Package ‘robustX’

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Type Package

Title 'eXtra' / 'eXperimental' Functionality for Robust Statistics

Version 1.2-5

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Maintainer Martin Maechler <maechler@stat.math.ethz.ch>

Description Robustness -- 'eXperimental', 'eXtraneous', or 'eXtraordinary' Functionality for Robust Statistics. Hence methods which are not well established, often related to methods in package 'robustbase'. Amazingly, 'BACON()', originally by Billor, Hadi, and Velleman (2000) <doi:10.1016/S0167-9473(99)00101-2> has become established in places. The ``barrow wheel'' `rbwheel()` is from Stahel and Mächler (2009) <doi:10.1111/j.1467-9868.2009.00706.x>.

Imports grDevices, graphics, stats, utils, robustbase (>= 0.92-3)

Suggests MASS, lattice

Enhances ICS

License GPL (>= 2)

Encoding UTF-8

NeedsCompilation no

Author Martin Maechler [aut, cre] (<https://orcid.org/0000-0002-8685-9910>),
Werner A. Stahel [aut],
Rolf Turner [ctb] (reclas()),
Ueli Oetliker [ctb] (original version of BACON() and mvBACON for S+),
Tobias Schoch [ctb] (init.sel=``V2'' for BACON; fix alpha)

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R topics documented:

`robustX-package` *eXperimental eXtraneous ... Functionality for Robust Statistics*

Description

The package **robustX** aims to be a collection of R functionality for robust statistics of methods and ideas that are considered as proposals, experimental, for experiences or just too much specialized to be part of the "Robust Basics" package **robustbase**.

Details

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Version:	1.2-5
Date:	2021-06-02
Authors@R:	c(person("Martin","Maechler", role=c("aut","cre"), email="maechler@stat.math.ethz.ch", comment = c(ORCI
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```

Author(s)

Werner Stahel, Martin Maechler and potentially others

Maintainer: Martin Maechler

See Also

Package **robustbase** which it complements and on which it depends; further package **robust** and the whole CRAN task view on robust statistics, https://cran.r-project.org/view=Robust

Examples

```
pairs( rbwheel(100, 4) )
```

BACON — *BACON for Regression or Multivariate Covariance Estimation*

Description

BACON, short for '**B**locked **A**daptive **C**omputationally-Efficient **O**utlier **N**ominators', is a somewhat robust algorithm (set), with an implementation for regression or multivariate covariance estimation.

`BACON()` applies the multivariate (covariance estimation) algorithm, using `mvBACON(x)` in any case, and when `y` is not `NULL` adds a regression iteration phase, using the auxiliary `.lmBACON()` function.

Usage

```
BACON(x, y = NULL, intercept = TRUE,
      m = min(collect * p, n * 0.5),
      init.sel = c("Mahalanobis", "dUniMedian", "random", "manual", "V2"),
      man.sel, init.fraction = 0, collect = 4,
      alpha = 0.05, alphaLM = alpha, maxsteps = 100, verbose = TRUE)

## *Auxiliary* function:
.lmBACON(x, y, intercept = TRUE,
         init.dis, init.fraction = 0, collect = 4,
         alpha = 0.05, maxsteps = 100, verbose = TRUE)
```

Arguments

x
: a multivariate matrix of dimension [n x p] considered as containing no missing values.

y
: the response (n vector) in the case of regression, or `NULL` for the multivariate case, where just `mvBACON()` is returned.

intercept
: logical indicating if an intercept has to be used for the regression.

m
: integer in `1:n` specifying the size of the initial basic subset; used only when `init.sel` is not `"manual"`; see `mvBACON`.

init.sel
: character string, specifying the initial selection mode; see `mvBACON`.

man.sel
: only when `init.sel == "manual"`, the indices of observations determining the initial basic subset (and `m <-length(man.sel)`).

init.dis
: the distances of the x matrix used for the initial subset determined by `mvBACON`.

init.fraction
: if this parameter is > 0 then the tedious steps of selecting the initial subset are skipped and an initial subset of size n * init.fraction is chosen (with smallest dis)

collect
: numeric factor chosen by the user to define the size of the initial subset (p * collect)

alpha
: number in $(0, 1)$ determining the cutoff value for the Mahalanobis distances (multivariate outlier nomination in `mvBACON()`), or the discrepancies for regression, see `alphaLM`.

alphaLM
: number in $(0, 1)$ where a `1-alphaM` t-quantile is the cutoff for the discrepancies (for regression, `.lmBACON()`); see details.

maxsteps
: the maximal number of iteration steps (to prevent infinite loops)

verbose
: logical indicating if messages are printed which trace progress of the algorithm.

Details

Notably about the initial selection mode, `init.sel`, see its description in the `mvBACON` arguments list.

The choice of `alpha` and `alphaLM`:

- Multivariate outlier nomination: see the Details section of `mvBACON`.
- Regression: Let $t_r(\alpha)$ denote the $1 - \alpha$ quantile of the Student t-distribution with r degrees of freedom, where r is the number of elements in the current subset; e.g., $t_r(0.05)$ is the 0.95 quantile. Following Billor et al. (2000), the cutoff value for the discrepancies is defined as $t_r(\alpha/(2r + 2))$, and they use $\alpha = 0.05$. Note that this is argument `alphaLM` (defualting to `alpha`) for `BACON()`.

Value

`BACON(x,y,..)` (for regression) returns a `list` with components

subset
: the observation indices (in `1:n`) denoting a subset of “good” supposedly outlier-free observations.

`tis`	the $t_i(y_m, X_m)$ of eq (6) in the reference; the clean "basic subset" in the algorithm is defined the observations i with the smallest $\|t_i\|$, and the t_i can be regarded as scaled predicted errors.
`mv.dis`	the (final) discrepancies or distances of `mvBACON()`.
`mv.subset`	the "good" subset from `mvBACON()`, used to start the regression iterations.

Note

"BACON" was also chosen in honor of Francis Bacon:

Whoever knows the ways of Nature will more easily notice her deviations; and, on the other hand, whoever knows her deviations will more accurately describe her ways.
Francis Bacon (1620), Novum Organum II 29.

Author(s)

Ueli Oetliker, Swiss Federal Statistical Office, for S-plus 5.1; 25.05.2001; modified six times till 17.6.2001.

Port to R, testing etc, by Martin Maechler. Daniel Weeks (at pitt.edu) proposed a fix to a long standing buglet in `GiveTis()` computing the t_i, which was further improved Maechler, for **robustX** version 1.2-3 (Feb. 2019).

Correction of `alpha` default, from 0.95 to 0.05, by Tobias Schoch, see `mvBACON`.

References

Billor, N., Hadi, A. S., and Velleman , P. F. (2000). BACON: Blocked Adaptive Computationally-Efficient Outlier Nominators; *Computational Statistics and Data Analysis* **34**, 279–298. doi: 10.1016/S01679473(99)001012

See Also

`mvBACON`, the multivariate version of the BACON algorithm.

Examples

```
data(starsCYG, package = "robustbase")
## Plot simple data and fitted lines
plot(starsCYG)
lmST <- lm(log.light ~ log.Te, data = starsCYG)
abline(lmST, col = "gray") # least squares line
str(B.ST <- with(starsCYG,  BACON(x = log.Te, y = log.light)))
## 'subset': A good set of of points (to determine regression):
colB <- adjustcolor(2, 1/2)
points(log.light ~ log.Te, data = starsCYG, subset = B.ST$subset,
       pch = 19, cex = 1.5, col = colB)
## A BACON-derived line:
lmB <- lm(log.light ~ log.Te, data = starsCYG, subset = B.ST$subset)
abline(lmB, col = colB, lwd = 2)

require(robustbase)
```

```
(RlmST <- lmrob(log.light ~ log.Te, data = starsCYG))
abline(RlmST, col = "blue")
```

---

covNNC *Robust Covariance Estimation via Nearest Neighbor Cleaning*

Description

covNNC() estimates robust covariance/dispersion matrices by the nearest neighbor variance estimation (NNVE) or (rather) "Nearest Neighbor Cleaning" (NNC) method of Wang and Raftery (2002, *JASA*).

Usage

```
covNNC(X, k = min(12, n - 1), pnoise = 0.05, emconv = 0.001,
       bound = 1.5, extension = TRUE, devsm = 0.01)
```

Arguments

X	matrix in which each row represents an observation or point and each column represents a variable.
k	desired number of nearest neighbors (default is 12)
pnoise	percent of added noise
emconv	convergence tolerance for EM
bound	value used to identify surges in variance caused by outliers wrongly included as signal points (bound = 1.5 means a 50 percent increase)
extension	whether or not to continue after reaching the last chi-square distance. The default is to continue, which is indicated by setting extension = TRUE.
devsm	when extension = TRUE, the algorithm stops if the relative difference in variance is less than devsm. (default is 0.01)

Value

A list with components

cov	covariance matrix
mu	mean vector
postprob	posterior probability
classification	classification (0=noise otherwise 1) obtained by rounding postprob
innc	list of initial nearest neighbor cleaning results (components are the covariance, mean, posterior probability and classification)

Note

Terms of use: GPL version 2 or newer.

MM: Even though `covNNC()` is backed by a serious scientific publication, I cannot recommend its use at all.

Author(s)

Naisyin Wang `<nwang@stat.tamu.edu>` and Adrian Raftery `<raftery@stat.washington.edu>` with contributions from Chris Fraley `<fraley@stat.washington.edu>`.

`covNNC()`, then named `cov.nnve()`, used to be (the only function) in CRAN package **covRobust** (2003), which was archived in 2012.

Martin Maechler allowed `ncol(X) == 1`, sped up the original code, by reducing the amount of scaling; further, the accuracy was increased (using internal `q.dDk()`). The original version is available, unexported as `robustX:::covNNC1`.

References

Wang, N. and Raftery, A. (2002) Nearest neighbor variance estimation (NNVE): Robust covariance estimation via nearest neighbor cleaning (with discussion). *Journal of the American Statistical Association* **97**, 994–1019.

See also University of Washington Statistics Technical Report 368 (2000); see at https://stat.uw.edu/research/tech-reports/

See Also

`cov.mcd` from package **MASS**; `covMcd`, and `covOGK` from package **robustbase**.

The whole package **rrcov**.

Examples

```
data(iris)
covNNC(iris[-5])

data(hbk, package="robustbase")
hbk.x <- data.matrix(hbk[, 1:3])
covNNC(hbk.x)
```

`L1median` *Compute the Multivariate L1-Median aka 'Spatial Median'*

Description

Compute the multivariate L_1-median m, also called "Spatial Median", i.e., the minimizer of

$$\sum_{i=1}^{n} \|x_i - m\|,$$

where $\|u\| = \sqrt{\sum_{j=1}^{p} u_j^2}$.

As a convex problem, there's always a global minimizer, computable not by a closed formula but rather an iterative search. As the (partial) first derivatives of the objective function is undefined at the data points, the minimization is not entirely trivial.

Usage

```
L1median(X, m.init = colMedians(X), weights = NULL,
method = c("nlm", "HoCrJo", "VardiZhang", optimMethods, nlminbMethods),
pscale = apply(abs(centr(X, m.init)), 2, mean, trim = 0.40),
tol = 1e-08, maxit = 200, trace = FALSE,
zero.tol = 1e-15, ...)
```

Arguments

`X`	numeric `matrix` of dimension $n \times p$, say.
`m.init`	starting value for m; typically and by default the coordinatewise median.
`weights`	optional numeric vector of non-negative weights; currently only implemented for method `"VardiZhang"`.
`method`	character string specifying the computational method, i.e., the algorithm to be used (can be abbreviated).
`pscale`	numeric p-vector of positive numbers, the coordinate-wise scale (typical size of δm_j), where m is the problem's solution.
`tol`	positive number specifying the (relative) convergence tolerance.
`maxit`	positive integer specifying the maximal number of iterations (before the iterations are stopped prematurely if necessary).
`trace`	an integer specifying the tracing level of the iterations; `0` does no tracing
`zero.tol`	for method `"VardiZhang"`, a small positive number specifying the tolerance for determining that the iteration is 'exactly' at a data point (which is a singularity).
`...`	optional arguments to `nlm()` or the `control` (list) arguments of `optim()`, or `nlminb()`, respectively.

Details

Currently, we have to refer to the "References" below.

Value

currently the result *depends* strongly on the `method` used.

FIXME. This will change considerably.

Author(s)

Martin Maechler. Method "HoCrJo" is mostly based on Kristel Joossens' R function, implementing Hossjer and Croux (1995).

References

Hossjer and Croux, C. (1995). Generalizing Univariate Signed Rank Statistics for Testing and Estimating a Multivariate Location Parameter. *Non-parametric Statistics* **4**, 293–308.

Vardi, Y. and Zhang, C.-H. (2000). The multivariate L_1-median and associated data depth. *Proc. National Academy of Science* **97**(4), 1423–1426.

Fritz, H. and Filzmoser, P. and Croux, C. (2012) A comparison of algorithms for the multivariate L1-median. *Computational Statistics* **27**, 393–410.

Kent, J. T., Er, F. and Constable, P. D. L. (2015) Algorithms for the spatial median;, in K. Nordhausen and S. Taskinen (eds), *Modern Nonparametric, Robust and Multivariate Methods: Festschrift in Honour of Hannu Oja*, Springer International Publishing, chapter 12, pp. 205–224. doi: 10.1007/9783319224046_12

See Also

median, covMcd

CRAN package **pcaPP** added more L1 median methods, re-implementing our R versions in C++, see Fritz et al.(2012) and e.g., l1median_NLM().

Examples

```
data(stackloss)
L1median(stackloss)
L1median(stackloss, method = "HoCrJo")


## Explore all methods:
m <- eval(formals(L1median)$method); allMeths <- m[m != "Brent"]
L1m <- sapply(allMeths, function(meth) L1median(stackloss, method = meth))
## --> with a warning for L-BFGS-B
str(L1m)
pm <- sapply(L1m, function(.) if(is.numeric(.)) . else .$par)
t(pm) # SANN differs a bit; same objective ?
```

---

mvBACON *BACON: Blocked Adaptive Computationally-Efficient Outlier Nominators*

Description

This function performs an outlier identification algorithm to the data in the x array [n x p] and y vector [n] following the lines described by Hadi et al. for their BACON outlier procedure.

Usage

```
mvBACON(x, collect = 4, m = min(collect * p, n * 0.5), alpha = 0.05,
        init.sel = c("Mahalanobis", "dUniMedian", "random", "manual", "V2"),
        man.sel, maxsteps = 100, allowSingular = FALSE, verbose = TRUE)
```

Arguments

`x` numeric matrix (of dimension $[nxp]$), not supposed to contain missing values.

`collect` a multiplication factor c, when `init.sel` is not `"manual"`, to define m, the size of the initial basic subset, as $m := c \cdot p$, in practice, `m <-min(p * collect,n/2)`.

`m` integer in `1:n` specifying the *size* of the initial basic subset; used only when `init.sel` is not `"manual"`.

`alpha` determines the cutoff value for the Mahalanobis distances (see details).

`init.sel` character string, specifying the initial selection mode; implemented modes are:

"Mahalanobis" based on Mahalanobis distances (default); the version $V1$ of the reference; affine invariant but not robust.

"dUniMedian" based on the distances from the **uni**variate medians; similar to the version $V2$ of the reference; robust but not affine invariant.

"random" based on a random selection, i.e., reproducible only via `set.seed()`.

"manual" based on manual selection; in this case, a vector `man.sel` containing the indices of the selected observations must be specified.

"V2" based on the Euclidean norm from the **uni**variate medians; this is the version $V2$ of the reference; robust but not affine invariant.

`"Mahalanobis"` and `"V2"` where proposed by Hadi and the other authors in the reference as versions 'V_1' and 'V_2', as well as `"manual"`, while `"random"` is provided in order to study the behaviour of BACON. Option `"dUniMedian"` is similar to `"V2"` and is due to U. Oetliker.

`man.sel` only when `init.sel == "manual"`, the indices of observations determining the initial basic subset (and `m <-length(man.sel)`).

`maxsteps` maximal number of iteration steps.

`allowSingular` logical indicating a solution should be sought also when no matrix of rank p is found.

`verbose` logical indicating if messages are printed which trace progress of the algorithm.

Details

Remarks on the tuning parameter `alpha`: Let χ^2_p be a chi-square distributed random variable with p degrees of freedom (p is the number of variables; n is the number of observations). Denote the $(1-\alpha)$ quantile by $\chi^2_p(\alpha)$, e.g., $\chi^2_p(0.05)$ is the 0.95 quantile. Following Billor et al. (2000), the cutoff value for the Mahalanobis distances is defined as $\chi_p(\alpha/n)$ (the square root of chi^2_p) times a correction factor $c(n,p)$, n and p, and they use $\alpha = 0.05$.

Value

a list with components

subset	logical vector of length n where the i-th entry is true iff the i-th observation is part of the final selection.
dis	numeric vector of length n with the (Mahalanobis) distances.
cov	$p \times p$ matrix, the corresponding robust estimate of covariance.

Author(s)

Ueli Oetliker, Swiss Federal Statistical Office, for S-plus 5.1. Port to R, testing etc, by Martin Maechler; Init selection "V2" and correction of default alpha from 0.95 to 0.05, by Tobias Schoch, FHNW Olten, Switzerland.

References

Billor, N., Hadi, A. S., and Velleman , P. F. (2000). BACON: Blocked Adaptive Computationally-Efficient Outlier Nominators; *Computational Statistics and Data Analysis* **34**, 279–298. doi: 10.1016/S01679473(99)001012

See Also

covMcd for a high-breakdown (but more computer intensive) method; BACON for a "generalization", notably to *regression*.

Examples

```
require(robustbase) # for example data and covMcd():
## simple 2D example :
plot(starsCYG, main = "starsCYG  data  (n=47)")
B.st <- mvBACON(starsCYG)
points(starsCYG[ ! B.st$subset,], pch = 4, col = 2, cex = 1.5)
stopifnot(identical(which(!B.st$subset), c(7L,11L,20L,30L,34L)))
## finds the 4 clear outliers (and 1 "borderline");
## it does not find obs. 14 which is an outlier according to covMcd(.)

iniS <- setNames(, eval(formals(mvBACON)$init.sel)) # all initialization methods, incl "random"
set.seed(123)
Bs.st <- lapply(iniS[iniS != "manual"], function(s)
                mvBACON(as.matrix(starsCYG), init.sel = s, verbose=FALSE))
ii <- - match("steps", names(Bs.st[[1]]))
Bs.s1 <- lapply(Bs.st, `[`, ii)
stopifnot(exprs = {
   length(Bs.s1) >= 4
   length(unique(Bs.s1)) == 1 # all 4 methods give the same
})

## Example where "dUniMedian" and "V2" differ :
data(pulpfiber, package="robustbase")
dU.plp <- mvBACON(as.matrix(pulpfiber), init.sel = "dUniMedian")
V2.plp <- mvBACON(as.matrix(pulpfiber), init.sel = "V2")
```

```
(oU <- which(! dU.plp$subset))
(o2 <- which(! V2.plp$subset))
stopifnot(setdiff(o2, oU) %in% c(57L,58L,59L,62L))
## and 57, 58, 59, and 62 *are* outliers according to covMcd(.)

## 'coleman' from pkg 'robustbase'
coleman.x <- data.matrix(coleman[, 1:6])
Cc <- covMcd (coleman.x) # truly robust
summary(Cc) # -> 6 outliers (1,3,10,12,17,18)
Cb1 <- mvBACON(coleman.x) ##-> subset is all TRUE hmm??
Cb2 <- mvBACON(coleman.x, init.sel = "dUniMedian")
stopifnot(all.equal(Cb1, Cb2))
## try 20 different random starts:
Cb.r <- lapply(1:20, function(i) { set.seed(i)
                    mvBACON(coleman.x, init.sel="random", verbose=FALSE) })
nm <- names(Cb.r[[1]]); nm <- nm[nm != "steps"]
all(eqC <- sapply(Cb.r[-1], function(CC) all.equal(CC[nm], Cb.r[[1]][nm]))) # TRUE
## --> BACON always  breaks down, i.e., does not see the outliers here

## breaks down even when manually starting with all the non-outliers:
Cb.man <- mvBACON(coleman.x, init.sel = "manual",
                  man.sel = setdiff(1:20, c(1,3,10,12,17,18)))
which( ! Cb.man$subset) # the outliers according to mvBACON : _none_
```

Qrot *Rotation Matrix to Specific Direction*

Description

Construct the $p \times p$ rotation matrix that rotates the unit vector (1,0,....0), i.e., the x_1-axis, onto (1,1,1,...1)/$\sqrt{p}$, or more generally to $u/\|u\|$ ($u :=$`unit.image`).

Usage

```
Qrot(p, transpose = FALSE, unit.image = rep(1, p))
```

Arguments

`p`	integer; the dimension (of the vectors involved).
`transpose`	logical indicating if the *transposed* matrix is to returned.
`unit.image`	numeric vector of length p onto which the unit vector should be rotated; defaults to *"the diagonal"* $\propto (1, 1, 1, ..., 1)$.

Details

The `qr` decomposition is used for a Gram-Schmitt basis orthogonalization.

Value

$p \times p$ orthogonal matrix which rotates $(1, 0, ..., 0)$ onto a vector proportional to `unit.image`.

Author(s)

Martin Maechler

See Also

qr, matrix (and vector) multiplication, %*%.

Examples

```
Q <- Qrot(6)
zapsmall(crossprod(Q)) # 6 x 6 unity <==> Q'Q = I  <==> Q orthogonal

if(require("MASS")) {
  Qt <- Qrot(6, transpose = TRUE)
  stopifnot(all.equal(Qt, t(Q)))
  fractions(Qt ^2) # --> 1/6  1/30  etc, in an almost lower-triagonal matrix
}
```

---

rbwheel *Multivariate Barrow Wheel Distribution Random Vectors*

Description

Generate p-dimensional random vectors according to Stahel's Barrow Wheel Distribution.

Usage

```
rbwheel(n, p, frac = 1/p, sig1 = 0.05, sig2 = 1/10,
        rGood = rnorm,
        rOut = function(n) sqrt(rchisq(n, p - 1)) * sign(runif(n, -1, 1)),
        U1 = rep(1, p),
        scaleAfter = TRUE, scaleBefore = FALSE, spherize = FALSE,
        fullResult = FALSE)
```

Arguments

n	integer, specifying the sample size.
p	integer, specifying the dimension (aka number of variables).
frac	numeric, the proportion of outliers. The default, $1/p$, corresponds to the (asymptotic) breakdown point of M-estimators.
sig1	thickness of the "wheel", ($= \sigma$ (good[,1])), a non-negative numeric.
sig2	thickness of the "axis" (compared to 1).
rGood	function; the generator for "good" observations.
rOut	function, generating the outlier observations.
U1	p-vector to which $(1, 0, \ldots, 0)$ is rotated.

scaleAfter
: logical indicating if the matrix is re-scaled *after* rotation (via `scale()`).. Default `TRUE`; note that this used to be false by default in the first public version.

scaleBefore
: logical indicating if the matrix is re-scaled before rotation (via `scale()`).

spherize
: logical indicating if the matrix is to be "spherized", i.e., rotated and scaled to have empirical covariance I_p. This means that the principal components are used (before rotation).

fullResult
: logical indicating if in addition to the $n \times p$ matrix, some intermediate quantities are returned as well.

Details

....

Value

By default (when `fullResult` is `FALSE`), an $n \times p$ matrix of n sample vectors of the p dimensional barrow wheel distribution, with an attribute, `n1` specifying the exact number of "good" observations, $n1 \approx (1 - f) \cdot n$, $f =$`frac`.

If `fullResult` is `TRUE`, a list with components

X
: the $n \times p$ matrix of above, `X = X0 %*% A`, where `A <-Qrot(p,u = U1)`, and `X0` is the corresponding matrix before rotation, see below.

X0
: ....

A
: the $p \times p$ rotation matrix, see above.

n1
: the number of "good" observations, see above.

n2
: the number of "outlying" observations, $n2 = n - n1$.

Author(s)

Werner Stahel and Martin Maechler

References

http://stat.ethz.ch/people/maechler/robustness

Stahel, W.~A. and Mächler, M. (2009). Comment on "invariant co-ordinate selection", *Journal of the Royal Statistical Society B* **71**, 584–586. doi: 10.1111/j.14679868.2009.00706.x

Examples

```
set.seed(17)
rX8 <- rbwheel(1000,8, fullResult = TRUE, scaleAfter=FALSE)
with(rX8, stopifnot(all.equal(X, X0 %*% A,    tol = 1e-15),
                    all.equal(X0, X %*% t(A), tol = 1e-15)))
##--> here, don't need to keep X0 (nor A, since that is Qrot(p))

## for n = 100,  you  don't see "it", but may guess .. :
n <- 100
pairs(r <- rbwheel(n,6))
```

```
n1 <- attr(r,"n1") ; pairs(r, col=1+((1:n) > n1))

## for n = 500, you *do* see it :
n <- 500
pairs(r <- rbwheel(n,6))
## show explicitly
n1 <- attr(r,"n1") ; pairs(r, col=1+((1:n) > n1))

## but increasing sig2 does help:
pairs(r <- rbwheel(n,6, sig2 = .2))

## show explicitly
n1 <- attr(r,"n1") ; pairs(r, col=1+((1:n) > n1))

set.seed(12)
pairs(X <- rbwheel(n, 7, spherize=TRUE))
colSums(X) # already centered

if(require("ICS") && require("robustbase")) {
  # ICS: Compare M-estimate [Max.Lik. of t_{df = 2}] with high-breakdown :
  stopifnot(require("MASS"))
  X.paM <- ics(X, S1 = cov, S2 = function(.) cov.trob(., nu=2)$cov, stdKurt = FALSE)
  X.paM.<- ics(X, S1 = cov, S2 = function(.) tM(., df=2)$V, stdKurt = FALSE)
  X.paR <- ics(X, S1 = cov, S2 = function(.) covMcd(.)$cov, stdKurt = FALSE)
  plot(X.paM) # not at all clear
  plot(X.paM.)# ditto
  plot(X.paR)# very clear
}
## Similar such experiments --->  demo(rbwheel_d)  and   demo(rbwheel_ics)
##                                --------------        -----------------
```

reclas *Recursive Robust Median-like Location and Scale*

Description

Calculate an estimate of location, asymptotically equivalent to the median, and an estimate of scale equal to the **MEAN** absolute deviation. Both done recursively.

Usage

```
reclas(y, b = 0.2, mfn = function(n) 0.1 * n^(-0.25),
     nstart = 30, m0 = median(y0),
     scon=NULL, updateScale = is.null(scon))
```

Arguments

y	numeric vector of i.i.d. data whose location and scale parameters are to be estimated.
b	numeric tuning parameter (default value equal to that used by Holst, 1987).
mfn	a `function` of the index of the data which must be positive and and tend to 0 as the index tends to infinity. The default function is that used by Holst, 1987.
nstart	number of starting values: Starting values for the algorithm are formed from the first `nstart` values of `y`. The default value is that used in Cameron and Turner, 1993.
m0	value for the initial approximate median; by default, the `median` of the first `nstart` observations.
scon	value for the scale parameter `s`, a `function` or `NULL`. When `NULL`, as by default, the scale is initialized to the mean of the absolute differences between the first `nstart` `y` values and `m0`. If scon is a function, the initial scale is set to `scon(y0,m0)`, where `y0` is the vector of the first `nstart` `y` values. Note that `scon` also determines the default for `updateScale`.
updateScale	a logical indicating if the scale, initialized from `scon` should be updated in each iteration. Otherwise, the the scale is held constant throughout and the algorithm becomes equivalent to the algorithm of Holst.

Value

An S3 "object" of `class` `"reclas"`; simply a list with entries

locn	the successive recursive estimates of location. The first `nstart -1` of these are `NA`.
scale	the successive recursive estimates of scale **if** `updateScale` is true; otherwise the constant value used for the scale.
updateScale	the same as the function argument.
call	the function call, i.e., `match.call`.

There is a `plot` method for `"reclas"`, see the examples.

Author(s)

`<r.turner@auckland.ac.nz>` http://www.stat.auckland.ac.nz/~rolf

Extensions by Martin Maechler (`scon` as function; `updateScale`, `plot()`).

References

Cameron, Murray A. and Turner, T. Rolf (1993). Recursive location and scale estimators. *Commun. Statist. — Theory Meth.* **22**(9) 2503–2515.

Holst, U. (1987). Recursive estimators of location. *Commun. Statist. — Theory Meth.* **16** (8) 2201–2226.

Examples

```
set.seed(42)
y <- rt(10000, df = 1.5) # not quite Gaussian ...
z1 <- reclas(y)
z3 <- reclas(y, scon= 1  ) # correct fixed scale
z4 <- reclas(y, scon= 100) # wrong fixed scale
z2 <- reclas(y, # a more robust initial scale:
           scon = function(y0, m0) robustbase::Qn(y0 - m0),
           updateScale = TRUE) # still updated

## Visualizing -- using the plot() method for "reclas":
M <- median(y) ; yl <- c(-1,1)* 0.5
OP <- par(mfrow=c(2,2), mar=.1+c(3,3,1,1), mgp=c(1.5, .6, 0))
 plot(z1, M=M, ylim=yl)
 plot(z2, M=M, ylim=yl)
 plot(z3, M=M, ylim=yl)
 plot(z4, M=M, ylim=yl)
par(OP)
```

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