree/segment combinations in the examples and, for
## crsiv() and crsivderiv(), ensures that the warm-start strategy is used.
model.iv <- crsiv(y=y,z=z,w=w,cv.threshold=0)
phi.iv <- predict(model.iv,newdata=evaldata)

## For the plots, restrict focal attention to the bulk of the data
## (i.e. for the plotting area trim out 1/4 of one percent from each
## tail of y and z)

trim <- 0.0025

curve(phi,min(z),max(z),
      xlim=quantile(z,c(trim,1-trim)),
      ylim=quantile(y,c(trim,1-trim)),
      ylab="Y",
      xlab="Z",
      main="Nonparametric Instrumental Spline Regression",
      sub=paste("Landweber-Fridman: iterations = ", model.iv$num.iterations,sep=""),
      lwd=1,lty=1)

points(z,y,type="p",cex=.25,col="grey")

lines(evaldata$z,evaldata$z^2 -0.325*evaldata$z,lwd=1,lty=1)

lines(evaldata$z,phi.iv,col="blue",lwd=2,lty=2)

lines(evaldata$z,mean.noniv,col="red",lwd=2,lty=4)

legend(quantile(z,trim),quantile(y,1-trim),
      c(expression(paste(varphi(z),"", E(y|z)",sep="")),
        expression(paste("Nonparametric ",hat(varphi)(z))),
        "Nonparametric E(y|z)"),
      lty=c(1,2,4),

```

```

col=c("black","blue","red"),
lwd=c(1,2,2))

## End(Not run)

```

---

crsivderiv

*Nonparametric Instrumental Derivatives*


---

## Description

crsivderiv uses the approach of Florens and Racine (2012) to compute the partial derivative of a nonparametric estimation of an instrumental regression function  $\varphi$  defined by conditional moment restrictions stemming from a structural econometric model:  $E[Y - \varphi(Z, X)|W] = 0$ , and involving endogenous variables  $Y$  and  $Z$  and exogenous variables  $X$  and instruments  $W$ . The derivative function  $\varphi'$  is the solution of an ill-posed inverse problem, and is computed using Landweber-Fridman regularization.

## Usage

```

crsivderiv(y, ...)

## Default S3 method:
crsivderiv(y,
  z,
  w,
  x = NULL,
  zeval = NULL,
  weval = NULL,
  xeval = NULL,
  constant = 0.5,
  display.nomad.progress = TRUE,
  display.warnings = TRUE,
  iterate.diff.tol = 1.0e-08,
  iterate.max = 1000,
  opts = list("MAX_BB_EVAL"=10000,
             "EPSILON"=.Machine$double.eps,
             "INITIAL_MESH_SIZE"="r1.0e-01",
             "MIN_MESH_SIZE"=paste("r",sqrt(.Machine$double.eps),sep=""),
             "MIN_FRAME_SIZE"=paste("r",1,sep=""),
             "DISPLAY_DEGREE"=0),
  penalize.iteration = TRUE,
  smooth.residuals = TRUE,
  start.from = c("Eyz","EEyz"),
  starting.values = NULL,
  stop.on.increase = TRUE,
  ...)

```

**Arguments**

<code>y</code>	a one (1) dimensional numeric or integer vector of dependent data, each element $i$ corresponding to each observation (row) $i$ of $z$
<code>z</code>	a one-column data frame of continuous endogenous predictors. The current implementation of <code>crsivderiv</code> supports univariate continuous $z$ only
<code>w</code>	a $q$ -variate data frame of instruments. The data types may be continuous, discrete (unordered and ordered factors), or some combination thereof
<code>x</code>	an $r$ -variate data frame of exogenous predictors. The data types may be continuous, discrete (unordered and ordered factors), or some combination thereof
<code>zeval</code>	a one-column data frame of continuous endogenous predictors on which the regression will be estimated (evaluation data). By default, evaluation takes place on the data provided by <code>z</code>
<code>weval</code>	a $q$ -variate data frame of instruments on which the regression will be estimated (evaluation data). By default, evaluation takes place on the data provided by <code>w</code>
<code>xeval</code>	an $r$ -variate data frame of exogenous predictors on which the regression will be estimated (evaluation data). By default, evaluation takes place on the data provided by <code>x</code>
<code>constant</code>	the constant to use when using Landweber-Fridman iteration
<code>display.nomad.progress</code>	a logical value indicating whether to display the progress of the NOMAD solver (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>iterate.diff.tol</code>	the search tolerance for the difference in the stopping rule from iteration to iteration when using Landweber-Fridman (disable by setting to zero)
<code>iterate.max</code>	an integer indicating the maximum number of iterations permitted before termination occurs when using Landweber-Fridman iteration
<code>opts</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>penalize.iteration</code>	a logical value indicating whether to penalize the norm by the number of iterations or not (default <code>TRUE</code> )
<code>smooth.residuals</code>	a logical value (defaults to <code>TRUE</code> ) indicating whether to optimize bandwidths for the regression of $y - \varphi(z)$ on $w$ or for the regression of $\varphi(z)$ on $w$ during iteration
<code>start.from</code>	a character string indicating whether to start from $E(Y z)$ (default, "Eyz") or from $E(E(Y z) z)$ (this can be overridden by providing <code>starting.values</code> below)
<code>starting.values</code>	a value indicating whether to commence Landweber-Fridman assuming $\varphi'_{-1} = \text{starting.values}$ (proper Landweber-Fridman) or instead begin from $E(y z)$ (defaults to <code>NULL</code> , see details below)

stop.on.increase  
 a logical value (defaults to TRUE) indicating whether to halt iteration if the stopping criterion (see below) increases over the course of one iteration (i.e. it may be above the iteration tolerance but increased)

... additional arguments supplied to `crs`

## Details

For Landweber-Fridman iteration, an optimal stopping rule based upon  $\|E(y|w) - E(\varphi_k(z, x)|w)\|^2$  is used to terminate iteration. However, if local rather than global optima are encountered the resulting estimates can be overly noisy. To best guard against this eventuality set `nmulti` to a larger number than the default `nmulti=5` for `crs` when using `cv="nomad"` or instead use `cv="exhaustive"` if possible (this may not be feasible for non-trivial problems).

Note that for subsequent Landweber-Fridman iterations, a “warm start” strategy is employed. The optimal parameters (spline degree, number of segments, and bandwidths or inclusion indicators) from the previous iteration are used as starting values for the current iteration. The user-supplied `nmulti` is respected for all iterations. For iterations after the first successful one, these optimal parameters serve as the first of the multiple initial points (a warm start), while any remaining restarts are cold starts. If `nmulti` is not explicitly supplied by the user, it defaults to the `crs` default (5) for the first iteration and to 1 for all subsequent iterations. This strategy provides a balance between computational efficiency and robustness, allowing the NOMAD solver to refine the structural parameters as the residuals evolve incrementally while still guarding against local optima.

When using Landweber-Fridman iteration, iteration will terminate when either the change in the value of  $\|(E(y|w) - E(\varphi_k(z, x)|w))/E(y|w)\|^2$  from iteration to iteration is less than `iterate.diff.tol` or we hit `iterate.max` or  $\|(E(y|w) - E(\varphi_k(z, x)|w))/E(y|w)\|^2$  stops falling in value and starts rising.

When your problem is a simple one (e.g. univariate  $Z$ ,  $W$ , and  $X$ ) you might want to avoid `cv="nomad"` and instead use `cv="exhaustive"` since exhaustive search may be feasible (for `degree.max` and `segments.max` not overly large). This will guarantee an exact solution for each iteration (i.e. there will be no errors arising due to numerical search).

The current implementation supports a single continuous endogenous regressor only. Instrument and exogenous regressor data may still be mixed continuous and categorical.

## Value

`crsivderiv` returns a `crsivderiv` object (which inherits from the `crs` class). The generic functions `print`, `summary`, `fitted`, `residuals`, `predict`, and `plot` support objects of this type.

For the `plot` function, the options are `plot.data=FALSE` (a logical value indicating whether to plot the data as a scatter plot) and `phi=FALSE` (a logical value indicating whether to plot the reconstructed structural function rather than its derivative). Note that the `plot` method for `crsivderiv` objects currently only supports a univariate continuous endogenous predictor  $z$ .

See `crs` for details on the return object components.

In addition to the standard `crs` components, `crsivderiv` returns components `phi.prime`, `phi`, `phi.prime.mat`, `phi.mat`, `num.iterations`, `norm.stop`, `norm.value` and `convergence`.

**Note**

This function currently supports univariate  $z$  only. This function should be considered to be in ‘beta test’ status until further notice.

**Author(s)**

Jeffrey S. Racine <racinej@mcmaster.ca>

**References**

- Carrasco, M. and J.P. Florens and E. Renault (2007), “Linear Inverse Problems in Structural Econometrics Estimation Based on Spectral Decomposition and Regularization,” In: James J. Heckman and Edward E. Leamer, Editor(s), Handbook of Econometrics, Elsevier, 2007, Volume 6, Part 2, Chapter 77, Pages 5633-5751
- Darolles, S. and Y. Fan and J.P. Florens and E. Renault (2011), “Nonparametric Instrumental Regression,” *Econometrica*, 79, 1541-1565.
- Fève, F. and J.P. Florens (2010), “The Practice of Non-parametric Estimation by Solving Inverse Problems: The Example of Transformation Models,” *Econometrics Journal*, 13, S1-S27.
- Florens, J.P. and J.S. Racine (2012), “Nonparametric Instrumental Derivatives,” Working Paper.
- Fridman, V. M. (1956), “A Method of Successive Approximations for Fredholm Integral Equations of the First Kind,” *Uspekhi, Math. Nauk.*, 11, 233-334, in Russian.
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- Landweber, L. (1951), “An Iterative Formula for Fredholm Integral Equations of the First Kind,” *American Journal of Mathematics*, 73, 615-24.
- Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

**See Also**

npreg, [crsiv](#), [crs](#)

**Examples**

```
## Not run:
## This illustration was made possible by Samuele Centorrino
## <samuele.centorrino@univ-tlse1.fr>

set.seed(42)
n <- 1000

## For trimming the plot (trim .5% from each tail)

trim <- 0.005

## The DGP is as follows:

## 1)  $y = \phi(z) + u$ 
```

```

## 2)  $E(u|z) \neq 0$  (endogeneity present)

## 3) Suppose there exists an instrument  $w$  such that  $z = f(w) + v$  and
##  $E(u|w) = 0$ 

## 4) We generate  $v$ ,  $w$ , and generate  $u$  such that  $u$  and  $z$  are
## correlated. To achieve this we express  $u$  as a function of  $v$  (i.e.  $u =$ 
##  $\gamma v + \epsilon$ )

v <- rnorm(n,mean=0,sd=0.27)
eps <- rnorm(n,mean=0,sd=0.05)
u <- -0.5*v + eps
w <- rnorm(n,mean=0,sd=1)

## In Darolles et al (2011) there exist two DGPs. The first is
##  $\phi(z)=z^2$  and the second is  $\phi(z)=\exp(-\text{abs}(z))$  (which is
## discontinuous and has a kink at zero).

fun1 <- function(z) { z^2 }
fun2 <- function(z) { exp(-abs(z)) }

z <- 0.2*w + v

## Generate two y vectors for each function.

y1 <- fun1(z) + u
y2 <- fun2(z) + u

## You set y to be either y1 or y2 (ditto for phi) depending on which
## DGP you are considering:

y <- y1
phi <- fun1

## Sort on z (for plotting)

ivdata <- data.frame(y,z,w,u,v)
ivdata <- ivdata[order(ivdata$z),]
rm(y,z,w,u,v)
attach(ivdata)

## Setting cv.threshold = 0 forces NOMAD search instead of exhaustive search
## when no categorical predictors are present. This avoids unnecessary
## evaluation of all degree/segment combinations in the examples and, for
## crsiv() and crsivderiv(), ensures that the warm-start strategy is used.
model.ivderiv <- crsivderiv(y=y,z=z,w=w,cv.threshold=0)

ylim <-c(quantile(model.ivderiv$phi.prime,trim),
         quantile(model.ivderiv$phi.prime,1-trim))

plot(z,model.ivderiv$phi.prime,
     xlim=quantile(z,c(trim,1-trim)),

```

```

    main="",
    ylim=ylim,
    xlab="Z",
    ylab="Derivative",
    type="l",
    lwd=2)
rug(z)

## End(Not run)

```

---

crssigtest

*Regression Spline Significance Test with Mixed Data Types*


---

## Description

crssigtest implements a consistent test of significance of an explanatory variable in a nonparametric regression setting that is analogous to a simple  $t$ -test in a parametric regression setting. The test is based on Ma and Racine (2011).

## Usage

```

crssigtest(model = NULL,
           index = NULL,
           boot = TRUE,
           boot.num = 399,
           boot.type = c("residual", "reorder"),
           random.seed = 42)

```

## Arguments

model	a crs model object.
index	a vector of indices for the columns of model\$xz for which the test of significance is to be conducted. Defaults to $(1, 2, \dots, p)$ where $p$ is the number of columns in model\$xz.
boot	a logical value (default TRUE) indicating whether to compute the bootstrap P-value or simply return the asymptotic P-value.
boot.num	an integer value specifying the number of bootstrap replications to use. Defaults to 399.
boot.type	whether to conduct ‘residual’ bootstrapping (iid) or permute (reorder) in place the predictor being tested when imposing the null.
random.seed	an integer used to seed R’s random number generator. This is to ensure replicability. Defaults to 42.

**Value**

crssigtest returns an object of type sigtest. [summary](#) supports sigtest objects. It has the following components:

index	the vector of indices input
P	the vector of bootstrap P-values for each statistic in F
P.asy	the vector of asymptotic P-values for each statistic in index
F	the vector of pseudo F-statistics F
F.boot	the matrix of bootstrapped pseudo F-statistics generated under the null (one column for each statistic in F)
df1	the vector of numerator degrees of freedom for each statistic in F (based on the smoother matrix)
df2	the vector of denominator degrees of freedom for each statistic in F (based on the smoother matrix)
rss	the vector of restricted sums of squared residuals for each statistic in F
uss	the vector of unrestricted sums of squared residuals for each statistic in F
boot.num	the number of bootstrap replications
boot.type	the boot.type
xnames	the names of the variables in model\$xz

**Usage Issues**

This function should be considered to be in ‘beta status’ until further notice.

Caution: bootstrap methods are, by their nature, *computationally intensive*. This can be frustrating for users possessing large datasets. For exploratory purposes, you may wish to override the default number of bootstrap replications, say, setting them to `boot.num=99`.

**Author(s)**

Jeffrey S. Racine <racinej@mcmaster.ca>

**References**

Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

Ma, S. and J.S. Racine, (2011), “Inference for Regression Splines with Categorical and Continuous Predictors,” Working Paper.

**Examples**

```
## Not run:
options(crs.messages=FALSE)
set.seed(42)

n <- 1000
```

```

z <- rbinom(n,1,.5)
x1 <- rnorm(n)
x2 <- runif(n,-2,2)
z <- factor(z)
## z is irrelevant
y <- x1 + x2 + rnorm(n)

model <- crs(y~x1+x2+z,complexity="degree",segments=c(1,1))
summary(model)

model.sigstest <- crssigstest(model)
summary(model.sigstest)

## End(Not run)

```

---

Engel95

*1995 British Family Expenditure Survey*


---

### Description

British cross-section data consisting of a random sample taken from the British Family Expenditure Survey for 1995. The households consist of married couples with an employed head-of-household between the ages of 25 and 55 years. There are 1655 household-level observations in total.

### Usage

```
data("Engel95")
```

### Format

A data frame with 10 columns, and 1655 rows.

**food** expenditure share on food, of type numeric  
**catering** expenditure share on catering, of type numeric  
**alcohol** expenditure share on alcohol, of type numeric  
**fuel** expenditure share on fuel, of type numeric  
**motor** expenditure share on motor, of type numeric  
**fares** expenditure share on fares, of type numeric  
**leisure** expenditure share on leisure, of type numeric  
**logexp** logarithm of total expenditure, of type numeric  
**logwages** logarithm of total earnings, of type numeric  
**nkids** number of children, of type numeric

### Source

Richard Blundell and Dennis Kristensen

## References

Blundell, R. and X. Chen and D. Kristensen (2007), "Semi-Nonparametric IV Estimation of Shape-Invariant Engel Curves," *Econometrica*, 75, 1613-1669.

Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

## Examples

```
## Not run:
## Example - we compute nonparametric instrumental regression of an
## Engel curve for food expenditure shares using Landweber-Fridman
## iteration of Fredholm integral equations of the first kind.

## We consider an equation with an endogenous predictor ('z') and an
## instrument ('w'). Let  $y = \phi(z) + u$  where  $\phi(z)$  is the function of
## interest. Here  $E(u|z)$  is not zero hence the conditional mean  $E(y|z)$ 
## does not coincide with the function of interest, but if there exists
## an instrument  $w$  such that  $E(u|w) = 0$ , then we can recover the
## function of interest by solving an ill-posed inverse problem.

data(Engel95)

## Sort on logexp (the endogenous predictor) for plotting purposes
## (i.e. so we can plot a curve for the fitted values versus logexp)

Engel95 <- Engel95[order(Engel95$logexp),]

attach(Engel95)

## Setting cv.threshold = 0 forces NOMAD search instead of exhaustive search
## when no categorical predictors are present. This avoids unnecessary
## evaluation of all degree/segment combinations in the examples and, for
## crsiv() and crsivderiv(), ensures that the warm-start strategy is used.
model.iv <- crsiv(y=food,z=logexp,w=logwages,method="Landweber-Fridman",cv.threshold=0)
phihat <- model.iv$phi

## Compute the non-IV regression (i.e. regress y on z)

## Setting cv.threshold = 0 forces NOMAD search instead of exhaustive search
## when no categorical predictors are present. This avoids unnecessary
## evaluation of all degree/segment combinations in the examples and, for
## crsiv() and crsivderiv(), ensures that the warm-start strategy is used.
ghat <- crs(food~logexp,cv.threshold=0)

## For the plots, we restrict focal attention to the bulk of the data
## (i.e. for the plotting area trim out 1/4 of one percent from each
## tail of y and z). This is often helpful as estimates in the tails of
## the support are less reliable (i.e. more variable) so we are
## interested in examining the relationship 'where the action is'.

trim <- 0.0025
```

```

plot(logexp, food,
     ylab="Food Budget Share",
     xlab="log(Total Expenditure)",
     xlim=quantile(logexp, c(trim, 1-trim)),
     ylim=quantile(food, c(trim, 1-trim)),
     main="Nonparametric Instrumental Regression Splines",
     type="p",
     cex=.5,
     col="lightgrey")

lines(logexp, phihat, col="blue", lwd=2, lty=2)

lines(logexp, fitted(ghat), col="red", lwd=2, lty=4)

legend(quantile(logexp, trim), quantile(food, 1-trim),
       c(expression(paste("Nonparametric IV: ", hat(varphi)(logexp))),
         "Nonparametric Regression: E(food | logexp)"),
       lty=c(2, 4),
       col=c("blue", "red"),
       lwd=c(2, 2),
       bty="n")

## End(Not run)

```

---

frscv

*Categorical Factor Regression Spline Cross-Validation*


---

## Description

frscv computes exhaustive cross-validation directed search for a regression spline estimate of a one (1) dimensional dependent variable on an r-dimensional vector of continuous predictors and nominal/ordinal ([factor/ordered](#)) predictors.

## Usage

```

frscv(xz,
      y,
      basis = c("additive", "tensor", "glp", "auto"),
      complexity = c("degree-knots", "degree", "knots"),
      cv.func = c("cv.ls", "cv.gcv", "cv.aic"),
      degree = degree,
      degree.max = 10,
      degree.min = 0,
      display.nomad.progress = TRUE,
      display.warnings = TRUE,
      knots = c("quantiles", "uniform", "auto"),
      segments = segments,
      segments.max = 10,

```

```

segments.min = 1,
singular.ok = FALSE,
tau = NULL,
weights = NULL)

```

## Arguments

<code>xz</code>	continuous and/or nominal/ordinal ( <a href="#">factor/ordered</a> ) predictors
<code>y</code>	continuous univariate vector
<code>basis</code>	a character string (default <code>basis="additive"</code> ) indicating whether the additive or tensor product B-spline basis matrix for a multivariate polynomial spline or generalized B-spline polynomial basis should be used. Note this can be automatically determined by cross-validation if <code>cv=TRUE</code> and <code>basis="auto"</code> , and is an ‘all or none’ proposition (i.e. interaction terms for all predictors or for no predictors given the nature of ‘tensor products’). Note also that if there is only one predictor this defaults to <code>basis="additive"</code> to avoid unnecessary computation as the spline bases are equivalent in this case
<code>complexity</code>	a character string (default <code>complexity="degree-knots"</code> ) indicating whether model ‘complexity’ is determined by the degree of the spline or by the number of segments (‘knots’). This option allows the user to use cross-validation to select either the spline degree (number of knots held fixed) or the number of knots (spline degree held fixed) or both the spline degree and number of knots
<code>cv.func</code>	a character string (default <code>cv.func="cv.ls"</code> ) indicating which method to use to select smoothing parameters. <code>cv.gcv</code> specifies generalized cross-validation (Craven and Wahba (1979)), <code>cv.aic</code> specifies expected Kullback-Leibler cross-validation (Hurvich, Simonoff, and Tsai (1998)), and <code>cv.ls</code> specifies least-squares cross-validation
<code>degree</code>	integer/vector specifying the degree of the B-spline basis for each dimension of the continuous $x$
<code>degree.max</code>	the maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.max=10</code> )
<code>degree.min</code>	the minimum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=0</code> )
<code>display.nomad.progress</code>	a logical value indicating whether to display NOMAD progress (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>knots</code>	a character string (default <code>knots="quantiles"</code> ) specifying where knots are to be placed. ‘quantiles’ specifies knots placed at equally spaced quantiles (equal number of observations lie in each segment) and ‘uniform’ specifies knots placed at equally spaced intervals. If <code>knots="auto"</code> , the knot type will be automatically determined by cross-validation
<code>segments</code>	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous $x$ (i.e. number of knots minus one)
<code>segments.max</code>	the maximum segments of the B-spline basis for each of the continuous predictors (default <code>segments.max=10</code> )

<code>segments.min</code>	the minimum segments of the B-spline basis for each of the continuous predictors (default <code>segments.min=1</code> )
<code>singular.ok</code>	a logical value (default <code>singular.ok=FALSE</code> ) that, when <code>FALSE</code> , discards singular bases during cross-validation (a check for ill-conditioned bases is performed).
<code>tau</code>	if non-null a number in (0,1) denoting the quantile for which a quantile regression spline is to be estimated rather than estimating the conditional mean (default <code>tau=NULL</code> )
<code>weights</code>	an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector. If non-NULL, weighted least squares is used with weights 'weights' (that is, minimizing 'sum(w*e^2)'); otherwise ordinary least squares is used.

### Details

`frscv` computes exhaustive cross-validation for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and nominal/ordinal (`factor/ordered`) predictors. The optimal  $K/I$  combination (i.e. degree/segments/ $I$ ) is returned along with other results (see below for return values).

For the continuous predictors the regression spline model employs either the additive or tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>) and the `tensor.prod.model.matrix` function.

For the nominal/ordinal (`factor/ordered`) predictors the regression spline model uses indicator basis functions.

### Value

`frscv` returns a `crscv` object. Furthermore, the function `summary` supports objects of this type. The returned objects have the following components:

<code>K</code>	scalar/vector containing optimal degree(s) of spline or number of segments
<code>I</code>	scalar/vector containing an indicator of whether the predictor is included or not for each dimension of the nominal/ordinal ( <code>factor/ordered</code> ) predictors
<code>K.mat</code>	vector/matrix of values of $K$ evaluated during search
<code>cv.func</code>	objective function value at optimum
<code>cv.func.vec</code>	vector of objective function values at each degree of spline or number of segments in <code>K.mat</code>

### Author(s)

Jeffrey S. Racine <[racinej@mcmaster.ca](mailto:racinej@mcmaster.ca)>

## References

Craven, P. and G. Wahba (1979), "Smoothing Noisy Data With Spline Functions," *Numerische Mathematik*, 13, 377-403.

Hurvich, C.M. and J.S. Simonoff and C.L. Tsai (1998), "Smoothing Parameter Selection in Non-parametric Regression Using an Improved Akaike Information Criterion," *Journal of the Royal Statistical Society B*, 60, 271-293.

Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

Ma, S. and J.S. Racine and L. Yang (2015), "Spline Regression in the Presence of Categorical Predictors," *Journal of Applied Econometrics*, Volume 30, 705-717.

Ma, S. and J.S. Racine (2013), "Additive Regression Splines with Irrelevant Categorical and Continuous Regressors," *Statistica Sinica*, Volume 23, 515-541.

## See Also

[loess](#), [npregbw](#)

## Examples

```
set.seed(42)
## Simulated data
n <- 1000

x <- runif(n)
z <- round(runif(n,min=-0.5,max=1.5))
z.unique <- uniquecombs(as.matrix(z))
ind <- attr(z.unique,"index")
ind.vals <- sort(unique(ind))
dgp <- numeric(length=n)
for(i in 1:nrow(z.unique)) {
  zz <- ind == ind.vals[i]
  dgp[zz] <- z[zz]+cos(2*pi*x[zz])
}

y <- dgp + rnorm(n,sd=.1)

xdata <- data.frame(x,z=factor(z))

## Compute the optimal K and I, determine optimal number of knots, set
## spline degree for x to 3

cv <- frscv(x=xdata,y=y,complexity="knots",degree=c(3))
summary(cv)
```

## Description

frscvNOMAD computes NOMAD-based (Nonsmooth Optimization by Mesh Adaptive Direct Search, Abramson, Audet, Couture and Le Digabel (2011)) cross-validation directed search for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous predictors and nominal/ordinal ([factor/ordered](#)) predictors.

## Usage

```
frscvNOMAD(xz,
           y,
           basis = c("additive", "tensor", "glp", "auto"),
           complexity = c("degree-knots", "degree", "knots"),
           cv.df.min = 1,
           cv.func = c("cv.ls", "cv.gcv", "cv.aic"),
           degree = degree,
           degree.max = 10,
           degree.min = 0,
           display.nomad.progress = TRUE,
           display.warnings = TRUE,
           include = include,
           initial.mesh.size.integer = "1",
           knots = c("quantiles", "uniform", "auto"),
           max.bb.eval = 10000,
           min.mesh.size.integer = "1",
           min.frame.size.integer = "1",
           nmulti = 0,
           opts=list(),
           random.seed = 42,
           segments = segments,
           segments.max = 10,
           segments.min = 1,
           singular.ok = FALSE,
           tau = NULL,
           weights = NULL)
```

## Arguments

xz	continuous and/or nominal/ordinal ( <a href="#">factor/ordered</a> ) predictors
y	continuous univariate vector
basis	a character string (default basis="additive") indicating whether the additive or tensor product B-spline basis matrix for a multivariate polynomial spline or generalized B-spline polynomial basis should be used. Note this can be automatically determined by cross-validation if cv=TRUE and basis="auto", and is

an ‘all or none’ proposition (i.e. interaction terms for all predictors or for no predictors given the nature of ‘tensor products’). Note also that if there is only one predictor this defaults to `basis="additive"` to avoid unnecessary computation as the spline bases are equivalent in this case

<code>complexity</code>	a character string (default <code>complexity="degree-knots"</code> ) indicating whether model ‘complexity’ is determined by the degree of the spline or by the number of segments (‘knots’). This option allows the user to use cross-validation to select either the spline degree (number of knots held fixed) or the number of knots (spline degree held fixed) or both the spline degree and number of knots
<code>cv.df.min</code>	the minimum degrees of freedom to allow when conducting cross-validation (default <code>cv.df.min=1</code> )
<code>cv.func</code>	a character string (default <code>cv.func="cv.ls"</code> ) indicating which method to use to select smoothing parameters. <code>cv.gcv</code> specifies generalized cross-validation (Craven and Wahba (1979)), <code>cv.aic</code> specifies expected Kullback-Leibler cross-validation (Hurvich, Simonoff, and Tsai (1998)), and <code>cv.ls</code> specifies least-squares cross-validation
<code>degree</code>	integer/vector specifying the degree of the B-spline basis for each dimension of the continuous $x$
<code>degree.max</code>	the maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.max=10</code> )
<code>degree.min</code>	the minimum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=0</code> )
<code>display.nomad.progress</code>	a logical value indicating whether to display the progress of the NOMAD solver (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>include</code>	integer/vector for the categorical predictors. If it is not NULL, it will be the initial value for the fitting
<code>initial.mesh.size.integer</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>knots</code>	a character string (default <code>knots="quantiles"</code> ) specifying where knots are to be placed. ‘quantiles’ specifies knots placed at equally spaced quantiles (equal number of observations lie in each segment) and ‘uniform’ specifies knots placed at equally spaced intervals. If <code>knots="auto"</code> , the knot type will be automatically determined by cross-validation
<code>max.bb.eval</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.mesh.size.integer</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.frame.size.integer</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>nmulti</code>	integer number of times to restart the process of finding extrema of the cross-validation function from different (random) initial points (default <code>nmulti=0</code> )

opts	list of optional arguments to be passed to <code>snomadr</code> . If not user-specified, this function applies the NOMAD4 path defaults <code>QUAD_MODEL_SEARCH="no"</code> , <code>EVAL_QUEUE_SORT="DIR_LAST"</code> , <code>SIMPLE_LINE_SEARCH="yes"</code> , and <code>SPECULATIVE_SEARCH="no"</code> , and <code>DIRECTION_TYPE="ORTHO N+1 NEG"</code> for faster mixed-integer search in this specific <code>frscvNOMAD</code> path. User-supplied <code>opts</code> entries always take precedence.
random.seed	when it is not missing and not equal to 0, the initial points will be generated using this seed when <code>nmulti &gt; 0</code>
segments	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous $x$ (i.e. number of knots minus one)
segments.max	the maximum segments of the B-spline basis for each of the continuous predictors (default <code>segments.max=10</code> )
segments.min	the minimum segments of the B-spline basis for each of the continuous predictors (default <code>segments.min=1</code> )
singular.ok	a logical value (default <code>singular.ok=FALSE</code> ) that, when <code>FALSE</code> , discards singular bases during cross-validation (a check for ill-conditioned bases is performed).
tau	if non-null a number in (0,1) denoting the quantile for which a quantile regression spline is to be estimated rather than estimating the conditional mean (default <code>tau=NULL</code> )
weights	an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector. If non-NULL, weighted least squares is used with weights 'weights' (that is, minimizing ' $\sum(w*e^2)$ '); otherwise ordinary least squares is used.

## Details

`frscvNOMAD` computes NOMAD-based cross-validation for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and nominal/ordinal (`factor/ordered`) predictors. Numerical search for the optimal degree/segments/ $I$  is undertaken using `snomadr`.

The optimal  $K/I$  combination is returned along with other results (see below for return values).

For the continuous predictors the regression spline model employs either the additive or tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>) and the `tensor.prod.model.matrix` function.

For the nominal/ordinal (`factor/ordered`) predictors the regression spline model uses indicator basis functions.

## Value

`frscvNOMAD` returns a `crscv` object. Furthermore, the function `summary` supports objects of this type. The returned objects have the following components:

K	scalar/vector containing optimal degree(s) of spline or number of segments
I	scalar/vector containing an indicator of whether the predictor is included or not for each dimension of the nominal/ordinal ( <code>factor/ordered</code> ) predictors

K.mat	vector/matrix of values of K evaluated during search
degree.max	the maximum degree of the B-spline basis for each of the continuous predictors (default degree.max=10)
segments.max	the maximum segments of the B-spline basis for each of the continuous predictors (default segments.max=10)
degree.min	the minimum degree of the B-spline basis for each of the continuous predictors (default degree.min=0)
segments.min	the minimum segments of the B-spline basis for each of the continuous predictors (default segments.min=1)
cv.func	objective function value at optimum
cv.func.vec	vector of objective function values at each degree of spline or number of segments in K.mat

### Author(s)

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### References

- Abramson, M.A. and C. Audet and G. Couture and J.E. Dennis Jr. and S. Le Digabel (2011), “The NOMAD project”. Software available at <https://www.gerad.ca/nomad>.
- Craven, P. and G. Wahba (1979), “Smoothing Noisy Data With Spline Functions,” *Numerische Mathematik*, 13, 377-403.
- Hurvich, C.M. and J.S. Simonoff and C.L. Tsai (1998), “Smoothing Parameter Selection in Nonparametric Regression Using an Improved Akaike Information Criterion,” *Journal of the Royal Statistical Society B*, 60, 271-293.
- Le Digabel, S. (2011), “Algorithm 909: NOMAD: Nonlinear Optimization With the MADS Algorithm”. *ACM Transactions on Mathematical Software*, 37(4):44:1-44:15.
- Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.
- Ma, S. and J.S. Racine and L. Yang (2015), “Spline Regression in the Presence of Categorical Predictors,” *Journal of Applied Econometrics*, Volume 30, 705-717.
- Ma, S. and J.S. Racine (2013), “Additive Regression Splines with Irrelevant Categorical and Continuous Regressors,” *Statistica Sinica*, Volume 23, 515-541.

### See Also

[loess](#), [npregbw](#)

### Examples

```
set.seed(42)
## Simulated data
n <- 1000

x <- runif(n)
```

```

z <- round(runif(n,min=-0.5,max=1.5))
z.unique <- uniquecombs(as.matrix(z))
ind <- attr(z.unique,"index")
ind.vals <- sort(unique(ind))
dgp <- numeric(length=n)
for(i in 1:nrow(z.unique)) {
  zz <- ind == ind.vals[i]
  dgp[zz] <- z[zz]+cos(2*pi*x[zz])
}

y <- dgp + rnorm(n,sd=.1)

xdata <- data.frame(x,z=factor(z))

## Compute the optimal K and I, determine optimal number of knots, set
## spline degree for x to 3

cv <- frscvNOMAD(x=xdata,y=y,complexity="knots",degree=c(3),segments=c(5))
summary(cv)

```

---

glp.model.matrix

*Utility function for constructing generalized polynomial smooths*


---

### Description

Produce model matrices for a generalized polynomial smooth from the model matrices for the marginal bases of the smooth.

### Usage

```
glp.model.matrix(X)
```

### Arguments

X                    a list of model matrices for the marginal bases of a smooth

### Details

This function computes a generalized polynomial where the orders of each term entering the polynomial may vary.

### Value

A model matrix for a generalized polynomial smooth.

### Author(s)

Jeffrey S. Racine <racinej@mcmaster.ca>

## References

Hall, P. and J.S. Racine (2015), “Infinite Order Cross-Validated Local Polynomial Regression,” *Journal of Econometrics*, 185, 510-525.

## Examples

```
X <- list(matrix(1:4,2,2),matrix(5:10,2,3))
glp.model.matrix(X)
```

---

gsl.bs

*GSL (GNU Scientific Library) B-spline/B-spline Derivatives*

---

## Description

gsl.bs generates the B-spline basis matrix for a polynomial spline and (optionally) the B-spline basis matrix derivative of a specified order with respect to each predictor

## Usage

```
gsl.bs(..., display.warnings = TRUE)
## Default S3 method:
gsl.bs(x,
       degree = 3,
       nbreak = 2,
       deriv = 0,
       x.min = NULL,
       x.max = NULL,
       intercept = FALSE,
       knots = NULL,
       display.warnings = TRUE,
       ...)
```

## Arguments

x	the predictor variable. Missing values are not allowed
degree	degree of the piecewise polynomial - default is '3' (cubic spline)
nbreak	number of breaks in each interval - default is '2'
deriv	the order of the derivative to be computed-default if 0
x.min	the lower bound on which to construct the spline - defaults to min(x)
x.max	the upper bound on which to construct the spline - defaults to max(x)
intercept	if 'TRUE', an intercept is included in the basis; default is 'FALSE'
knots	a vector (default knots="NULL") specifying knots for the spline basis (default enables uniform knots, otherwise those provided are used)
display.warnings	a logical value indicating whether to display warnings (default display.warnings=TRUE)
...	optional arguments

**Details**

Typical usages are (see below for a list of options and also the examples at the end of this help file)

```
B <- gsl.bs(x,degree=10)
B.predict <- predict(gsl.bs(x,degree=10),newx=xeval)
```

**Value**

`gsl.bs` returns a `gsl.bs` object. A matrix of dimension `'c(length(x), degree+nbreak-1)'`. The generic function `predict` extracts (or generates) predictions from the returned object.

A primary use is in modelling formulas to directly specify a piecewise polynomial term in a model. See <https://www.gnu.org/software/gsl/> for further details.

**Author(s)**

Jeffrey S. Racine <racinej@mcmaster.ca>

**References**

Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

Ma, S. and J.S. Racine and L. Yang (2015), "Spline Regression in the Presence of Categorical Predictors," *Journal of Applied Econometrics*, Volume 30, 705-717.

Ma, S. and J.S. Racine (2013), "Additive Regression Splines with Irrelevant Categorical and Continuous Regressors," *Statistica Sinica*, Volume 23, 515-541.

**See Also**

[bs](#)

**Examples**

```
## Plot the spline bases and their first order derivatives
x <- seq(0,1,length=100)
matplot(x,gsl.bs(x,degree=5),type="l")
matplot(x,gsl.bs(x,degree=5,deriv=1),type="l")

## Regression example
n <- 1000
x <- sort(runif(n))
y <- cos(2*pi*x) + rnorm(n,sd=.25)
B <- gsl.bs(x,degree=5,intercept=FALSE)
plot(x,y,cex=.5,col="grey")
lines(x,fitted(lm(y~B)))
```

## Description

krscv computes exhaustive cross-validation directed search for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and nominal/ordinal ([factor/ordered](#)) predictors.

## Usage

```
krscv(xz,
      y,
      basis = c("additive", "tensor", "glp", "auto"),
      complexity = c("degree-knots", "degree", "knots"),
      cv.func = c("cv.ls", "cv.gcv", "cv.aic"),
      degree = degree,
      degree.max = 10,
      degree.min = 0,
      display.nomad.progress = TRUE,
      display.warnings = TRUE,
      knots = c("quantiles", "uniform", "auto"),
      restarts = 0,
      segments = segments,
      segments.max = 10,
      segments.min = 1,
      singular.ok = FALSE,
      tau = NULL,
      weights = NULL)
```

## Arguments

xz	continuous and/or nominal/ordinal ( <a href="#">factor/ordered</a> ) predictors
y	continuous univariate vector
basis	a character string (default basis="additive") indicating whether the additive or tensor product B-spline basis matrix for a multivariate polynomial spline or generalized B-spline polynomial basis should be used. Note this can be automatically determined by cross-validation if cv=TRUE and basis="auto", and is an 'all or none' proposition (i.e. interaction terms for all predictors or for no predictors given the nature of 'tensor products'). Note also that if there is only one predictor this defaults to basis="additive" to avoid unnecessary computation as the spline bases are equivalent in this case
complexity	a character string (default complexity="degree-knots") indicating whether model 'complexity' is determined by the degree of the spline or by the number of segments ('knots'). This option allows the user to use cross-validation to select either the spline degree (number of knots held fixed) or the number of knots (spline degree held fixed) or both the spline degree and number of knots

<code>cv.func</code>	a character string (default <code>cv.func="cv.ls"</code> ) indicating which method to use to select smoothing parameters. <code>cv.gcv</code> specifies generalized cross-validation (Craven and Wahba (1979)), <code>cv.aic</code> specifies expected Kullback-Leibler cross-validation (Hurvich, Simonoff, and Tsai (1998)), and <code>cv.ls</code> specifies least-squares cross-validation
<code>degree</code>	integer/vector specifying the degree of the B-spline basis for each dimension of the continuous $x$
<code>degree.max</code>	the maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.max=10</code> )
<code>degree.min</code>	the minimum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=0</code> )
<code>display.nomad.progress</code>	a logical value indicating whether to display NOMAD progress (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>knots</code>	a character string (default <code>knots="quantiles"</code> ) specifying where knots are to be placed. 'quantiles' specifies knots placed at equally spaced quantiles (equal number of observations lie in each segment) and 'uniform' specifies knots placed at equally spaced intervals. If <code>knots="auto"</code> , the knot type will be automatically determined by cross-validation
<code>restarts</code>	number of times to restart <code>optim</code> from different initial random values (default <code>restarts=0</code> ) when searching for optimal bandwidths for the categorical predictors for each unique $K$ combination (i.e. degree/segments)
<code>segments</code>	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous $x$ (i.e. number of knots minus one)
<code>segments.max</code>	the maximum segments of the B-spline basis for each of the continuous predictors (default <code>segments.max=10</code> )
<code>segments.min</code>	the minimum segments of the B-spline basis for each of the continuous predictors (default <code>segments.min=1</code> )
<code>singular.ok</code>	a logical value (default <code>singular.ok=FALSE</code> ) that, when <code>FALSE</code> , discards singular bases during cross-validation (a check for ill-conditioned bases is performed).
<code>tau</code>	if non-null a number in (0,1) denoting the quantile for which a quantile regression spline is to be estimated rather than estimating the conditional mean (default <code>tau=NULL</code> )
<code>weights</code>	an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector. If non-NULL, weighted least squares is used with weights 'weights' (that is, minimizing 'sum(w*e^2)'); otherwise ordinary least squares is used.

## Details

`krscv` computes exhaustive cross-validation for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and nominal/ordinal ([factor/ordered](#)) predictors. The optimal  $K/\lambda$  combination is returned along with other results (see below for

return values). The method uses kernel functions appropriate for categorical (ordinal/nominal) predictors which avoids the loss in efficiency associated with sample-splitting procedures that are typically used when faced with a mix of continuous and nominal/ordinal ([factor/ordered](#)) predictors.

For the continuous predictors the regression spline model employs either the additive or tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>) and the [tensor.prod.model.matrix](#) function.

For the discrete predictors the product kernel function is of the ‘Li-Racine’ type (see Li and Racine (2007) for details).

For each unique combination of degree and segment, numerical search for the bandwidth vector `lambda` is undertaken using [optim](#) and the box-constrained L-BFGS-B method (see [optim](#) for details). The user may restart the [optim](#) algorithm as many times as desired via the `restarts` argument. The approach ascends from `K=0` through `degree.max/segments.max` and for each value of `K` searches for the optimal bandwidths for this value of `K`. After the most complex model has been searched then the optimal `K/Lambda` combination is selected. If any element of the optimal `K` vector coincides with `degree.max/segments.max` a warning is produced and the user ought to restart their search with a larger value of `degree.max/segments.max`.

## Value

`krscv` returns a `crscv` object. Furthermore, the function [summary](#) supports objects of this type. The returned objects have the following components:

<code>K</code>	scalar/vector containing optimal degree(s) of spline or number of segments
<code>K.mat</code>	vector/matrix of values of <code>K</code> evaluated during search
<code>restarts</code>	number of restarts during search, if any
<code>lambda</code>	optimal bandwidths for categorical predictors
<code>lambda.mat</code>	vector/matrix of optimal bandwidths for each degree of spline
<code>cv.func</code>	objective function value at optimum
<code>cv.func.vec</code>	vector of objective function values at each degree of spline or number of segments in <code>K.mat</code>

## Author(s)

Jeffrey S. Racine <[racinej@mcmaster.ca](mailto:racinej@mcmaster.ca)>

## References

Craven, P. and G. Wahba (1979), “Smoothing Noisy Data With Spline Functions,” *Numerische Mathematik*, 13, 377-403.

Hurvich, C.M. and J.S. Simonoff and C.L. Tsai (1998), “Smoothing Parameter Selection in Non-parametric Regression Using an Improved Akaike Information Criterion,” *Journal of the Royal Statistical Society B*, 60, 271-293.

Li, Q. and J.S. Racine (2007), *Nonparametric Econometrics: Theory and Practice*, Princeton University Press.

Ma, S. and J.S. Racine and L. Yang (2015), “Spline Regression in the Presence of Categorical Predictors,” *Journal of Applied Econometrics*, Volume 30, 705-717.

Ma, S. and J.S. Racine (2013), “Additive Regression Splines with Irrelevant Categorical and Continuous Regressors,” *Statistica Sinica*, Volume 23, 515-541.

### See Also

[loess](#), [npregbw](#)

### Examples

```
set.seed(42)
## Simulated data
n <- 1000

x <- runif(n)
z <- round(runif(n,min=-0.5,max=1.5))
z.unique <- uniquecombs(as.matrix(z))
ind <- attr(z.unique,"index")
ind.vals <- sort(unique(ind))
dgp <- numeric(length=n)
for(i in 1:nrow(z.unique)) {
  zz <- ind == ind.vals[i]
  dgp[zz] <- z[zz]+cos(2*pi*x[zz])
}
y <- dgp + rnorm(n,sd=.1)

xdata <- data.frame(x,z=factor(z))

## Compute the optimal K and lambda, determine optimal number of knots, set
## spline degree for x to 3

cv <- krscv(x=xdata,y=y,complexity="knots",degree=c(3))
summary(cv)
```

### Description

krscvNOMAD computes NOMAD-based (Nonsmooth Optimization by Mesh Adaptive Direct Search, Abramson, Audet, Couture and Le Digabel (2011)) cross-validation directed search for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and nominal/ordinal ([factor/ordered](#)) predictors.

**Usage**

```
krscvNOMAD(xz,
           y,
           basis = c("additive", "tensor", "glp", "auto"),
           complexity = c("degree-knots", "degree", "knots"),
           cv.df.min = 1,
           cv.func = c("cv.ls", "cv.gcv", "cv.aic"),
           degree = degree,
           degree.max = 10,
           degree.min = 0,
           display.nomad.progress = TRUE,
           display.warnings = TRUE,
           initial.mesh.size.integer = "1",
           initial.mesh.size.real = "r0.1",
           knots = c("quantiles", "uniform", "auto"),
           lambda = lambda,
           lambda.discrete = FALSE,
           lambda.discrete.num = 100,
           max.bb.eval = 140,
           min.mesh.size.integer = "1",
           min.mesh.size.real = paste("r", sqrt(.Machine$double.eps), sep=""),
           min.frame.size.integer = "1",
           min.frame.size.real = "1",
           nmulti = 0,
           opts=list(),
           random.seed = 42,
           segments = segments,
           segments.max = 10,
           segments.min = 1,
           singular.ok = FALSE,
           tau = NULL,
           weights = NULL)
```

**Arguments**

xz	continuous and/or nominal/ordinal ( <a href="#">factor/ordered</a> ) predictors
y	continuous univariate vector
basis	a character string (default basis="additive") indicating whether the additive or tensor product B-spline basis matrix for a multivariate polynomial spline or generalized B-spline polynomial basis should be used. Note this can be automatically determined by cross-validation if cv=TRUE and basis="auto", and is an 'all or none' proposition (i.e. interaction terms for all predictors or for no predictors given the nature of 'tensor products'). Note also that if there is only one predictor this defaults to basis="additive" to avoid unnecessary computation as the spline bases are equivalent in this case
complexity	a character string (default complexity="degree-knots") indicating whether model 'complexity' is determined by the degree of the spline or by the number

	of segments ('knots'). This option allows the user to use cross-validation to select either the spline degree (number of knots held fixed) or the number of knots (spline degree held fixed) or both the spline degree and number of knots
<code>cv.df.min</code>	the minimum degrees of freedom to allow when conducting cross-validation (default <code>cv.df.min=1</code> )
<code>cv.func</code>	a character string (default <code>cv.func="cv.ls"</code> ) indicating which method to use to select smoothing parameters. <code>cv.gcv</code> specifies generalized cross-validation (Craven and Wahba (1979)), <code>cv.aic</code> specifies expected Kullback-Leibler cross-validation (Hurvich, Simonoff, and Tsai (1998)), and <code>cv.ls</code> specifies least-squares cross-validation
<code>degree</code>	integer/vector specifying the degree of the B-spline basis for each dimension of the continuous $x$
<code>degree.max</code>	the maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.max=10</code> )
<code>degree.min</code>	the minimum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=0</code> )
<code>display.nomad.progress</code>	a logical value indicating whether to display the progress of the NOMAD solver (default <code>display.nomad.progress=TRUE</code> )
<code>display.warnings</code>	a logical value indicating whether to display warnings (default <code>display.warnings=TRUE</code> )
<code>initial.mesh.size.integer</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>initial.mesh.size.real</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>knots</code>	a character string (default <code>knots="quantiles"</code> ) specifying where knots are to be placed. 'quantiles' specifies knots placed at equally spaced quantiles (equal number of observations lie in each segment) and 'uniform' specifies knots placed at equally spaced intervals. If <code>knots="auto"</code> , the knot type will be automatically determined by cross-validation
<code>lambda</code>	real/vector for the categorical predictors. If it is not NULL, it will be the starting value(s) for lambda
<code>lambda.discrete</code>	if <code>lambda.discrete=TRUE</code> , the bandwidth will be discretized into <code>lambda.discrete.num+1</code> points and lambda will be chosen from these points
<code>lambda.discrete.num</code>	a positive integer indicating the number of discrete values that lambda can assume - this parameter will only be used when <code>lambda.discrete=TRUE</code>
<code>max.bb.eval</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details). Default is 140 for the aggressive speed-oriented profile.
<code>min.mesh.size.integer</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.mesh.size.real</code>	argument passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)

<code>min.frame.size.integer</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>min.frame.size.real</code>	arguments passed to the NOMAD solver (see <a href="#">snomadr</a> for further details)
<code>nmulti</code>	integer number of times to restart the process of finding extrema of the cross-validation function from different (random) initial points (default <code>nmulti=0</code> )
<code>opts</code>	list of optional arguments to be passed to <a href="#">snomadr</a> . If not user-specified, this function applies the NOMAD4 path defaults <code>QUAD_MODEL_SEARCH="no"</code> , <code>EVAL_QUEUE_SORT="DIR_LAST"</code> and <code>DIRECTION_TYPE="ORTHO 2N"</code> for an aggressive, speed-oriented mixed-integer search profile in this specific <code>krscvNOMAD</code> path. User-supplied <code>opts</code> entries always take precedence.
<code>random.seed</code>	when it is not missing and not equal to 0, the initial points will be generated using this seed when <code>nmulti &gt; 0</code>
<code>segments</code>	integer/vector specifying the number of segments of the B-spline basis for each dimension of the continuous $x$ (i.e. number of knots minus one)
<code>segments.max</code>	the maximum segments of the B-spline basis for each of the continuous predictors (default <code>segments.max=10</code> )
<code>segments.min</code>	the minimum segments of the B-spline basis for each of the continuous predictors (default <code>segments.min=1</code> )
<code>singular.ok</code>	a logical value (default <code>singular.ok=FALSE</code> ) that, when <code>FALSE</code> , discards singular bases during cross-validation (a check for ill-conditioned bases is performed).
<code>tau</code>	if non-null a number in (0,1) denoting the quantile for which a quantile regression spline is to be estimated rather than estimating the conditional mean (default <code>tau=NULL</code> )
<code>weights</code>	an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector. If non-NULL, weighted least squares is used with weights 'weights' (that is, minimizing 'sum(w*e^2)'); otherwise ordinary least squares is used.

## Details

`krscvNOMAD` computes NOMAD-based cross-validation for a regression spline estimate of a one (1) dimensional dependent variable on an  $r$ -dimensional vector of continuous and nominal/ordinal ([factor/ordered](#)) predictors. Numerical search for the optimal degree/segments/lambda is undertaken using [snomadr](#).

The optimal  $K/\lambda$  combination is returned along with other results (see below for return values). The method uses kernel functions appropriate for categorical (ordinal/nominal) predictors which avoids the loss in efficiency associated with sample-splitting procedures that are typically used when faced with a mix of continuous and nominal/ordinal ([factor/ordered](#)) predictors.

For the continuous predictors the regression spline model employs either the additive or tensor product B-spline basis matrix for a multivariate polynomial spline via the B-spline routines in the GNU Scientific Library (<https://www.gnu.org/software/gsl/>) and the `tensor.prod.model.matrix` function.

For the discrete predictors the product kernel function is of the 'Li-Racine' type (see Li and Racine (2007) for details).

**Value**

krscvNOMAD returns a crscv object. Furthermore, the function `summary` supports objects of this type. The returned objects have the following components:

<code>K</code>	scalar/vector containing optimal degree(s) of spline or number of segments
<code>K.mat</code>	vector/matrix of values of <code>K</code> evaluated during search
<code>degree.max</code>	the maximum degree of the B-spline basis for each of the continuous predictors (default <code>degree.max=10</code> )
<code>segments.max</code>	the maximum segments of the B-spline basis for each of the continuous predictors (default <code>segments.max=10</code> )
<code>degree.min</code>	the minimum degree of the B-spline basis for each of the continuous predictors (default <code>degree.min=0</code> )
<code>segments.min</code>	the minimum segments of the B-spline basis for each of the continuous predictors (default <code>segments.min=1</code> )
<code>restarts</code>	number of restarts during search, if any
<code>lambda</code>	optimal bandwidths for categorical predictors
<code>lambda.mat</code>	vector/matrix of optimal bandwidths for each degree of spline
<code>cv.func</code>	objective function value at optimum
<code>cv.func.vec</code>	vector of objective function values at each degree of spline or number of segments in <code>K.mat</code>

**Author(s)**

Jeffrey S. Racine <racinej@mcmaster.ca> and Zhenghua Nie <niez@mcmaster.ca>

**References**

- Abramson, M.A. and C. Audet and G. Couture and J.E. Dennis Jr. and S. Le Digabel (2011), “The NOMAD project”. Software available at <https://www.gerad.ca/nomad>.
- Craven, P. and G. Wahba (1979), “Smoothing Noisy Data With Spline Functions,” *Numerische Mathematik*, 13, 377-403.
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- Ma, S. and J.S. Racine (2013), “Additive Regression Splines with Irrelevant Categorical and Continuous Regressors,” *Statistica Sinica*, Volume 23, 515-541.

**See Also**

[loess](#), [npregbw](#)

**Examples**

```

set.seed(42)
## Simulated data
n <- 1000

x <- runif(n)
z <- round(runif(n,min=-0.5,max=1.5))
z.unique <- uniquecombs(as.matrix(z))
ind <- attr(z.unique,"index")
ind.vals <- sort(unique(ind))
dgp <- numeric(length=n)
for(i in 1:nrow(z.unique)) {
  zz <- ind == ind.vals[i]
  dgp[zz] <- z[zz]+cos(2*pi*x[zz])
}
y <- dgp + rnorm(n,sd=.1)

xdata <- data.frame(x,z=factor(z))

## Compute the optimal K and lambda, determine optimal number of knots, set
## spline degree for x to 3

cv <- krscvNOMAD(x=xdata,y=y,complexity="knots",degree=c(3),segments=c(5))
summary(cv)

```

---

 snomadr

*R interface to NOMAD*


---

**Description**

snomadr is an R interface to NOMAD (Nonsmooth Optimization by Mesh Adaptive Direct Search, Abramson, Audet, Couture and Le Digabel (2011)), an open source software C++ implementation of the Mesh Adaptive Direct Search (MADS, Le Digabel (2011)) algorithm designed for constrained optimization of blackbox functions.

NOMAD is designed to find (local) solutions of mathematical optimization problems of the form

$$\begin{aligned}
 & \min && f(x) \\
 & x \text{ in } && R^n \\
 \\
 & \text{s. t.} && g(x) \leq 0 \\
 & && x_L \leq x \leq x_U
 \end{aligned}$$

where  $f(x): R^n \rightarrow R^k$  is the objective function, and  $g(x): R^n \rightarrow R^m$  are the constraint functions. The vectors  $x_L$  and  $x_U$  are the bounds on the variables  $x$ . The functions  $f(x)$  and  $g(x)$

can be nonlinear and nonconvex. The variables can be integer, continuous real number, binary, and categorical.

Kindly see <https://www.gerad.ca/en/software/nomad> and the references below for details.

## Usage

```
snomadr(eval.f,
        n,
        bbin = NULL,
        bbout = NULL,
        x0 = NULL,
        lb = NULL,
        ub = NULL,
        nmulti = 0,
        random.seed = 0,
        opts = list(),
        display.nomad.progress = TRUE,
        information = list(),
        snomadr.environment = new.env(),
        ... )
```

## Arguments

eval.f	function that returns the value of the objective function
n	the number of variables
bbin	types of variables. Variable types are 0 (CONTINUOUS), 1 (INTEGER), 2 (CATEGORICAL), 3 (BINARY)
bbout	types of output of eval.f. See the NOMAD User Guide <a href="https://nomad-4-user-guide.readthedocs.io/en/latest/#">https://nomad-4-user-guide.readthedocs.io/en/latest/#</a>
x0	vector with starting values for the optimization. If it is provided and nmulti is bigger than 1, x0 will be the first initial point for multiple initial points
lb	vector with lower bounds of the controls (use -1.0e19 for controls without lower bound)
ub	vector with upper bounds of the controls (use 1.0e19 for controls without upper bound)
nmulti	when it is missing, or it is equal to 0 and x0 is provided, snomadRSolve will be called to solve the problem. Otherwise, smultinomadRSolve will be called
random.seed	when it is not missing and not equal to 0, the initial points will be generated using this seed when nmulti > 0
opts	list of options for NOMAD, see the NOMAD user guide <a href="https://nomad-4-user-guide.readthedocs.io/en/latest/#">https://nomad-4-user-guide.readthedocs.io/en/latest/#</a> . Options can also be set by nomad.opt which should be in the folder where R (snomadr) is executed. This interface uses NOMAD 4 option names directly (for example MIN_FRAME_SIZE). A complete option catalog generated from the embedded NOMAD 4.5.0 definitions is bundled at system.file("nomad", "NOMAD_4_5_0_OPTIONS_REFERENCE.md", package="crs").

To improve comparability with historical NOMAD 3.9.1 behavior, snomadr applies a small NOMAD4 compatibility profile when these options are not user-supplied (user opts always take precedence): QUAD\_MODEL\_SEARCH, SGTelib\_MODEL\_SEARCH, NM\_SEARCH, SPECULATIVE\_SEARCH, EVAL\_OPPORTUNISTIC, EVAL\_QUEUE\_SORT, DIRECTION\_TYPE, QUAD\_MODEL\_SEARCH\_BOX\_FACTOR, and QUAD\_MODEL\_BOX\_FACTOR.

A few high-impact options are:

"MAX\_BB\_EVAL"=10000

"INITIAL\_MESH\_SIZE"=1

"MIN\_MESH\_SIZE"="r1.0e-10"

"MIN\_FRAME\_SIZE"=1

Note that the "r..." denotes relative measurement (relative to lb and ub)

Note that decreasing the maximum number of black box evaluations ("MAX\_BB\_EVAL") will terminate search sooner and may result in a less accurate solution. For complicated problems you may want to increase this value. When experimenting it is desirable to set "DISPLAY\_DEGREE"=1 (or a larger integer) to get some sense for how the algorithm is progressing

display.nomad.progress

when FALSE, no output from snomadr is displayed on the screen. If the NOMAD option "DISPLAY\_DEGREE"=0, is set, there will also be no output from NOMAD. Higher integer values for "DISPLAY\_DEGREE"= provide successively more detail

information

is a list. snomadr will call snomadRInfo to return the information about NOMAD according to the values of "info", "version" and "help".

"info"="-i": display the usage and copyright of NOMAD

"version"="-v": display the version of NOMAD you are using

"help"="-h": display all options

You also can display a specific option, for example, "help"="-h x0", this will tell you how to set x0

snomadr.environment

environment that is used to evaluate the functions. Use this to pass additional data or parameters to a function

...

arguments that will be passed to the user-defined objective and constraints functions. See the examples below

## Details

snomadr is used in the `crs` package to numerically minimize an objective function with respect to the spline degree, number of knots, and optionally the kernel bandwidths when using `crs` with the option `cv="nomad"` (default). This is a constrained mixed integer combinatoric problem and is known to be computationally 'hard'. See `frscvNOMAD` and `krscvNOMAD` for the functions called when `cv="nomad"` while using `crs`.

However, the user should note that for simple problems involving one predictor exhaustive search may be faster and potentially more accurate, so please bear in mind that `cv="exhaustive"` can be useful when using `crs`.

Naturally, exhaustive search is also useful for verifying solutions returned by snomadr. See `frscv` and `krscv` for the functions called when `cv="exhaustive"` while using `crs`.

**Value**

The return value contains a list with the inputs, and additional elements

call	the call that was made to solve
status	integer value with the status of the optimization
message	more informative message with the status of the optimization
iterations	number of iterations that were executed, if multiple initial points are set, this number will be the sum for each initial point.
objective	value if the objective function in the solution
solution	optimal value of the controls

**Author(s)**

Zhenghua Nie <niez@mcmaster.ca>

**References**

Abramson, M.A. and C. Audet and G. Couture and J.E. Dennis Jr. and S. Le Digabel (2011), “The NOMAD project”. Software available at <https://www.gerad.ca/en/software/nomad/>

Le Digabel, S. (2011), “Algorithm 909: NOMAD: Nonlinear Optimization With The MADS Algorithm”. ACM Transactions on Mathematical Software, 37(4):44:1-44:15.

**See Also**

[optim](#), [nlm](#), [nlminb](#)

**Examples**

```
## Not run:
## List all options
snomadr(information=list("help"="-h"))

## Print given option, for example, MESH_SIZE
snomadr(information=list("help"="-h MESH_SIZE"))

## Print the version of NOMAD
snomadr(information=list("version"="-v"))

## Print usage and copyright
snomadr(information=list("info"="-i"))

## This is the example found in
## NOMAD/examples/basic/library/single_obj/basic_lib.cpp

eval.f <- function ( x ) {
  f <- c(Inf, Inf, Inf);
  n <- length (x);
```

```

    if ( n == 5 && ( is.double(x) || is.integer(x) ) ) {
      f[1] <- x[5];
      f[2] <- sum ( (x-1)^2 ) - 25;
      f[3] <- 25 - sum ( (x+1)^2 );
    }

    return ( as.double(f) );
  }

## Initial values
x0 <- rep(0.0, 5 )

bbin <-c(1, 1, 1, 1, 1)
## Bounds
lb <- rep(-6.0,5 )
ub <- c(5.0, 6.0, 7.0, 1000000, 100000)

bbout <-c(0, 2, 1)
## Options
opts <-list("MAX_BB_EVAL"=500,
           "MIN_MESH_SIZE"=0.001,
           "INITIAL_MESH_SIZE"=0.1,
           "MIN_FRAME_SIZE"=1)

snomadr(eval.f=eval.f,n=5, x0=x0, bbin=bbin, bbout=bbout, lb=lb, ub=ub, opts=opts)

## How to transfer other parameters into eval.f
##
## First example: supply additional arguments in user-defined functions
##

## objective function and gradient in terms of parameters
eval.f.ex1 <- function(x, params) {
  return( params[1]*x^2 + params[2]*x + params[3] )
}

## Define parameters that we want to use
params <- c(1,2,3)

## Define initial value of the optimization problem
x0 <- 0

## solve using snomadr
snomadr( n           =1,
        x0           = x0,
        eval.f       = eval.f.ex1,
        params       = params )

##
## Second example: define an environment that contains extra parameters
##

```

```

## Objective function and gradient in terms of parameters
## without supplying params as an argument
eval.f.ex2 <- function(x) {
  return( params[1]*x^2 + params[2]*x + params[3] )
}

## Define initial value of the optimization problem
x0 <- 0

## Define a new environment that contains params
auxdata      <- new.env()
auxdata$params <- c(1,2,3)

## pass The environment that should be used to evaluate functions to snomadr
snomadr(n      =1,
        x0      = x0,
        eval.f  = eval.f.ex2,
        snomadr.environment = auxdata )

## Solve using algebra
cat( paste( "Minimizing f(x) = ax^2 + bx + c\n" ) )
cat( paste( "Optimal value of control is -b/(2a) = ", -params[2]/(2*params[1]), "\n" ) )
cat( paste( "With value of the objective function f(-b/(2a)) = ",
           eval.f.ex1( -params[2]/(2*params[1]), params ), "\n" ) )

## The following example is NOMAD/examples/advanced/multi_start/multi.cpp
## This will call smultinomadRSolve to resolve the problem.
eval.f.ex1 <- function(x, params) {
  M<-as.numeric(params$M)
  NBC<-as.numeric(params$NBC)

  f<-rep(0, M+1)
  x<-as.numeric(x)

  x1 <- rep(0.0, NBC)
  y1 <- rep(0.0, NBC)

  x1[1]<-x[1]
  x1[2]<-x[2]
  y1[3]<-x[3]
  x1[4]<-x[4]
  y1[4]<-x[5]

  epi <- 6
  for(i in 5:NBC){
    x1[i]<-x[epi]
    epi <- epi+1
    y1[i]<-x[epi]
    epi<-epi+1
  }
  constraint <- 0.0
  ic <- 1

```

```

f[ic]<-constraint
ic <- ic+1

constraint <- as.numeric(1.0)
distmax <- as.numeric(0.0)
avg_dist <- as.numeric(0.0)
dist1<-as.numeric(0.0)

for(i in 1:(NBC-1)){
  for (j in (i+1):NBC){
    dist1 <- as.numeric((x1[i]-x1[j])*(x1[i]-x1[j])+(y1[i]-y1[j])*(y1[i]-y1[j]))

    if((dist1 > distmax)) {distmax <- as.numeric(dist1)}
    if((dist1[1]) < 1) {constraint <- constraint*sqrt(dist1)}
    else if((dist1) > 14) {avg_dist <- avg_dist+sqrt(dist1)}
  }
}

if(constraint < 0.9999) constraint <- 1001.0-constraint
else constraint = sqrt(distmax)+avg_dist/(10.0*NBC)

f[2] <- 0.0
f[M+1] <- constraint

return(as.numeric(f) )
}

## Define parameters that we want to use
params<-list()
NBC <- 5
M <- 2
n<-2*NBC-3

params$NBC<-NBC
params$M<-M
x0<-rep(0.1, n)
lb<-rep(0, n)
ub<-rep(4.5, n)

eval.f.ex1(x0, params)

bbout<-c(2, 2, 0)
nmulti=5
bbin<-rep(0, n)
## Define initial value of the optimization problem

## Solve using snomadRSolve
snomadr(n          = as.integer(n),
        x0         = x0,
        eval.f     = eval.f.ex1,
        bbin       = bbin,
        bbout      = bbout,

```

```

        lb          = lb,
        ub          = ub,
        params      = params )

## Solve using smultinomadRSolve, if x0 is provided, x0 will
## be the first initial point, otherwise, the program will
## check best_x.txt, if it exists, it will be read in as
## the first initial point. Other initial points will be
## generated by uniform distribution.
## nmulti represents the number of mads will run.
##
snomadr(n          = as.integer(n),
        eval.f     = eval.f.ex1,
        bbin       = bbin,
        bbout      = bbout,
        lb         = lb,
        ub         = ub,
        nmulti     = as.integer(nmulti),
        display.nomad.progress = TRUE,
        params     = params )

## End(Not run)

```

---

tensor.prod.model.matrix

*Utility functions for constructing tensor product smooths*

---

## Description

Produce model matrices or penalty matrices for a tensor product smooth from the model matrices or penalty matrices for the marginal bases of the smooth.

## Usage

```
tensor.prod.model.matrix(X)
```

## Arguments

X a list of model matrices for the marginal bases of a smooth

## Details

If  $X[[1]]$ ,  $X[[2]]$  ...  $X[[m]]$  are the model matrices of the marginal bases of a tensor product smooth then the  $i$ th row of the model matrix for the whole tensor product smooth is given by  $X[[1]][i, ] \%x\% X[[2]][i, ] \%x\% \dots X[[m]][i, ]$ , where  $\%x\%$  is the Kronecker product. Of course the routine operates column-wise, not row-wise!

**Value**

Either a single model matrix for a tensor product smooth, or a list of penalty terms for a tensor product smooth.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Wood, S.N. (2006) “Low Rank Scale Invariant Tensor Product Smooths for Generalized Additive Mixed Models”. *Biometrics* 62(4):1025-1036

**See Also**

[te](#), [smooth.construct.tensor.smooth.spec](#)

**Examples**

```
X <- list(matrix(1:4,2,2),matrix(5:10,2,3))
tensor.prod.model.matrix(X)
```

---

uniquecombs

*Find the unique rows in a matrix*

---

**Description**

This routine returns a matrix containing all the unique rows of the matrix supplied as its argument. That is, all the duplicate rows are stripped out. Note that the ordering of the rows on exit is not the same as on entry. It also returns an index attribute for relating the result back to the original matrix.

**Usage**

```
uniquecombs(x)
```

**Arguments**

x is an R matrix (numeric)

**Details**

Models with more parameters than unique combinations of covariates are not identifiable. This routine provides a means of evaluating the number of unique combinations of covariates in a model. The routine calls compiled C code.

**Value**

A matrix consisting of the unique rows of  $x$  (in arbitrary order).

The matrix has an "index" attribute. `index[i]` gives the row of the returned matrix that contains row  $i$  of the original matrix.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

[unique](#) can do the same thing, including for non-numeric matrices, but more slowly and without returning the index.

**Examples**

```
X<-matrix(c(1,2,3,1,2,3,4,5,6,1,3,2,4,5,6,1,1,1),6,3,byrow=TRUE)
print(X)
Xu <- uniquecombs(X);Xu
ind <- attr(Xu,"index")
## find the value for row 3 of the original from Xu
Xu[ind[3],];X[3,]
```

---

wage1

*Cross-Sectional Data on Wages*


---

**Description**

Cross-section wage data consisting of a random sample taken from the U.S. Current Population Survey for the year 1976. There are 526 observations in total.

**Usage**

```
data("wage1")
```

**Format**

A data frame with 24 columns, and 526 rows.

**wage** column 1, of type numeric, average hourly earnings

**educ** column 2, of type numeric, years of education

**exper** column 3, of type numeric, years potential experience

**tenure** column 4, of type numeric, years with current employer

**nonwhite** column 5, of type factor, ="Nonwhite" if nonwhite, "White" otherwise

**female** column 6, of type factor, ="Female" if female, "Male" otherwise

**married** column 7, of type factor, ="Married" if Married, "Nonmarried" otherwise

**numdep** column 8, of type numeric, number of dependents  
**smsa** column 9, of type numeric, =1 if live in SMSA  
**northcen** column 10, of type numeric, =1 if live in north central U.S  
**south** column 11, of type numeric, =1 if live in southern region  
**west** column 12, of type numeric, =1 if live in western region  
**construc** column 13, of type numeric, =1 if work in construc. indus.  
**ndurman** column 14, of type numeric, =1 if in nondur. manuf. indus.  
**trcommpu** column 15, of type numeric, =1 if in trans, commun, pub ut  
**trade** column 16, of type numeric, =1 if in wholesale or retail  
**services** column 17, of type numeric, =1 if in services indus.  
**profserv** column 18, of type numeric, =1 if in prof. serv. indus.  
**profocc** column 19, of type numeric, =1 if in profess. occupation  
**clerocc** column 20, of type numeric, =1 if in clerical occupation  
**servocc** column 21, of type numeric, =1 if in service occupation  
**lwage** column 22, of type numeric, log(wage)  
**expersq** column 23, of type numeric,  $\text{exper}^2$   
**tenursq** column 24, of type numeric,  $\text{tenure}^2$

### Source

Jeffrey M. Wooldridge

### References

Wooldridge, J.M. (2000), *Introductory Econometrics: A Modern Approach*, South-Western College Publishing.

### Examples

```
## Not run:
data(wage1)

## Cross-validated model selection for spline degree and bandwidths Note
## - we override the default degree.max and segments.max here given the
## large number of predictors and small sample size (the tensor spline basis
## will become singular hampering search)

model <- crs(lwage~married+
             female+
             nonwhite+
             educ+
             exper+
             tenure,
             degree.max=5,
             segments.max=5,
             data=wage1)
```

```
summary(model)

## Residual plots
plot(model)
## Partial mean plots (control for non axis predictors)
plot(model,mean=TRUE)
## Partial first derivative plots (control for non axis predictors)
plot(model,deriv=1)
## Partial second derivative plots (control for non axis predictors)
plot(model,deriv=2)

## End(Not run)
```

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