

# Package ‘colf’

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**Type** Package

**Title** Constrained Optimization on Linear Function

**Version** 0.1.3

**URL** <https://github.com/Lyzander/colf>

**BugReports** <https://github.com/Lyzander/colf/issues>

**Depends** R (>= 3.2.0), nlsr, stats, utils

**Description** Performs least squares constrained optimization on a linear objective function. It contains a number of algorithms to choose from and offers a formula syntax similar to `lm()`.

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**LazyData** TRUE

**RoxygenNote** 5.0.1

**Suggests** testthat, knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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coef.colf_nlxb	<i>Coefficients for colf_nlxb</i>
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**Description**

Coefficients for colf\_nlxb

**Usage**

```
## S3 method for class 'colf_nlxb'
coef(object, ...)
```

**Arguments**

object	A colf_nlxb object i.e. the result of running colf_nlxb
...	Currently not used

**Value**

A vector with the coefficients

**Examples**

```
mymod <- colf_nlxb(mpg ~ hp + cyl, mtcars)

#coefficients
coef(mymod)
```

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colf_nls	<i>Non linear Least Squares Optimization on a Linear Objective Function</i>
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**Description**

Non linear least squares optimization using the port algorithm on a linear objective function.

**Usage**

```
colf_nls(formula, data, start = NULL, trace = FALSE, control = NULL,
na.action = c("na.omit", "na.fail", "na.exclude"), lower = -Inf,
upper = Inf, ...)
```

**Arguments**

formula	The formula. This has the same syntax and supports the same features as the formula in <code>lm</code> . See examples.
data	A data frame containing the data of the variables in the formula.
start	An atomic vector of same length as the number of parameters. If not provided a cheap guess will be made. If categorical variables are included these need to be taken into consideration as number of categories minus one. See examples and details.
trace	Logical. Defaults to FALSE. Set to TRUE if you want the intermediate progress to be reported
control	an optional list of control settings. See <code>nls.control</code> for the names of the settable control values and their effect.
na.action	A function which indicates what should happen if NAs are present in the data set. Defaults to <code>options('na.action')</code> . <code>na.fail</code> , or <code>na.exclude</code> can be used.
lower	Lower bounds of the parameters (atomic vector). If a single number, this will be applied to all parameters. Defaults to <code>-Inf</code> (unconstrained).
upper	Upper bounds of the parameters (atomic vector). If a single number, this will be applied to all parameters. Defaults to <code>Inf</code> (unconstrained).
...	Other arguments passed on to optimiser

**Details**

`colf_nls` uses `nls`, in an attempt to find the minimum of the residual sum of squares. The algorithm is applied on a linear objective function.

The function provides an easy way to apply the optimizer on a linear objective function in a similar way to `lm`.

`start`, `lower` and `upper`, if provided, can be either an atomic vector which has the same length as the number of parameters or a single number which will be replicated to match the length of the parameters. If categorical variables exist in the function these will be dummified. Out of one categorical variable, `n - 1` will be created where `n` is the total number of categories in the variable. This needs to be taken into account when providing an atomic vector for `start`, `lower` or `upper`. Also, as with `lm` an intercept will be added which also needs to be taken into account.

**Value**

Same as `nls`

**See Also**

[nls](#), [nls.control](#)

**Examples**

```
#no constraints
colf_nls(mpg ~ cyl + disp, mtcars)
```

```

#no intercept
colf_nls(mpg ~ 0 + cyl + disp, mtcars)

#including categorical variables. These will be dummified.
colf_nls(Sepal.Length ~ Sepal.Width + Species, iris)

#lower boundary will be replicated for all parameters
colf_nls(Sepal.Length ~ Sepal.Width + Species, iris, lower = 0.5)

#species is categorical and contains 3 categories, thus we need to specify 4 lower bounds:
#the first one for the intercept.
#the second one for Sepal.Width
#the two next for the dummy variables constructed from Species.
colf_nls(Sepal.Length ~ Sepal.Width + Species, iris, lower = rep(0.5, 4))

```

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colf_nlxb	<i>Nash Variant of the Marquardt algorithm on a linear objective function</i>
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## Description

Non linear least squares solution via qr linear solver on a linear objective function.

## Usage

```

colf_nlxb(formula, data, start = NULL, trace = FALSE, lower = -Inf,
  upper = Inf, na.action = c("na.omit", "na.fail", "na.exclude"),
  masked = NULL, control = NULL, ...)

```

## Arguments

formula	The formula. This has the same syntax and supports the same features as the formula in <code>lm</code> . See examples.
data	A data frame containing the data of the variables in the formula.
start	An atomic vector of same length as the number of parameters. If not provided a cheap guess will be made. If categorical variables are included these need to be taken into consideration as number of categories minus one. See examples and details.
trace	Logical. Defaults to FALSE. Set to TRUE if you want the intermediate progress to be reported
lower	Lower bounds of the parameters (atomic vector). If a single number, this will be applied to all parameters. Defaults to -Inf (unconstrained).
upper	Upper bounds of the parameters (atomic vector). If a single number, this will be applied to all parameters. Defaults to Inf (unconstrained).
na.action	A function which indicates what should happen if NAs are present in the data set. Defaults to <code>options('na.action')</code> . <code>na.fail</code> , or <code>na.exclude</code> can be used.

masked	Character vector of parameter names. These parameters will not be altered by the algorithm.
control	A list of controls for the algorithm. These are: <ul style="list-style-type: none"> <li>• watch - Monitor progress. Logical, defaults to FALSE</li> <li>• phi - Adds <math>\phi \cdot \text{identity}</math> to Jacobian inner product. Defaults to 1.</li> <li>• lamda - Initial Marquardt adjustment. Defaults to 0.0001.</li> <li>• offset - Shift to test floating point equality. Defaults to 100.</li> <li>• laminc - Factor to use to increase lamda. Defaults to 10.</li> <li>• lamdec - Factor to use to decrease lamda (<math>\text{lamdec} / \text{laminc}</math>). Defaults to 4.</li> <li>• femax - Maximum evaluations of sum of squares function. Defaults to 10000.</li> <li>• jemax - Maximum evaluations of the Jacobian. Defaults to 5000.</li> <li>• roffttest - Use a termination of the relative offset orthogonality type.</li> <li>• smallstest - Exit the function if the sum of squares falls below <math>(100 * \text{Machine}\\$double.eps)^4</math> times the initial sumsquares. Defaults to TRUE.</li> </ul>
...	Other arguments passed on to optimiser

### Details

colf\_nlxb uses Nash's (Nash, 1979) variant of the Marquardt algorithm, in an attempt to find the minimum of the residual sum of squares. The algorithm is applied on a linear objective function.

The function provides an easy way to apply the optimizer on a linear objective function in a similar way to lm.

start, lower and upper, if provided, can be either an atomic vector which has the same length as the number of parameters or a single number which will be replicated to match the length of the parameters. If categorical variables exist in the function these will be dummified. Out of one categorical variable,  $n - 1$  will be created where  $n$  is the total number of categories in the variable. This needs to be taken into account when providing an atomic vector for start, lower or upper. Also, as with lm an intercept will be added which also needs to be taken into account.

### Value

Same as nlxb

### See Also

[nlxb](#)

### Examples

```
#no constraints
colf_nlxb(mpg ~ cyl + disp, mtcars)

#no intercept
colf_nlxb(mpg ~ 0 + cyl + disp, mtcars)

#including categorical variables. These will be dummified.
```

```
colf_nlxb(Sepal.Length ~ Sepal.Width + Species, iris)

#lower boundary will be replicated for all parameters
colf_nlxb(Sepal.Length ~ Sepal.Width + Species, iris, lower = 0.5)

#species is categorical and contains 3 categories, thus we need to specify 4 lower bounds:
#the first one for the intercept.
#the second one for Sepal.Width
#the two next for the dummy variables constructed from Species.
colf_nlxb(Sepal.Length ~ Sepal.Width + Species, iris, lower = rep(0.5, 4))
```

---

construct_formula	<i>Construct an nls-compatible formula from an lm style formula</i>
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---

### Description

Construct an nls-compatible formula from an lm style formula

### Usage

```
construct_formula(formula, data)
```

### Arguments

formula	The formula. This has the same syntax and supports the same features as the formula in lm. See examples.
data	A data frame containing the data of the variables in the formula.

### Details

construct\_formula creates the parameters needed for the formula to be compatible with nls style functions. It also creates and returns the modelling set.

construct\_formula will make syntactically valid names (if applicable) otherwise the optimizers will fail. To make these names make.names is used. Check examples.

### Value

A list of three elements:

- model\_formula - An nls compatible formula
- model\_data - The modelling set created (including dummy variables, if any)
- x\_param\_names - The names of the parameters

### See Also

[nls](#), [make.names](#)

## Examples

```
#simple syntax
construct_formula(mpg ~ hp + cyl, mtcars)

#example of make.names to create syntactically valid names
make.names('(foo/^\@bar)')

#function will create syntactically valid names (if applicable)
#otherwise the optimizers will fail
construct_formula(mpg ~ I(hp + cyl), mtcars)
construct_formula(mpg ~ (hp + cyl + disp)^3, mtcars)
```

---

fitted.colf_nlxb	<i>Fitted values for colf_nlxb</i>
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---

## Description

Fitted values for colf\_nlxb

## Usage

```
## S3 method for class 'colf_nlxb'
fitted(object, ...)
```

## Arguments

object	A colf_nlxb object i.e. the result of running colf_nlxb
...	Currently not used

## Value

A vector with the fitted values

## Examples

```
mymod <- colf_nlxb(mpg ~ hp + cyl, mtcars)

#fitted values
fitted(mymod)
```

predict.colf\_nls      *Predict method for colf\_nls*

---

### Description

Predict method for colf\_nls

### Usage

```
## S3 method for class 'colf_nls'  
predict(object, newdata, ...)
```

### Arguments

object	A colf_nls object
newdata	A new data.frame which contains the same column names and classes as the original data.frame
...	Currently not used

### Details

predict.colf\_nls will use the fit model to predict on a new data set.

When using predict.colf\_nls make sure the column names and classes of the new data set are the same as the data the model was trained on.

### Value

A vector with the predictions

### Examples

```
mymod <- colf_nls(mpg ~ hp + cyl, mtcars)  
  
#prediction  
predict(mymod, mtcars)
```



---

predict.colf_nlxb	<i>Predict method for colf_nlxb</i>
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---

## Description

Predict method for colf\_nlxb

## Usage

```
## S3 method for class 'colf_nlxb'  
predict(object, newdata, ...)
```

## Arguments

object	A colf_nls object
newdata	A new data.frame which contains the same column names and classes as the original data.frame
...	Currently not used

## Details

predict.colf\_nlxb will use the fit model to predict on a new data set.

When using predict.colf\_nlxb make sure the column names and classes of the new data set are the same as the data the model was trained on.

## Value

A vector with the predictions

## Examples

```
mymod <- colf_nlxb(mpg ~ hp + cyl, mtcars)  
  
#prediction  
predict(mymod, mtcars)
```

print.colf\_nlxb      *colf\_nlxb Print method*

---

### Description

colf\_nlxb Print method

### Usage

```
## S3 method for class 'colf_nlxb'  
print(x, ...)
```

### Arguments

x                    A colf\_nlxb object i.e. the result of running colf\_nlxb  
...                   Currently not used

### Value

Printing the colf\_nlxb object

### Examples

```
mymod <- colf_nlxb(mpg ~ hp + cyl, mtcars)  
  
#print  
print(mymod)
```

---

residuals.colf\_nlxb      *Residuals for colf\_nlxb*

---

### Description

Residuals for colf\_nlxb

### Usage

```
## S3 method for class 'colf_nlxb'  
residuals(object, ...)
```

### Arguments

object                A colf\_nlxb object i.e. the result of running colf\_nlxb  
...                    Currently not used

**Value**

A vector with the residuals

**Examples**

```
mymod <- colf_nlxb(mpg ~ hp + cyl, mtcars)

#residuals
residuals(mymod)
resid(mymod)
```

---

summary.colf\_nlxb      *colf\_nlxb Summary*

---

**Description**

colf\_nlxb Summary

**Usage**

```
## S3 method for class 'colf_nlxb'
summary(object, ...)
```

**Arguments**

object	A colf_nlxb object i.e. the result of running colf_nlxb
...	Currently not used

**Value**

The summary of the model

**Examples**

```
mymod <- colf_nlxb(mpg ~ hp + cyl, mtcars)

#summary
summary(mymod)
```

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