Use of the package **fitdistrplus** to specify a distribution from non-censored or censored data

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Here you will find some easy examples of use of the functions of the package **fitdistrplus**. The aim is to show you by examples how to use these functions to help you to specify a parametric distribution from data corresponding to a random sample drawn from a theoretical distribution that you want to describe. For details, see the documentation of each function, using the R help command (ex.: ?fitdist). Do not forget to load the package using the function **library** or **require** before testing following examples.

> library(fitdistrplus)

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1 Specification of a distribution from non-censored continuous data

1.1 Graphical display of the observed distribution

First of all, the observed distribution may be plotted using the function `plotdist`.

```r
> x1 <- c(6.4, 13.3, 4.1, 1.3, 14.1, 10.6, 9.9, 9.6, 15.3, 22.1,
+       13.4, 13.2, 8.4, 6.3, 8.9, 5.2, 10.9, 14.4)
> plotdist(x1)
```

![Histogram](image1)

![Cumulative distribution](image2)

1.2 Characterization of the observed distribution

Descriptive parameters of the empirical distribution may be computed using the function `descdist`. This function will also provide by default a skewness-kurtosis plot which may help you to select which distribution(s) to fit among the potential candidates.

```r
> descdist(x1)

summary statistics
-------
min:  1.3  max: 22.1
median:  10.2
mean:  10.4  sample sd:  4.75
sample skewness:  0.314
sample kurtosis:  3.25
```
In order to take into account the uncertainty of the estimated values of kurtosis and skewness, the data set may be bootstrapped by fixing the argument `boot` to an integer above 10 in `descdist`. Boot values of skewness and kurtosis corresponding to the boot nonparametric bootstrap samples are then computed and reported in blue color on the skewness-kurtosis plot.

```r
> descdist(x1, boot = 1000)
```

Summary statistics

```
-------
min: 1.3  max: 22.1
median: 10.2
mean: 10.4
sample sd: 4.75
sample skewness: 0.314
sample kurtosis: 3.25
```
1.3 Fitting of a distribution

One or more parametric distributions may then be fitted to the data set, one at a time, using the function `fitdist`. This function uses the maximum likelihood method if the argument `method="mle"` (or if it is omitted) or the matching moments estimation if the argument `method="mme"`. When fitting continuous distributions, Kolmogorov-Smirnov and Anderson-Darling statistics are computed and corresponding tests are performed when possible. Even if less appropriate for continuous distributions, the Chi-squared statistic is also computed when possible. For this calculation, cells are defined by the argument `chisqbreaks` or automatically defined from the data set and from the argument `meancount` (the approximate mean count per cell) which is fixed to \((4n)^{2/5}\) if omitted (with \(n\) the length of the data set). For more details, see the help of the function `fitdist`. Four goodness of fit plots are also provided.

Below is the result of a fit of a gamma distribution by maximum likelihood.

```r
> fig <- fitdist(x1, "gamma")
> plot(fig)
> summary(fig)
```

FITTING OF THE DISTRIBUTION ' gamma ' BY MAXIMUM LIKELIHOOD

PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>3.575</td>
</tr>
<tr>
<td>rate</td>
<td>0.343</td>
</tr>
</tbody>
</table>

Loglikelihood: -54.4  AIC: 113  BIC: 115

Correlation matrix:

<table>
<thead>
<tr>
<th></th>
<th>shape</th>
<th>rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>1.000</td>
<td>0.931</td>
</tr>
<tr>
<td>rate</td>
<td>0.931</td>
<td>1.000</td>
</tr>
</tbody>
</table>

GOODNESS-OF-FIT STATISTICS

<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Chi-squared</td>
<td>7.93</td>
</tr>
<tr>
<td>Degree of freedom of the Chi-squared distribution</td>
<td>3</td>
</tr>
<tr>
<td>Chi-squared p-value</td>
<td>0.0475</td>
</tr>
</tbody>
</table>

!!! For continuous distributions, Kolmogorov-Smirnov and...
Anderson-Darling statistics should be preferred !!!

_________ Kolmogorov-Smirnov_________
Kolmogorov-Smirnov statistic: 0.138
Kolmogorov-Smirnov test: not calculated

_________ Anderson-Darling_________
Anderson-Darling statistic: 0.457
Anderson-Darling test: not rejected

Below is the result of another fit of the same distribution by matching moments.

```R
> f1gbis <- fitdist(x1, "gamma", method = "mme")
> summary(f1gbis)

FITTING OF THE DISTRIBUTION ' gamma ' BY MATCHING MOMENTS
PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
</tr>
<tr>
<td>rate</td>
</tr>
</tbody>
</table>

GOODNESS-OF-FIT STATISTICS

_________ Chi-squared_________
Chi-squared statistic: 7.27
Degree of freedom of the Chi-squared distribution: 3
Chi-squared p-value: 0.0637
!!! the p-value may be wrong

with some theoretical counts < 5 !!!

!!! For continuous distributions, Kolmogorov-Smirnov and
Anderson-Darling statistics should be preferred !!!

_________ Kolmogorov-Smirnov_________
Kolmogorov-Smirnov statistic: 0.144
Kolmogorov-Smirnov test: not calculated

_________ Anderson-Darling_________
Anderson-Darling statistic: 0.471
Anderson-Darling test: not rejected
As can be seen in this returned summary, the automatic definition of the cells required to calculate the Chi-squared statistic does not give theoretical counts large enough to validate the use of the test in this example. It is often the case for small data sets. The observed and theoretical counts may be printed as below:

```r
> fig$chisqtable

obscounts  theocounts
<= 5.2   3.000   2.895
<= 8.4   3.000   4.596
<= 9.9   3.000   2.108
<= 13.2  3.000   3.706
<= 14.1  3.000   0.758
> 14.1   3.000   3.936
```

Below is the fit of a lognormal distribution.

```r
> f1l <- fitdist(x1, "lnorm")
> plot(f1l)
> summary(f1l)

FITTING OF THE DISTRIBUTION 'lnorm' BY MAXIMUM LIKELIHOOD
PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>meanlog</td>
<td>2.197</td>
</tr>
<tr>
<td>sdlog</td>
<td>0.622</td>
</tr>
</tbody>
</table>

Loglikelihood: -56.5  AIC: 117  BIC: 119
Correlation matrix:

<table>
<thead>
<tr>
<th></th>
<th>meanlog</th>
<th>sdlog</th>
</tr>
</thead>
<tbody>
<tr>
<td>meanlog</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>sdlog</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

GOODNESS-OF-FIT STATISTICS

Chi-squared statistic: 11.1
Degree of freedom of the Chi-squared distribution: 3
Chi-squared p-value: 0.0110
!!! the p-value may be wrong with some theoretical counts < 5 !!!

For continuous distributions, Kolmogorov-Smirnov and Anderson-Darling statistics should be prefered !!!

Kolmogorov-Smirnov statistic: 0.178
Kolmogorov-Smirnov test: not calculated

Anderson-Darling statistic: 0.793
Anderson-Darling test: rejected
Below is the fit of a normal distribution.

```r
> f1n <- fitdist(x1, "norm")
> plot(f1n)
> summary(f1n)
```

**Fitting of the distribution 'norm' by maximum likelihood**

**Parameters**

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean</td>
<td>10.41</td>
</tr>
<tr>
<td>sd</td>
<td>4.75</td>
</tr>
</tbody>
</table>

Loglikelihood: -53.6  AIC: 111  BIC: 113

**Correlation matrix:**

<table>
<thead>
<tr>
<th></th>
<th>mean</th>
<th>sd</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>sd</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

**Goodness-of-fit statistics**

---

**Chi-squared**

Chi-squared statistic: 4.83
Degree of freedom of the Chi-squared distribution: 3
Chi-squared p-value: 0.185
!!! the p-value may be wrong

with some theoretical counts < 5 !!!

!!! For continuous distributions, Kolmogorov-Smirnov and Anderson-Darling statistics should be preferred !!!
Below is the fit of a Weibull distribution.

```r
> f1w <- fitdist(x1, "weibull")
> plot(f1w)
> summary(f1w)
```

**FITTING OF THE DISTRIBUTION 'weibull' BY MAXIMUM LIKELIHOOD**

**PARAMETERS**

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>2.29</td>
</tr>
<tr>
<td>scale</td>
<td>11.70</td>
</tr>
</tbody>
</table>

Loglikelihood: -53.5  
AIC: 111  
BIC: 113

**Correlation matrix:**

<table>
<thead>
<tr>
<th></th>
<th>shape</th>
<th>scale</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>1.0</td>
<td>0.3</td>
</tr>
<tr>
<td>scale</td>
<td>0.3</td>
<td>1.0</td>
</tr>
</tbody>
</table>

------

**GOODNESS-OF-FIT STATISTICS**

<table>
<thead>
<tr>
<th>Distribution</th>
<th>Statistic</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chi-squared</td>
<td>5.87</td>
<td>0.118</td>
</tr>
</tbody>
</table>

!!! the p-value may be wrong with some theoretical counts < 5 !!!

!!! For continuous distributions, Kolmogorov-Smirnov and Anderson-Darling statistics should be preferred !!!

<table>
<thead>
<tr>
<th>Distribution</th>
<th>Statistic</th>
<th>Test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kolmogorov-Smirnov</td>
<td>0.121</td>
<td>not calculated</td>
</tr>
<tr>
<td>Anderson-Darling</td>
<td>0.282</td>
<td>not rejected</td>
</tr>
</tbody>
</table>
The values of the Anderson-Darling statistic (or another result of the fit: see the help of `fitdist` for details) for the different fittings may be extracted and compared to help the selection of a distribution:

```r
> anderson <- list(lnorm = f1l$ad, gamma = f1g$ad, norm = f1n$ad,
+                 weibull = f1w$ad)
> anderson

$lnorm
[1] 0.793

$gamma
[1] 0.457

$norm
[1] 0.226

$weibull
[1] 0.282
```

For some distributions (see the help of `fitdist` for details), it is necessary to specify initial values for the distribution parameters in the argument `start` when using the maximum likelihood method. `start` must be a named list of parameters initial values. The names of the parameters in `start` must correspond exactly to their definition in R or to their definition in a previous R code. The function `plotdist` may help to find correct initial values for the distribution parameters in non trivial cases, by an manual iterative use if necessary.

For example, below is the definition of the Gumbel distribution (also named extreme value distribution) and a first plot of the data set with the Gumbel distribution with arbitrary values for parameters.

```r
> dgumbel <- function(x, a, b) 1/b * exp((a - x)/b) * exp(-exp((a - x)/b))
> pgumbel <- function(q, a, b) exp(-exp((a - q)/b))
> qgumbel <- function(p, a, b) a - b * log(-log(p))
> plotdist(x1, "gumbel", para = list(a = 3, b = 2))
```
The same data set may be plotted with a Gumbel distribution with modified values for parameters.

> plotdist(x1, "gumbel", para = list(a = 10, b = 5))

And a Gumbel distribution may be fitted to data with these values for initial parameter values.

> fgu <- fitdist(x1, "gumbel", start = list(a = 10, b = 5))
> plot(fgu)
> summary(fgu)

Fitting of the distribution 'gumbel' by maximum likelihood
Parameters
  estimate Std. Error
a        8.09  1.092
Loglikelihood: -54.1  AIC: 112  BIC: 114

Correlation matrix:
<table>
<thead>
<tr>
<th></th>
<th>a</th>
<th>b</th>
</tr>
</thead>
<tbody>
<tr>
<td>a</td>
<td>1.000</td>
<td>0.330</td>
</tr>
<tr>
<td>b</td>
<td>0.330</td>
<td>1.000</td>
</tr>
</tbody>
</table>

GOODNESS-OF-FIT STATISTICS

Chi-squared statistic: 7.56
Degree of freedom of the Chi-squared distribution: 3
Chi-squared p-value: 0.056

!!! the p-value may be wrong with some theoretical counts < 5 !!!

!!! For continuous distributions, Kolmogorov-Smirnov and Anderson-Darling statistics should be preferred !!!

Kolmogorov-Smirnov statistic: 0.121
Kolmogorov-Smirnov test: not calculated

Anderson-Darling statistic: 0.34
Anderson-Darling test: not calculated

1.4 Simulation of the uncertainty by bootstrap

The uncertainty in the parameters of the fitted distribution may be simulated by parametric or nonparametric bootstrap using the function \texttt{boodist}. This function returns the bootstrapped values of parameters which may be plotted to visualize the bootstrap region. It also calculates the 95 percent confidence intervals for each parameter from the 2.5 and 97.5 percentiles of the bootstrapped values of each parameter (see the help of the function \texttt{boodist} for details).

Below is an example of the use of this function with the previous fit of the gamma distribution.

```r
> big <- bootdist(f1g)
> plot(big)
```
> summary(big)

Parametric bootstrap medians and 95% percentile CI
   Median 2.5% 97.5%
shape  3.965  2.20  8.463
rate   0.385  0.21  0.864

Maximum likelihood method converged for 1001 among 1001 iterations

2 Specification of a distribution from non-censored discrete data

A discrete data set may be considered as a continuous one for example for a large data set from a binomial distribution converging to a normal one. A discrete plot of the distribution may also be provided, fixing the argument discrete of the function plotdist to TRUE.

> x2 <- rbinom(n = 100, size = 2, prob = 0.3)
> plotdist(x2, discrete = TRUE)
As for continuous distributions, descriptive parameters of the empirical distribution may be computed using the function `descdist` which also provides a skewness-kurtosis plot which may help you to choose which distribution(s) to fit.

```r
> descdist(x2, discrete = T)

summary statistics
------
min: 0 max: 16
median: 4
mean: 4.87
sample sd: 3.75
sample skewness: 1.03
sample kurtosis: 3.43
```
As for continuous distributions, one or more parametric distributions may then be fitted to the data set by maximum likelihood or matching moments.

Below is the result of the fit of a Poisson distribution with the bootstrap simulations.

```
> f2p <- fitdist(x2, "pois")
> plot(f2p)
> summary(f2p)
```

```
FITTING OF THE DISTRIBUTION ' pois ' BY MAXIMUM LIKELIHOOD
PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>lambda</td>
<td>4.87</td>
</tr>
<tr>
<td></td>
<td>0.221</td>
</tr>
</tbody>
</table>

Loglikelihood: -297  AIC: 596  BIC: 599

GOODNESS-OF-FIT STATISTICS

Chi-squared statistic: 141
Degree of freedom of the Chi-squared distribution:  6
Chi-squared p-value:  5.9e-28
!!! the p-value may be wrong

with some theoretical counts < 5 !!!

```
> b2p <- bootdist(f2p)
> summary(b2p)
```

```
Parametric bootstrap medians and 95% percentile CI

<table>
<thead>
<tr>
<th>Median</th>
<th>2.5%</th>
<th>97.5%</th>
</tr>
</thead>
<tbody>
<tr>
<td>4.89</td>
<td>4.48</td>
<td>5.34</td>
</tr>
</tbody>
</table>

Maximum likelihood method converged for 1001 among 1001 iterations
Below is the result of the fit of a negative binomial distribution with the bootstrap simulations.

```r
> f2n <- fitdist(x2, "nbinom")
> plot(f2n)
> summary(f2n)

FITTING OF THE DISTRIBUTION ' nbinom ' BY MAXIMUM LIKELIHOOD
PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>size</td>
<td>2.52</td>
</tr>
<tr>
<td>mu</td>
<td>4.87</td>
</tr>
</tbody>
</table>

Loglikelihood: -258  AIC: 521  BIC: 526
Correlation matrix:

<table>
<thead>
<tr>
<th></th>
<th>size</th>
<th>mu</th>
</tr>
</thead>
<tbody>
<tr>
<td>size</td>
<td>1.00e+00</td>
<td>-1.18e-05</td>
</tr>
<tr>
<td>mu</td>
<td>-1.18e-05</td>
<td>1.00e+00</td>
</tr>
</tbody>
</table>

GOODNESS-OF-FIT STATISTICS

Chi-squared statistic: 4.07
Degree of freedom of the Chi-squared distribution: 5
Chi-squared p-value: 0.54

> b2n <- bootdist(f2n)
> summary(b2n)

Parametric bootstrap medians and 95% percentile CI

<table>
<thead>
<tr>
<th></th>
<th>Median</th>
<th>2.5%</th>
<th>97.5%</th>
</tr>
</thead>
<tbody>
<tr>
<td>size</td>
<td>2.60</td>
<td>1.74</td>
<td>4.33</td>
</tr>
<tr>
<td>mu</td>
<td>4.89</td>
<td>4.14</td>
<td>5.61</td>
</tr>
</tbody>
</table>

Maximum likelihood method converged for 1001 among 1001 iterations
3 Specification of a distribution from censored data

Censored data may contain left censored, right censored and interval censored values, with several lower and upper bounds. Data must be coded into a dataframe with two columns, respectively named `left` and `right`, describing each observed value as an interval. The `left` column contains either `NA` for left censored observations, the left bound of the interval for interval censored observations, or the observed value for non-censored observations. The `right` column contains either `NA` for right censored observations, the right bound of the interval for interval censored observations, or the observed value for non-censored observations.

3.1 Graphical display of the observed distribution

First of all, the observed distribution may be plotted using the function `plotdistcens`. Data are reported directly as segments for interval, left and right censored data, and as points for non-censored data. For more details, see the help of the function `plotdistcens`.

```r
> d1 <- data.frame(left = c(1.73, 1.51, 0.77, 1.96, 1.96, -1.4, -1.4, NA, -0.11, 0.55, 0.41, 2.56, NA, -0.53, 0.63, -1.4, -1.4, -1.4, NA, 0.13), right = c(1.73, 1.51, 0.77, 1.96, 1.96, 0, -0.7, -1.4, -0.11, 0.55, 0.41, 2.56, -1.4, -0.53, 0.63, 0, -0.7, NA, -1.4, 0.13))
> plotdistcens(d1)
```
When left or right NA-values correspond to finite value (for example 0 for left NA-values of positive data), the arguments `leftNA` (or `rightNA`) must be affected to this finite value to ensure a correct plot of left (or right) censored observations, as in the example below.

```r
> d2 <- data.frame(left = 10^(d1$left), right = 10^(d1$right))
> plotdistcens(d2, leftNA = 0)
```

It is also possible to fix `rightNA` or `leftNA` to a realistic extreme value, even if not exactly known, to obtain a reasonable global ranking of observations, as in the example below for the first dataset.

```r
> plotdistcens(d1, rightNA = 3)
```
3.2 Fitting of a distribution

One or more parametric distributions may then be fitted to the censored data set, one at a time, using the function `fitdistcens`. This function always uses the maximum likelihood method. For more details, see the help of the function `fitdistcens`. Only one goodness of fit plot is provided for censored data, in cumulative frequencies. The uncertainty in the parameters of the fitted distribution may be simulated by nonparametric bootstrap only, using the function `boodistcens`.

Below is the result of a fit of a Weibull distribution by maximum likelihood and the results of the corresponding bootstrap simulations.

```r
> f2w <- fitdistcens(d2, "weibull")
> summary(f2w)
```

**FITTING OF THE DISTRIBUTION ' weibull ' BY MAXIMUM LIKELIHOOD ON CENSORED DATA**

**PARAMETERS**

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>0.324</td>
</tr>
<tr>
<td>scale</td>
<td>6.124</td>
</tr>
</tbody>
</table>

Loglikelihood: -68.5  AIC: 141  BIC: 143

Correlation matrix:

<table>
<thead>
<tr>
<th></th>
<th>shape</th>
<th>scale</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>1.000</td>
<td>0.326</td>
</tr>
<tr>
<td>scale</td>
<td>0.326</td>
<td>1.000</td>
</tr>
</tbody>
</table>

```r
> plot(f2w, leftNA = 0)
```
> b2w <- bootdistcens(f2w)
> summary(b2w)

Nonparametric bootstrap medians and 95% percentile CI
   Median  2.5%  97.5%
shape   0.335  0.246  0.497
scale    5.502  1.098  22.984

Maximum likelihood method converged for 1001 among 1001 iterations

> plot(b2w)
Goodness of fit statistics are not computed for fit on censored data, so the quality of fit may only be estimated from the loglikelihood and the goodness of fit plot.

Below is the fit of a lognormal distribution to the same censored data set.

```r
> f2l <- fitdistcens(d2, "lnorm")
> summary(f2l)

FITTING OF THE DISTRIBUTION ' lnorm ' BY MAXIMUM LIKELIHOOD ON CENSORED DATA
PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>meanlog</td>
<td>0.27</td>
</tr>
<tr>
<td>sdlog</td>
<td>3.28</td>
</tr>
</tbody>
</table>

Loglikelihood: -68.7  AIC: 141  BIC: 143

Correlation matrix:

<table>
<thead>
<tr>
<th></th>
<th>meanlog</th>
<th>sdlog</th>
</tr>
</thead>
<tbody>
<tr>
<td>meanlog</td>
<td>1.0000</td>
<td>-0.0739</td>
</tr>
<tr>
<td>sdlog</td>
<td>-0.0739</td>
<td>1.0000</td>
</tr>
</tbody>
</table>

> plot(f2l, leftNA = 0)
```

Below is the fit of an exponential distribution.

```r
> f2e <- fitdistcens(d2, "exp")
> summary(f2e)

FITTING OF THE DISTRIBUTION ' exp ' BY MAXIMUM LIKELIHOOD ON CENSORED DATA
PARAMETERS

<table>
<thead>
<tr>
<th>estimate</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>rate</td>
<td>0.0292</td>
</tr>
</tbody>
</table>

Loglikelihood: -99.6  AIC: 201  BIC: 202

> plot(f2e, leftNA = 0)
```
As with `fitdist`, for some distributions (see the help of `fitdistcens` for details), it is necessary to specify initial values for the distribution parameters in the argument `start`. `start` must be a named list of parameters initial values. The names of the parameters in `start` must correspond exactly to their definition in R or to their definition in a previous R code. The function `plotdistcens` may help to find correct initial values for the distribution parameters in non-trivial cases, by an manual iterative use if necessary, as explained previously for non-censored continuous data.

4 Changing the optimization algorithm used to maximize the likelihood

Sometimes the default algorithm used to maximize the likelihood fails to converge. It may then be interesting to change some options of the function `optim` or to use another optimization function than `optim` to maximize the likelihood.

4.1 Changing the arguments passed to `optim`

The argument `optim.method` may be used in the call to `fitdist` or `fitdistcens`. It will internally be passed to `mledist` and to `optim`. This argument may be fixed to "Nelder-Mead" (the robust Nelder and Mead method), "BFGS" (the BFGS quasi-Newton method), "CG" (a conjugate gradients method), "SANN" (a variant of simulated annealing) or "L-BFGS-B" (a modification of the BFGS quasi-Newton method which enables box constraints optimization). For the use of the last method the arguments `lower` and/or `upper` also have to be passed. More details on these optimization functions may be found in the help page of `optim` from the package `stats`.

Below are examples of fits of a gamma distribution to non-censored data with various options of `optim`.

```r
> fitdist(x1, "gamma", optim.method = "Nelder-Mead")
Fitting of the distribution ' gamma ' by maximum likelihood
Parameters:
  estimate
shape   3.575
rate    0.343

> fitdist(x1, "gamma", optim.method = "BFGS")
Fitting of the distribution ' gamma ' by maximum likelihood
Parameters:
  estimate
shape   3.577
rate    0.344

> fitdist(x1, "gamma", optim.method = "L-BFGS-B", lower = c(0, + 0))
```
4.2 Supplying another optimization function

You may also want to use another function than \texttt{optim} to maximize the likelihood. This optimization function has to be specified by the argument \texttt{custom.optim} in the call to \texttt{fitdist} or \texttt{fitdistcens}. But before that, it is necessary to customize this optimization function: \texttt{custom.optim} function must have (at least) the following arguments, \texttt{fn} for the function to be optimized, \texttt{par} for the initialized parameters. It is assumed that \texttt{custom.optim} should carry out a MINIMIZATION. Finally, it should return at least the following components: \texttt{par} for the estimate, \texttt{convergence} for the convergence code, \texttt{value} for \texttt{fn(par)} and \texttt{hessian}.

Below is an example of code written to customize \texttt{genoud} function from \texttt{rgenoud} package.

\begin{verbatim}
mygenoud <- function(fn, par, ...) {
  require(rgenoud)
  res <- genoud(fn, starting.values=par, ...)
  standardres <- c(res, convergence=0)
  return(standardres)
}
\end{verbatim}

The customized optimization function may then be passed as the argument \texttt{custom.optim} in the call to \texttt{fitdist} or \texttt{fitdistcens}. The following code may for example be used to fit a gamma distribution to the non censored data \texttt{x1}. Note that in this example various arguments are also passed from \texttt{fitdist} to \texttt{genoud}: \texttt{nvars}, \texttt{Domains}, \texttt{boundary.enforcement}, \texttt{print.level} and \texttt{hessian}.

\begin{verbatim}
fitdist(x1, "gamma", custom.optim=mygenoud, nvars=2,
   Domains=cbind(c(0,0), c(10, 10)), boundary.enforcement=1,
   print.level=1, hessian=TRUE)
\end{verbatim}