Package `regr` for an Augmented Regression Analysis

Werner A. Stahel, ETH Zurich

October 22, 2019

Abstract

The R function `regr` is a wrapper function that allows for fitting several different types of regression models by a unified call, and provides more informative numerical and graphical output than the traditional `summary` and `plot` methods. The package `regr` contains the functions that go along with `regr` and some more that help develop regression models. It is available from `R-forge` and is still in development.

```
## Loading required package:  plgraphics
## Registered S3 methods overwritten by 'regr':
##  method        from
##  add1.default  stats
##  add1.mlm      stats
##  drop1.default  stats
##  drop1.mlm      stats
##  drop1.multinom nnet
```

1 Introduction

Regression models are fitted in the statistical programming environment R by diverse functions, depending on the particular type of target variable. Outputs obtained by calling the function `summary` on the object produced by the fitting function look often quite similar. Graphical output for residual analysis is obtained by calling `plot`, but the result is not always informative.

The function `regr` allows for fitting various regression models with the same arguments. The result contains more informative numerical output than the calls to standard R functions. Residual analysis obtained by `plot`ing the result produces more appropriate and enhanced displays through the functions available from the package `plgraphics`.

`regr` proceeds by checking arguments, then calling the suitable fitting method from standard R or other packages, collecting useful statistics from the resulting object and a call of `summary` on it and adding a few to generate an object of class `regr`.

In particular, the following models can be fitted by `regr`:

- ordinary linear models, using Least Squares or robust estimation, by calling `lm` or `lmrob` from the `robustbase` package,
- generalized linear models, by calling `glm`,

- multinomial response models, by calling `multinom` of package `nnet`,
- ordered response models, by calling `polr` of package `MASS`,
- models for survival data and Tobit regression, by calling `survreg` or `coxph` of package `survival`,
- multivariate ordinary linear models, by calling `lm`,
- nonlinear models, by calling `nls`.

This document presents the main features of the package `regr` and explains the ideas behind them. It gives no details about the functions. They can be found in the help files.

The package is available from `R-forge`, e.g. by calling
`install.packages("regr", repos="http://r-forge.r-project.org")`.
The reason why it is not on CRAN is that the author is still developing additional features and does not yet want to guarantee upward compatibility. It also means that comments and suggestions are very welcome: `stahel-at-stat.math.ethz.ch`

2 Numerical Output

The useful numerical output of fitting functions is usually obtained by calling `summary` on the object produced by the fitting method. This results, for most functions, in a table showing the estimated regression coefficients, their standard errors, the value of a test statistic (t or z or deviance) and, for the ordinary linear model, a p value for the tests for zero coefficients. It is followed by an overall summary, usually including a test for the hypothesis that all coefficients are zero, and a standard deviation of the error and coefficient of determination, if applicable.

If there are factors (qualitative explanatory variables) in the model, the coefficients are not always interpreted adequately, and the respective standard errors, t and p values are of little use and often misinterpreted. On the other hand, the information whether a factor has a significant effect is not available from the summary but has to be obtained by calling `drop1` on the fit object. (The function `anova`, which seems to be suited according to its name, usually does not answer this question.)

This situation cannot be called user friendly. The function `regr` is meant to provide the results that are needed without having the user call different functions and select the output that is safe to be interpreted.

Here is a result of printing a `regr` object.

```
data(d.blast, package="plgraphics")
d.blast$location <- factor(d.blast$location)
regroptions("termcolumns")

## [1] "coef"     "df"       "ciLow"    "ciUp"     "R2.x"     "signif"
## [7] "p.value"  "p.symbol"
```

```
r.blast <- regr(logst(tremor) ~ location + log10(distance) + log10(charge),
    data = d.blast)
r.blast

##
##   Blasting for Tunnel Excavation
##
## Call:
## regr(formula = logst(tremor) ~ location + log10(distance) + log10(charge),
##     data = d.blast, na.action = nainf.exclude)
## Fitting function:  lm
##
## Terms:
##                       coef df      ciLow       ciUp   R2.x  signif p.value
## (Intercept)      2.9706240  1  2.7484193  3.1928286      .       .       .
## location                 .  7          .          . 0.1017   3.477       0
## log10(distance) -1.5061553  1 -1.6302824 -1.3820282 0.4768 -12.134       0
## log10(charge)    0.6225836  1  0.5463715  0.6987957 0.1024   8.169       0
##                 p.symbol
## (Intercept)            .
## location             ***
## log10(distance)      ***
## log10(charge)        ***
## ---
## Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1     1
##
## St.dev.error:  0.1409   on 352 degrees of freedom
## Multiple R^2:  0.7981    Adjusted R^2:  0.7929    AIC:  -1409.04
## F-statistic:   154.6   on 9 and 352 d.f.,  p.value: 1.549e-116
##
## Effects of factor levels:
## $location
##   loc1       loc2         loc3         loc4         loc5       loc6
##   -0.01739    0.13336 ***  0.11249 *** -0.18291 *** -0.05111 *  0.05302 *
##   loc7       loc8
##   -0.03150   -0.01596
```

2.1 Standard output for continuous explanatory variables

The "Terms:" table characterizes the effects of the individual terms in the model. For continuous explanatory variables (the last 2 lines in the example) it shows:

`coef`, the estimated value of the coefficient;

`df`, degrees of freedom, = 1 for continuous variables;

`ciLow, ciHigh`, the limits of the confidence interval;

`R2.x`, the coefficient of determination for regressing the explanatory variable in question on the other terms in the model. This is one of the wellknown collinearity diagnostics.

`signif`, a significance measure that is > 1 for estimated coefficients differing significantly from 0, see below for its definition;

`p.value`, the p value for testing if the coefficient could be zero;

`p.symb`, the usual significance symbols.

In fact, three more columns are contained in `rr$termtable`, but they are not printed by default:

`se`, the standard errors of the estimated coefficients;

`testst`, the test statistic used for testing if the coefficient could be zero;

`stcoef`, the estimated standardized coefficient, defined as `coef` times the standard deviation of the explanatory variable, divided by the standard deviation of the response (if the response is continuous as assumed here), see below for its use;

Regr options. The default for the columns to be printed is set by an option stored in the `.regroptions` list and controled by the function `regroptions` in the same way that the usual options are controled by the function `options`.

Significance. The usual `summary` output of fitting functions includes the t (or z) values of the coefficients as a column in the coefficients table. They are simply the ratios of the two preceding columns in the standard output. Nevertheless, they provide a kind of strength of the significance of the coefficients. The p value may also serve as such a measure, but it is less intuitive as it turns tiny for important variables, making comparisons somewhat more difficult than t values. The significance of t values depends on the number of degrees of freedom, but informed users will know that critical values are around ± 2, and they will therefore informally compare t values to ± 2. Based on these considerations, we introduce a new measure of significance here.

The new significance measure is defined as

$$\texttt{signif} = \texttt{t value} \,/\, \texttt{critical value}$$

where `critical value` is the critical value q_{df} of the t distribution and depends on the degrees of freedom of the residuals.

Confidence Intervals. The standard errors provided by the usual `summary` tables allow for calculating confidence intervals for continuous explanatory variables, by the formula `coef` $\pm$ q_{df} $\cdot$ `std.error`. In `regr` output, they are shown in the Terms table by default. If the table gets too wide,

the confidence limits may be suppressed by modifying the `termcolumns` option in `regroptions`. They can then be calculated as

$$\texttt{coef} \cdot \left(1 \pm 1/\texttt{signif}\right).$$

This is slightly more complicated for a calculation in the mind than $\texttt{coef} \pm 2\,\texttt{se}$, but the formula shows an additional interpretation of `signif` in terms of the confidence interval: If the input variable were scaled such that the confidence interval had half width 1, then the estimate would be `signif` units away from zero.

Standardized Coefficients. Standardized coefficients are meant to allow for a comparison of the importance of explanatory variables that have different variances. Each of them shows the effect on the response of increasing "its" carrier $X^{(j)}$ by one standard deviation, as a multiple of the response's standard deviation. This is often a more meaningful comparison of the relevance of the input variables. These coefficients are also stored in `rr$termtable` as the column `stcoef` and can therefore be seen as follows.

```
names(r.blast$termtable)

##  [1] "coef"     "se"       "ciLow"    "ciUp"     "df"       "testst"
##  [7] "signif"   "p.value"  "p.symbol" "stcoef"   "R2.x"

regroptions(termcolumns=c("coef", "stcoef", "df", "signif", "p.symb"))

r.blast

##
##   Blasting for Tunnel Excavation
##
## Call:
## regr(formula = logst(tremor) ~ location + log10(distance) + log10(charge),
##     data = d.blast, na.action = nainf.exclude)
## Fitting function:  lm
##
## Terms:
##                       coef     stcoef df  signif p.symbol
## (Intercept)      2.9706240          .  1       .        .
## location                 .          .  7   3.477      ***
## log10(distance) -1.5061553 -0.7902588  1 -12.134      ***
## log10(charge)    0.6225836  0.4061715  1   8.169      ***
## ---
## Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1     1
##
## St.dev.error:  0.1409   on 352 degrees of freedom
## Multiple R^2:  0.7981    Adjusted R^2:  0.7929    AIC:  -1409.04
```

```
## F-statistic:   154.6   on 9 and 352 d.f.,  p.value: 1.549e-116
##
## Effects of factor levels:
## $location
##   loc1       loc2         loc3         loc4         loc5       loc6
##   -0.01739    0.13336 ***  0.11249 *** -0.18291 *** -0.05111 *  0.05302 *
##   loc7       loc8
##   -0.03150   -0.01596

regroptions(default="all")  ## reset the options
```

Note, however, that increasing one $X^{(j)}$ without also changing others may not be possible in a given application, and therefore, an interpretation of coefficients can always be tricky. Furthermore, for binary input variables, increasing the variable by one standard deviation is impossible, since an increase can only occur from 0 to 1, and therefore, the standardized coeffient is somewhat counter-intuitive in this case.

2.2 Factors

For factors with more than two levels, (`location` in the example), there are several coefficients to be estimated. Their values depend on the scheme for generating the dummy variables characterizing the factor, which is determined by the `contrasts` option (or argument) in use. We come back to this point below ("Contrasts").

Note that for factors with only two levels, the problem does not arise, since the single coefficient can be interpreted in the straightforward manner as for continuous explanatory variables. `regr` therefore treats binary factors in the same way as continuous explanatory variables.

The test performed for factors with more than two levels, which is shown in the `Terms` table by the `p.value` entry, is the F test for the whole factor (hypothesis: all coefficients are 0). It is obtained by calling `drop1`. The significance measure is defined as

$$\texttt{signif} = \sqrt{\texttt{F value} \,/\, q_{df1,df2}}$$

where $q_{df1,df2}$ is the critical value of the F distribution. It reduces to the former one for binary factors.

The collinearity measure `R2.x` for factors is a formal generalization of `R2.x` for terms with one degree of freedom, determined by applying the relationship with the "variance inflation factor", `R2.x`$= 1/(1 - \text{vif})$ to the generalized vif. [More explanation planned.]

All coefficients for factors. The usual contrast option `contrasts="contr.treatment"` gives the coefficients of the dummy variables a clear interpretation: they estimate the difference of the response between level k and level 1 for $k > 1$. Another popular setting is `contrasts="contr.sum"`, for which the kth coefficient estimates the effect of the kth level in such a way that the sum of all coefficients is 0. For this setting, the last of these effects is not given in the vector of coefficients, `coefficients(r.blast)`.

In order to avoid ambiguities, the `regr` output lists the estimated effects for all levels of the factors after the term table. Even though the interpretation of significance and confidence intervals of the individual effects of the levels is delicate, `regr` objects include a full table, similar to the term table explained above, for each factor. By default, however, only the estimated effects are shown, together with the "star symbols" for their significance.

Contrasts. An advantage of `contr.sum` over the usual `contr.treatment` contrasts is that it avoids the (often unconscientious) choice of a reference level – the first level – and allows, for each level, to assess immediately how large its effect is as compared to an overall average effect. An even more important advantage appears when interactions between factors are included in the model: The main effects of one factor, including its significance, may still be interpreted (with caution) as average effects over the levels of the other factor.

The `contr.sum` setting is not well adapted to unbalanced factors, since the unweighted sum of coefficients is forced to be 0. This leads to large standard errors when one of the levels has a low frequency. The `regr` package provides the option `contr.wsum` for which the sum of coefficients weighted with the frequencies of the levels is zero. This type of contrasts is the default in `regr`.

2.3 Model summary

The last paragraph of the output gives the summary statistics. For ordinary linear models, the estimated standard deviation or the error term is given first. (It is labelled "Standard error of residual" in the `lm` output, which we would call a blunt misnomer.) The `Multiple R^2` is given next, together with its "adjusted" version, followed by the overall F test for the model.

For generalized linear models, the deviance test for the model is given. If applicable, a test for overdispersion based on residual deviance is also added.

3 Model Development

The functions `drop1` and `add1` are basic tools for model development. Their method for `regr` objects provide additional features.

First, they calculate tests by default. Second, `add1` has a useful default value for the argument `scope`: It consists of all squared continuous variables and all interactions between variables in the model. (These terms are calculated by `terms2order`.)

Since `drop1` and `add1` methods are available, `step` can be used to select a model automatically. However, it is preferable to use the version `step.regr` instead. It chooses "both" directions, backward and forward, by default, and extends the `scope` as in `add1`. There are two more features that are explained in the following.

```
add1(r.blast)

## Single term additions
##
## Model:
```

```
## logst(tremor) ~ location + log10(distance) + log10(charge)
##                                Df Sum of Sq    RSS     AIC F value
## <none>                                      6.9868 -1409.0
## I(log10(distance)^2)            1   0.00296 6.9839 -1407.2  0.1487
## I(log10(charge)^2)              1   0.14335 6.8435 -1414.5  7.3525
## location:log10(distance)        7   0.72645 6.2604 -1434.8  5.7191
## location:log10(charge)          7   0.11205 6.8748 -1400.9  0.8033
## log10(distance):log10(charge)   1   0.00016 6.9867 -1407.0  0.0080
##                                  Pr(>F)
## <none>
## I(log10(distance)^2)            0.700032
## I(log10(charge)^2)              0.007027 **
## location:log10(distance)       2.841e-06 ***
## location:log10(charge)          0.584971
## log10(distance):log10(charge)   0.928757
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

r.step <- step.regr(r.blast, k=4)
formula(r.step)

## logst(tremor) ~ location + log10(distance) + log10(charge)
```

Stopping rule. The usual stopping rule for stepwise model selection relies on the AIC criterion. Note that there is a funny argument for this choice: The rule that was commonly used early on stopped when all terms were formally significant. It has been criticized because of the multiplicity problem: The retained terms appear more significant than they are, because they are the most significant of an larger number of candidates. Thus, the formal significance tests for the terms are liberal to an unknown degree, and the selected models tend to be too large. Therefore, a new criterion was introduced, the AIC (or the BIC). Its justification is based on optimization of a prediction error sum of squares. It should be noted that it leads to even larger models than the significance criterion.

Unfortunately, it is not possible to specify the stopping criterion in `step`. However, setting its argument `k=4` – the default for `step.regr` –, one usually obtains a model with formally significant terms, for which every additional regressor would be non-signifcant.
($\mathrm{AIC}^{(k)}$ is $2L + k\mathrm{df}$, where L is the log likelihood. When dropping a single regressor from model 1 to obtain model 2, $2(L_1 - L_2)$ has a chisquared distribution with 1 degree of freedom, for which the critical value is 3.84. Thus, $\mathrm{AIC}_2^{(3.84)} - \mathrm{AIC}_1^{(3.84)} < 0$, if and only if $2(L_1 - L_2) < 3.84$, i.e., the test is non-significant, and the regressor will be dropped.)

Missing values. The `regr` methods for `drop1` and `step` behave more flexibly than in basic `R` when there are missing values:
`drop1` drops the rows in `data` that contain a missing value for the regressors in the current model and proceeds, rather than complaining about a variable number of missing observations.

`add1` drops the rows with missings in any variable used by the `scope` before calculations.
`step.regr` uses these two functions for the two directions. It only uses the observations without missing values in any variables in `scope`, but gives as the resulting fit the one based on the complete observations for the variables in the final formula.

3.1 Model Comparisons

When model development is part of the statistical analysis, it is useful to compare the terms that occur in different models under consideration. There is a function called `modelTable` that collects coefficients, p values, and other useful information, and a `format` and `print` method for showing the information in a useful way.

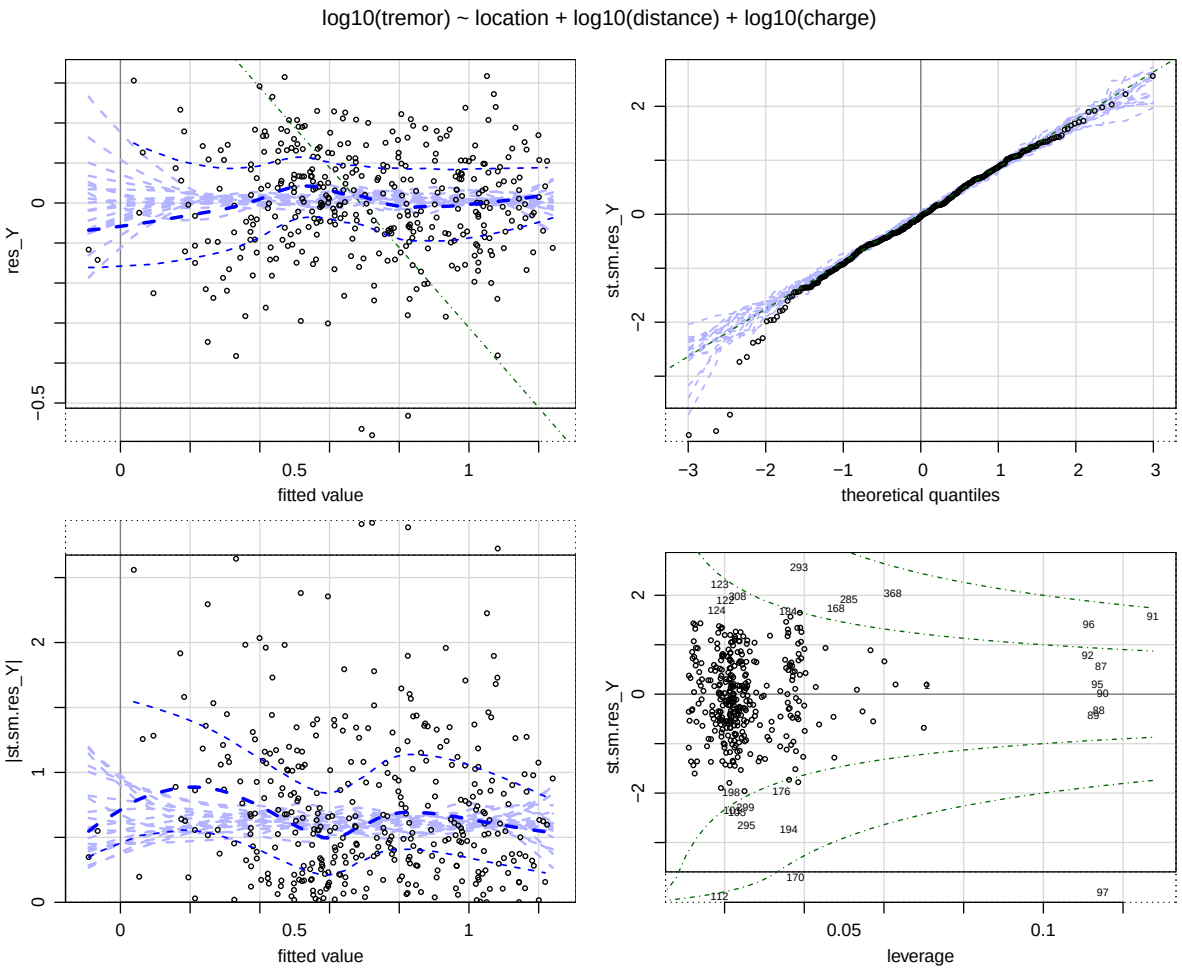
```
r.blast2 <-
  regr(logst(tremor) ~ ( location + log10(distance) + log10(charge) )^2,
       data=d.blast)
modelTable(c("r.blast", "r.blast2"))

##                                r.blast       r.blast2
## (Intercept)                     2.9706        2.8048
## location                          +++   ***     +++   ***
## log10(distance)                -1.5062   ***  -1.3548   ***
## log10(charge)                   0.6226   ***   0.7507   .
## location:log10(distance)           -            +++   ***
## location:log10(charge)             -            +++   .
## log10(distance):log10(charge)      -         -0.1085   .
## .sigma.                         0.1409        0.1358
## .df.                              10            25
```

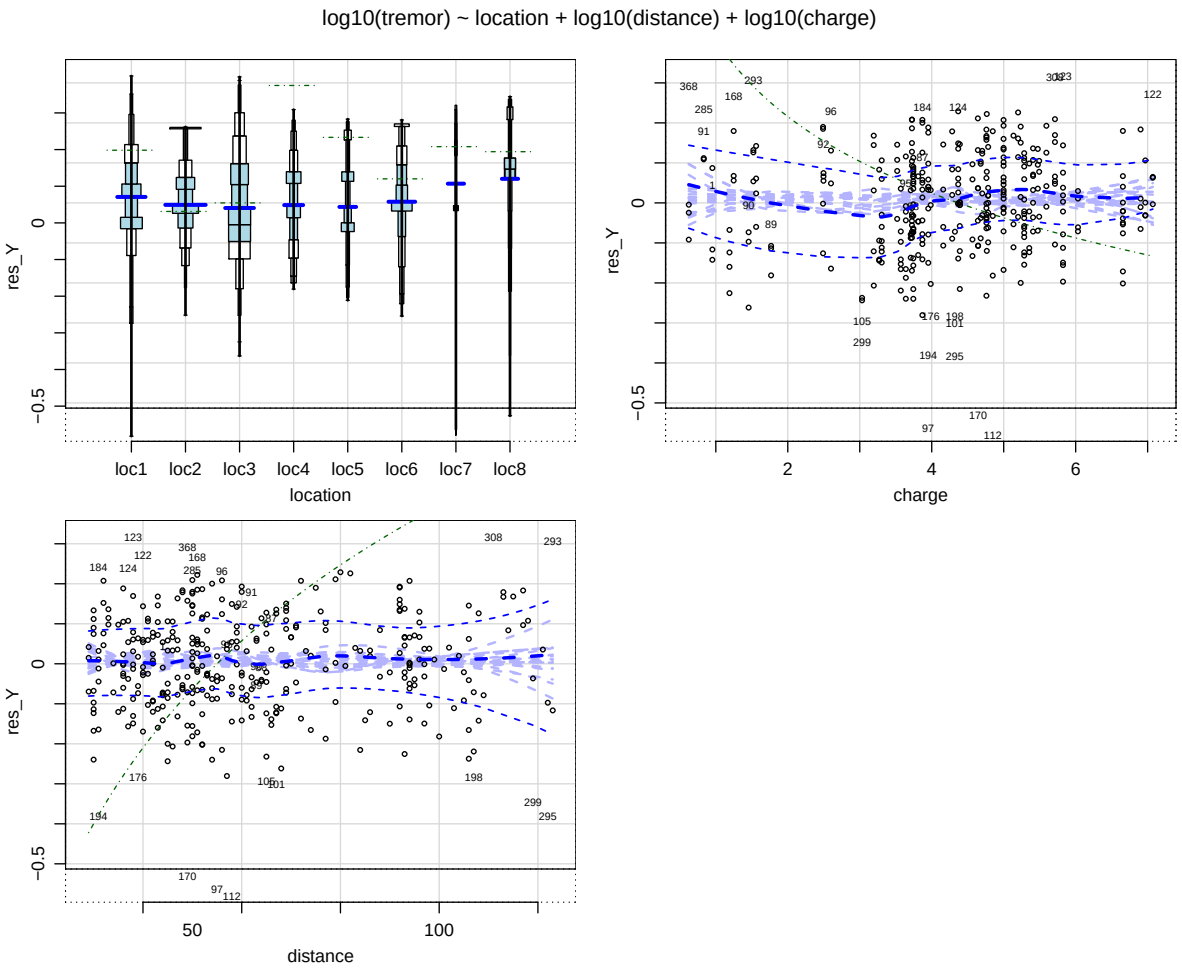
4 Residual Analysis

Various graphical displays involving residuals are of great help to check if assumptions are violated and to find improved models. Plain R provides four displays when the plot function is called for `lm` and similar objects. When `plot` is called on `regr` objects, it produces enhanced displays that are adapted to the type of fitted model and adds plots of residuals against input variables. This is implemented by making the function `plregr` in the package `plgraphics` the plot method for class `regr`. The `plgraphics` package features easy choices of most graphical elements, like plotting symbols, colors, tickmarks, etc. It implements methods for displaying censored variables, residuals from ordinal regression, plotting residuals against two variables, and more. See the package vignette and help files for details.

Here are the residual plots shown by default.

```
data(d.blast, package="plgraphics")
rr <- regr(log10(tremor)~location+log10(distance)+log10(charge),
           data=d.blast)
plot(rr)
```





Oct 22,01/9:10 | regr documentation

5 Details

5.1 regr options

Regr options shape the output of the `regr` function or even influence the way fitting functions are called.

Here is a list of the options.

digits number of digits used when printing `regr` objects

regr.contrasts contrasts used as a default in generating designs

show.termeffects logical: should term effects be shown?

termcolumns names of columns of the `termtable` component of the fitting result object which will be printed

termeffcolumns same for the term effects tables

coefcolumns same for the coefficients' table for each term

na.print symbol by which NA's are printed

This is the end of the story for the time being, 22.10.2019. I hope that you will get into using `regr` and have good success with your data analyses. Feedback is highly appreciated.

Werner Stahel, `stahel at stat.math.ethz.ch`